

**YIELD TRIAL AMONG ADVANCED POPULATIONS
OF RAPESEED (*Brassica rapa* L.)**

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**YIELD TRIAL AMONG ADVANCED POPULATIONS
OF RAPESEED (*Brassica rapa L.*)**

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*This is to certify that thesis entitled “YEILD TRIAL AMONG ADVANCED POPULATIONS OF RAPESEED (*Brassica rapa L.*)” submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment 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 **AFROZA AWAL SHOILY** Registration No. **19-10079** 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 2021

Dhaka, Bangladesh

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*Dedicated
to my
Beloved
family*

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LIST OF CONTENTS

Chapter	Title	Page No
Chapter I	Introduction	1
Chapter II	Review of literature	5
Chapter III	Materials and methods	15
Chapter IV	Results and discission	31
Chapter V	Summary and conclusion	78
Chapter VI	References	81
Chapter VI	Appendices	88

LIST OF TABLES

Tables	Title	Page
Table 1	Name of the advanced populations of mustard used in the study	17
Table 2	List of fertilizers and manures with doses and procedures of application	18
Table 3	Analysis of variance of 13 characters of 9 (nine) advanced populations of <i>Brassica rapa</i> L.	33
Table 4	Mean performance of yield and yield contributing characters of nine advanced populations <i>Brassica rapa</i> L.	34
Table 5	Estimation of some genetic parameters of 9 advanced populations of <i>Brassica rapa</i> L.	35
Table 6	Heritability, genetic advance and genetic advance in percentage of means for yield and yield contributing characters of 9 advanced populations of <i>Brassica rapa</i> L.	57
Table 7	Genotypic correlation coefficient among yield and yield contributing characters of 9 advanced populations of <i>Brassica rapa</i> L.	62
Table 8	Phenotypic correlation coefficient among yield and yield contributing characters of 9 advanced populations of <i>Brassica rapa</i> L.	63
Table 9	Partitioning of genotypic correlations into direct and indirect effects of important characters by path coefficient analysis of <i>Brassica rapa</i> L.	70
Table 10	Selection of most promising populations from different cross combinations of <i>Brassica rapa</i> L. based on mean performance	77

LIST OF FIGURES

Figures	Title	Page
Figure 1	Days to first flowering of nine advanced populations of <i>Brassica rapa</i> L.	37
Figure 2	Days to 50% flowering of nine advanced populations of <i>Brassica rapa</i> L.	38
Figure 3	Days to 80% Flowering of nine advanced populations of <i>Brassica rapa</i> L.	40
Figure 4	Days to maturity of nine advanced populations of <i>Brassica rapa</i> L.	41
Figure 5	Plant height of nine advanced populations of <i>Brassica rapa</i> L.	43
Figure 6	Root length of nine advanced populations of <i>Brassica rapa</i> L.	44
Figure 7	Number of primary branches per plant of nine advanced populations of <i>Brassica rapa</i> L.	46
Figure 8	Number of primary branches per plant of nine advanced populations of <i>Brassica rapa</i> L.	47
Figure 9	Number of siliquae per plant of nine advanced populations of <i>Brassica rapa</i> L.	49
Figure 10	Siliqua length of nine advanced populations of <i>Brassica rapa</i> L.	50
Figure 11	Number of seeds siliqua ¹ of nine advanced populations of <i>Brassica rapa</i> L.	52
Figure 12	Thousands seeds weight of nine advanced populations of <i>Brassica rapa</i> L.	53
Figure 13	Seed yield/m ² of nine advanced populations of <i>Brassica rapa</i> L.	55

LISTS OF ABBREVIATIONS

Abbreviation	Full Word
AEZ	Argo-Ecological Zone
Anova	Analysis of variance
<i>et al.</i>	And others
@	At the rate
BD	Bangladesh
BARI	Bangladesh Agricultural Research Institute
BAU	Bangladesh Agricultural University
BINA	Bangladesh Institute of Nuclear Agriculture
CV	Co-efficient of variation
DAS	Days after sowing
Df	Degrees of Freedom
σ^2e	Environmental variance
σ^2g	Genotypic variance
σ^2p	Phenotypic variance
FAO	Food and Agricultural Organization
RCBD	Randomized Complete Block Design
SAU	Sher-e-Bangla Agricultural University
USDA	United States Department of Agriculture

LIST OF APPENDICES

Appendix	Title	Page
Appendix I	Map showing the experimental site under the study	88
Appendix II	Physical and chemical characteristics of soils of the experimental site.	89
Appendix III	Monthly average temperature, relative humidity (RH), rainfall and sunshine of the experimental site during the experimental period (November, 2019 to February, 2020).	90
Appendix IV	The pictorial view of experimental field during seed sowing	91
Appendix V	The pictorial view of experimental plot during Intercultural operations	91
Appendix VI	The pictorial view of experimental plot during irrigation	91
Appendix VII	The pictorial view of experimental plot during harvesting stage	91

YIELD TRIAL AMONG ADVANCED POPULATIONS OF RAPESEED (*Brassica rapa* L.)

ABSTRACT

The present study was under taken using nine promising advanced populations of *Brassica rapa* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka during November 2019 to March 2020. Thirteen yield contributing characters were taken for evaluating the advanced populations. To find out the variations among the yield contributing characters of the populations heritability, genetic advance, correlation, direct and indirect effect of different characters on seed yield were analysed. Analysis of variance disclosed significant variations among all populations for all the traits. Minimum difference between phenotypic and genotypic variance was observed in days to first flowering, days to 50% flowering, root length, number of primary branches per plant, number of secondary branches per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and seed yield/m². However, high genotypic and phenotypic coefficient of variation was observed in the number of secondary branches per plant, number of siliquae per plant, thousand seed weight and seed yield/m². High heritability with low genetic advance was exhibited in days to first flowering, days to 50% flowering, days to 80% maturity, length of siliqua, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight and seed yield/m² whereas high heritability with high genetic advance was observed in the number of siliquae per plant indicating high potentiality for selection of the trait. Correlation study revealed that seed yield/m² had a significant positive correlation with days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua and thousand seed weight at the genotypic and phenotypic level. Direct positive effect on seed yield /m² was found in days to maturity, root length, the number of secondary branches per plant and thousand seed weight through path coefficient analysis. Higher seed yield/m² was observed in G5(244.38g), followed by G2(234.3g), G6(231.68 g). Among the populations, G5 was selected as the most promising population on the basis of days to maturity (76.33DAS), number of siliquae per plant (20.28), thousand seed weight (3.82g) and seed yield/m² (244.38g).

CHAPTER I

INTRODUCTION

Historically the brassicas are one of the earliest domesticated crop plants. In several ancient scripture and literature, it is mentioned that the crop might have been cultivated as early as 5000 BC. The Brassicaceae family (formerly Cruciferae) comprises of approximately 375 genera and 3200 species of plants. The Brassica genus consists of approximately 100 species with highly diverse morphology. Brassica have great economic and commercial value which play a major role in feeding the world population. All the major oleiferous species of this genus are grouped into two rapeseed and mustard. The oilseed brassicas comprise four species, namely *B. rapa*, *B. juncea*, *B. napus* and *B. carinata*. Among the species *Brassica rapa* and *Brassica napus* are regarded as commercial “rapeseed” while *Brassica juncea* is regarded as “mustard” (Weiss, 1983). *Brassica rapa* L. is commonly known as field mustard or rapeseed which is a cool season, thermosensitive as well as photosensitive crop (Ghosh and Chatterjee, 1988). It is the major sources of vegetable oil which is herbaceous cross-pollinated crop.

According to Vavilov (1926), the place of origin of rapeseed is Eastern Afghanistan and adjoining part of India and Pakistan. In the Indian sub-continent for hundreds of years mustard has been grown as an oil seed crop (Labana and Gupta, 1993). It is cultivating as a main commercial oil crop in Canada, China, Australia, India and as well as in Bangladesh.

Bangladesh produces 396594 metric tons of mustard seed from 339671 hectare of land during 2020-2021(www.bbs.portal.gov.bd). Major mustard growing districts of Bangladesh are Comilla, Tangail, Jessore, Sirajgonj, Sylhet, Faridpur, Pabna, Faridpur, Madaripur, Jamalpur, Rajshahi, Dinajpur, Kushtia, Kishoregonj, Rangpur and Dhaka. Rapeseed production holds third position in the world following soybean and palm. In Bangladesh rapeseed is grown widely and occupies the first position in respect of area and production among all the oil crops (Islam, 2013). Rapeseed crop account for almost 14 percent of the edible vegetable oil supply of the world demand (Kardam and Singh, 2005).

Mustard (rapeseed) seeds, generally contain 35-45% oil, 17-25% proteins, 8-10% fibers, 6-10% moisture after oil extraction. It is the most pungent of cultivated mustards and contains

glucoside. Rapeseed oil is high in unsaturated fats and vitamins E and K. It contains a beneficial ratio of omega-3 to omega-6 fats, which can positively influence heart health. Globally, after soybean the second most important economical protein source used in animal feed is rapeseed. The rapeseed oilcake contains high biological value of proteins and also possess sufficient quantity of phosphorus and calcium.

Although there is some controversy surrounding rapeseed oil, its use is associated with many benefits. Oilseeds are generally processed into protein meal, almost entirely used for feed, and into vegetable oil for food, oleo chemical, and biodiesel uses. It is also used as manure for various crops. Rapeseed oil is also used in food industry, as an illuminant and lubricant, and for soap manufacture. Rapeseed oil has potential market in emulsifying agents, polyamide fibers, and resins, detergent lubrication oils, and as a vegetable wax substitute.

As population of Bangladesh is growing fast and the economic prosperity has been increasing, it is now a challenge to us for accelerating the production of oils. Global market conditions of oilseeds resulted in rapid price increases in the second half of 2020, ensuing short-term market disruptions due to the COVID-19 pandemic (www.apps.fas.usda.gov).

The present yield of rapeseed-mustard is very low comparing to other oilseeds growing countries in the world. Bangladesh is passing through an enormous scarcity of edible oils for the last several decades because the cultivation area of mustard in Bangladesh is lower due to rice-based cropping pattern and existing low yielding varieties, unavailability of locally developed hybrids and low management practices. Beside that there is a lack of good quality seed, high yielding-short duration varieties and inadequate adoption of improved production technologies. In spite of being a principal oil crop in our country, cultivation of mustard is neglected by farmers and they generally cultivate the existing low yielding varieties associated with low inputs and management. This shortage also inherited from the past has been met through imports, using a huge amount of foreign exchange every year. In 2020 our internal production can meet only about 11.1% of our consumption; the rest 51.9% from imported palm oil and 37% from imported soybean oil (www.apps.fas.usda.gov). But the demand of edible oils is flourishing gradually. Hossain,

2013 stated that it is crucial to lessen the import dependence of oil seed to insulate the domestic market from the volatility of the world market.

Bangladesh expends a huge amount of foreign exchange on imports of edible oils and oilseeds to meet the rising demand of its population. For our country the value of imports is flourishing year after year which is regarded as an intimidation.

So, for avoiding import reliance and fulfil the demand, it is necessary to increase oil production notably. Realizing the importance and demand of oilseeds, Bangladesh government has given emphasis on R&D of oilseed crops and invested a lot of money for attaining their self-sufficiency in the country. Bangladesh Agricultural Research Institute (BARI), Bangladesh Institute of Nuclear Agriculture (BINA), and different agricultural universities of Bangladesh have started conducting research on oilseeds and they released a good number of high yielding varieties and improved management technologies of different oilseeds. The Department of Agricultural Extension (DAE) has also been involved in developmental programs for the technology transfer of oilseed crops through its countrywide networks.

There is a great scope of increasing yield of mustard by selecting high yielding varieties and improving management practices (Bhuiyan *et al.*, 2008). To fit mustard in existing cropping patterns farmers', need short durational higher yielding varieties. They want short durational variety of mustard that can grow successfully in between the two rice crops (T Aman & Boro). In Bangladesh short durational variety such as 'Tori-7' of *Brassica rapa* is still famous because it is compatible to the T. Aman-Mustard-Boro cropping pattern which covers about 1,84,620 hectares of land. The largest cropping patterns of the country is Boro-fallow -T. Aman having 23,6,005 hectares of land (Nasim *et al.*, 2017) in which mustard might be fit by short durational high yielding varieties. Hence, we should have initiative to produce short durational and high yielding varieties of *Brassica rapa* L. to fulfill the necessity of edible oils in Bangladesh.

The production potential of rapeseed may be well exploited if the population can be identified with early maturity, high yielding, large seed size, high oil content, short duration etc. In these circumstances, separate crossing programs have been inaugurated few years

ago which ultimately led to the selection of nine promising advanced populations of *Brassica rapa* L. in F₇, F₈, F₉, F₁₀ and F₁₆ generations.

The present experiment was aimed to find out the high yielding and short durational population of rapeseed among nine advanced populations of rapeseed (*Brassica rapa*). Another purpose of this work was to select a variety that can be grown between two growing crops all the year around in three crop rotations without hampering other crops. Thus, comparative yield trial was done for selecting high yielding advanced populations of rape seed for reaching the limit of higher yield within short duration time.

Objectives:

Conceiving the above scheme in thought, present study was undertaken to achieve the following objectives:

1. To select high yielding population(s) of *Brassica rapa*.
2. To study the genetic variability and character association in nine advanced populations of mustard.
3. To select short duration populations which can be fit in existing cropping patterns.

CHAPTER II

REVIEW OF LITERATURE

In Bangladesh context, *Brassica spp* is popular edible oil in rural area and it is considered important for improving the taste of a number of food items (Aziz *et al*, 2011a). *Brassica rapa L.* is self-incompatible species commonly called turnip, turnip rape, field mustard. These crops have received much attention by a large number of researchers on various aspects of its production and utilization. Some of the literature related to this investigation is reviewed in this chapter are given below under the following heads:

2.1 Genotypic and phenotypic variability

According to Sikarwar *et al*, (2017) analysis of variance pointed out highly significant differences for all the characters in 21 diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson) for ten yield contributing characters. He figured high genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) and for number of primary branches per plant, number of secondary branches per plant followed by seed yield per plant. And he found low PCV and GCV for days to first flowering, plant height and length of siliqua.

An experiment was performed by Sohail *et al*, (2017) on intra-specific quantitative characters among 253 *Brassica rapa* genotypes. Among the genotypes significant variations were recorded for leaf length and width, plant height, primary branches per plant, days to first flowering, days to 50% flowering, days to 80% flowering, days to maturity, main raceme length, pod length, pod width, stem thickness, thousand seed weight and seed yield per plant.

Siddika, (2015) did an experiment to study the genetic variability of *Brassica rapa L.* with 30 F₂ genotypes. The genotypes were significantly variable for all the characters. The value of Genotypic co-efficient of variation (GCV) is lower than the Phenotypic co-efficient of variation (PCV) values.

An experiment was conducted by Iqbal *et al*, (2014) using 10 indigenous variety with 8 important yields contributing characters of *Brassica rapa*. The result revealed highly significant differences in almost all character except siliqua width which observed significant variation.

An experiment was undertaken by Jahan *et al*, (2014) using 10 lines of *Brassica rapa* L. Among all the studied characters author found significant variation. High genotypic coefficient of variations (GCV) and low phenotypic coefficient of variations (PCV) were found for number of secondary branches per plant, siliquae per plant, yield per plant, whereas days to maturity showed very low GCV.

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

Halder (2013) conducted an experiment with 11 advanced lines of *Brassica rapa* L. and observed significant variations among the genotypes for all characters. Genotypic variance was lower than the phenotypic variances for characters. Difference between genotypic and phenotypic variances was minimum in number for primary branches per plant, days to 50% flowering and days to 80% flowering, length of siliqua, seeds per siliqua and thousand seed weight.

Khan *et al*, (2013) evaluated thirteen F₇, segregating lines and two parents of *Brassica rapa* to study variability, heritability and genetic advance. The result revealed that except thousand seed weight significant variation was presented among all the genotypes for all the traits. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliqua and followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliqua, and siliqua length showed high 5 heritability along with low genetic advance in percent of mean. Considering important performances, the genotypes G₁₅, G₁₉, O₁, G₃, O₄, G₁₀, G₁₈, G₂₁, and G₂₄ were found suitable for future breeding program.

An experiment was carried out by Alam *et al*, (2010) with twenty-six populations of some inter-varietal crosses of *Brassica rapa* L to study the variation. Higher phenotypic variation was observed than the genotypic variation. High heritability with high genetic advance was observed for, number of secondary branches per plant and number of siliquae per plant, plant height, number of primary branches per plant.

Aytac and Kinaci. (2009) performed an experiment for 2 years with 10 winter rapeseed genotypes for variation, genotypic and phenotypic correlations and broad sense heritability for seed yield and quality characters. They found significant differences for all yield and quality character indicated the presence of sufficient genetic variability for effective selection. Genetic advance, variability, broad sense heritability, was maximum for seed yield.

Saleh, (2009) conducted a field experiment utilizing 20 F₂ populations developed through inter-varietal crosses along with 3 check variety of *Brassica rapa* L. to find out the variation in different traits. Therefore, considerable variations present among all genotypes used in the experiment. Result showed 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 and secondary branches per plant, 1000 seed weight, length of siliqua, seeds per siliqua and yield per plant.

A study was conducted by Hosen, (2008) using 5 parental genotypes of *Brassica rapa* and their ten F₃ progenies including reciprocals. The result disclosed that there were large variations present among all the genotypes used in the experiment. Number of primary branches per plant, number of secondary branches per plant, days to 50 % flowering, length of siliqua, number of seeds per siliqua, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was considerable variation among the all characters except days to maturity. The plant height, days to 50 % flowering and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

Uddin, (2008) conducted an experiment to study the variability among seven parental genotypes and their twenty-one F₂ progenies of *Brassica rapa*. He observed that the phenotypic variance was than more genotypic variance. High GCV was observed in secondary branches per plant. High heritability with high genetic advance was observed in the number of secondary branches per plant.

To study inter genotypic variability an experiment was performed by Mahmud, (2008) with fifty-eight genotypes of *Brassica rapa*. Significant variation was observed among all the genotypes for all the traits studied except thousand seed weight. High GCV value was found for number of secondary branches per plant. High heritability values along with high genetic advance in percentage of mean were obtained for number of secondary branches per plant, days to 50 % flowering seeds per siliqua and siliqua length.

Parveen, (2007) studied on the variability in F₂ progenies of the inter-varietal crosses of 17 genotypes of *Brassica rapa*. Result showed significant variations among different genotypes were observed. High heritability coupled with high genetic advance in percent of mean was found in number of primary branches per plant.

Afroz *et al*, (2004) experimented 14 genotypes of mustard for studying genetic variability. The highest genetic advance was observed in percent of pollen sterility.

Ali *et al*, (2003) performed an experiment with 25 winter type rapeseed varieties introduced from diverse sources. He observed phenotypic and genotypic variances were highest for siliquae per plant and plant height, whereas the maximum genotypic and phenotypic coefficients of variability were observed in siliquae per plant and seed yield per plant.

2.2 Heritability and genetic advance in *Brassica sp*.

Sikarwar *et al*, (2017) carried out an experiment for the assessment heritability and genetic advance in twenty-one diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson) for 10 yield and yield contributing characters. Higher estimates of broad sense heritability were found for all studied characters. Here high genetic advance along with high heritability was observed for number of secondary branches per plant, number of

primary branches per plant, seed yield per plant, length of main raceme, number of siliquae on main raceme and number of seeds per siliquae.

Afrin *et al*, (2016) conducted an experiment on the 15 F₄ population considering different morphological attributes of *Brassica rapa*. Highest value for heritability was observed in the number of secondary branches per plant while the primary branches per plant found lowest value. Moderate heritability was observed in days to 50% flowering, days to 50% maturity, plant height yield per plant, thousand seed weight and siliquae length.

Naznin *et al*, (2015) performed an experiment to evaluate thirty-three genotypes of *Brassica rapa* L and observed that number of siliquae per plant, number of secondary branches per plant and number of primary branches per plant showed high heritability coupled with high genetic advance in percent of mean.

Sultana, (2015) carried out an experiment utilizing sixty-two F₄ genotypes of *Brassica napus* L. and observed that the highest value of heritability for number of secondary branches followed by seed yield per plant whereas days to maturity showed the lowest value of heritability.

Ejaz-Ul-Hasan *et al*, (2014) conducted an experiment on heritability of *Brassica napus* and reported that plant height, yield per plant and days to 50% flowering showed high heritability.

Khan *et al*, (2013) studied twenty genotypes of *Brassica napus* with a cheek variety and observed higher broad sense heritability in pods in main raceme. seed per siliqua primary branches per plant. seed yield per plant, seed yield per plant and number of siliquae per plant.

An experiment was carried out by Rameeh, (2013) to evaluated twenty-four rapeseed genotypes including 2 cultivars and 22 advanced lines, were based on randomized complete block design with three replications. Significant genotypes effects were exhibited for seed yield, plant height, indicating significant genetic difference among the genotypes. The

study showed high broad sense heritability was exhibited for pods on main axis and seed yield and duration of flowering and pods on main axis had exhibited high value of genetic coefficient of variation. The results of factor analysis showed 4 factors including sink factor (pods length, pod per plant and seed yield), fixed capital factor (phenological traits), and metric factor (plant height) and observed genetic diversity.

Ali et al, (2013) conducted an experiment with thirty lines of *Brassica carinata* and reported that PCV and GCV ranged from 4.9248.24 % and 3.2-38.1 % respectively. The highest heritability values were recorded for pod length (0.83) followed by pods on main raceme.

Rameeh, (2012) performed an experiment on twenty rapeseed genotypes including four cultivar and 16 advanced lines based on randomized complete block design with three replications. Significant genotypic effect was found for plant height, seed yield except seeds per siliqua. High broad sense heritability observed for plant height, siliqua per plant, 1000-seed weight. Here, days to maturity had low value of genetic coefficient of variation.

Patel et al, (2011) undertook experiment 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 grain weights. seed yield per plant. Moderate to high heritability associated with low genetic advance was recorded in days to maturity and days to flowering

Afrin et al, (2011) carried out an experiment in *Brassica napus* and studied heritability whereas the plant height exhibited highest value of broad sense heritability. Lowest heritability was found for number of secondary branches per plant, siliqua length, number of seed per Sequa, number of siliqua per plant, thousand seed weight and seed yield per plant.

Tahira et al, (2011) conducted an experiment with ten wide genetic ranged variety of *Brassica juncea* to study heritability in broad sense. The result showed high values of heritability in broad sense on siliqua length, plant height and seed yield.

Mahmud *et al*, (2011) executed an experiment with five advanced line of *Brassica rapa* along with 3 commercially cultivated varieties as check were evaluated to study the genetic divergence in respect of 10 different morphological characters. Relationship was not found between genetic divergence and geographic distribution of the genotypes. Number of secondary branches per plant, plant height and seeds per siliqua contributed maximum towards the total divergence. Hence, considering diversity pattern, genetic stains, line 39 and line 44 from cluster I; line 50, line 52; line 42 from cluster 11: line 2, line 43 and line 45 from cluster V; line 54 and line 58 from cluster VI- might be selected as suitable parents in future hybridization program.

Ara, (2010) studied on eight F₂ and eight F₄ populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* and found the variation. The result revealed that values of phenotypic variances were higher than genotypic variances. Days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, length of siliqua, seeds per siliqua, days to maturity, 1000-seed weight and yield per plant exhibited least difference between genotypic and phenotypic variances.

A research work was carried out by Rashid, (2007) on 40 Brassica species. The result revealed high heritability values along with high genetic advance in percentage of mean was showed for number of seeds per siliqua, siliqua length, number of primary and secondary branches per plant.

2.3 Analysis of correlation

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.

An experiment was carried out by Halder *et al*, (2016) to study the interrelationship among the characters of 11 advanced lines and three popular check varieties of *Brassica rapa* L. Through genotypic correlation coefficient, it was disclosed that yield per hectare had positive and highly significant correlation with number of primary branches per plant, days to first flowering, and days to 80% flowering and while days to 50% flowering and length of siliquae were negatively correlated with yield.

An experiment was executed by Bilal *et al*, (2015) with twenty-three genotypes of rapeseed for studying the correlation between the yield and yield contributing characters. The result stated positive significant correlation between days to maturity and yield per plant. Beside negative significant correlation was exhibited among plant height, pods per plant and 1000-seed weight. Number of pods per plant obtained positive significant correlation with 1000-seed weight.

Hussain, (2014) conducted an experiment with twenty-four genotypes including four check varieties of the species *Brassica rapa* L. for estimating the character associations. The significant positive correlation was found in thousand seed weight, number of primary branches per plant, number of siliquae per plant, with seed yield per plant.

Shakera (2014) executed an experiment with 20 F₃ and F₄ 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 early mature and high yielding plants. The result revealed that yield per plant exhibited significant and the positive correlation with plant height, number of secondary branches per plant, number of primary branches per plant, number of siliquae per plant and thousand seed weight.

Abideen *et al*, (2013) studied with eight genotypes of *Brassica napus* and the result stated that positive phenotypic 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.

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

Rameeh, (2011) conducted an experiment with 36 rapeseed genotypes and four cultivars and 32 advanced lines were evaluated in randomized complete block design with three replications. Siliquae per plant had significant positive correlation (0.80**) with seed yield was observed through correlation analysis.

A field experiment was undertaken by Khan, (2010) with 32 genotypes of *Brassica rapa* including two commercially cultivated varieties as checks to study correlation. The result of correlation disclosed highly significant positive association of seed yield per plant with number of primary and secondary branches per plant, and number of pods per plant.

Afrin, (2009) conducted a field experiment with 22 *Brassica napus* L. advanced lines to study the genetic variability. Here the significant positive correlation with seed yield per plant was observed in plant height, number of primary branches per plant and number of siliquae per plant. The highest significant positive correlation was found between plant height and days to 50% flowering.

Srivastava and Singh (2002) studied out an experiment to study the correlation in Indian mustard (*Brassica juncea* L.) for 10 characters in 24 strains of Indian mustard along with 2 varieties. They found that the number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and oil percent were positively associated with seed yield.

2.4 Path co-efficient analysis

In correlation study when more characters are involved it becomes difficult to find out the traits which really contribute towards the yield. Under such situation the path analysis helps to determine the direct and indirect contribution of these traits towards the yield.

A research work was experimented by Kumari *et al.*, (2017) to study the correlation among thirteen quantitative and qualitative characters of 44 genotypes of yellow sarson (*Brassica rapa* var. yellow sarson). Here the seed yield per plant showed significant and positive correlation with biological yield while positive but non-significant correlation with, seeds per siliquae, and days to maturity, 1000-seed weight, siliqua length while non-significant negative correlation with plant height and primary branches per plant. Significant but negative correlation coefficient of oil content was also observed. The 1000 seed weight showed significant positive correlation with siliqua length and seeds per siliqua. It was also observed that the path coefficient analysis of biological yield exerted maximum direct effect whereas siliqua length and oil content exhibited negative direct effect and days to 50% flowering exerted negative indirect effect on seed yield.

Islam et al. (2016) studied on twenty-one F₉ populations from inter- varietal crosses of *Brassica rapa* L. The result of path co-efficient analysis concluded that plant height, number of primary branches per plant, seeds per siliqua, siliqua length and number of siliquae per plant, exhibited the positive direct effect and days to 50% flowering, number of secondary branches per plant and thousand seed weight exhibited the negative direct effect on yield per plant.

Uddin *et al*, (2013) carried out an experiment with 7 parental and 21 F₂ progenies of *Brassica rapa* where study of the path coefficient revealed that number of primary branches per plant, days to 50 % flowering, number of secondary branches per plant, number of siliquae per plant, siliqua length, seed per siliqua and thousand seed weight exhibited direct positive association with seed yield per plant while days to maturity and the plant height had direct negative association.

An experiment was undertaken by Mahmud, (2008) with 58 genotypes of *Brassica rapa*. The result of path analysis disclosed that yield per plant had the highest direct effect on number of primary and secondary branches per plant, number of siliquae per plant, and number of seeds per siliqua.

Uddin (2008) conducted an experiment to study the correlation among seven parental genotypes and their twenty-one F₂ progenies of *Brassica rapa* and studied path coefficient analysis. He observed that the seed yield per plant had positive direct effect on days to 50 % flowering, number of primary branches per plant, number of primary branches per plant, number of secondary branches per plant. Number of siliqua per plant, siliqua length, seed per siliqua and thousand seed weight while days to maturity and plant height had direct negative effect on yield per plant.

Hosen (2008) exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seed per siliqua while working with five parental genotypes of *Brassica rapa* and their thirteen progenies including reciprocals.

CHAPTER III

MATERIALS AND METHODS

The present study was administered at Sher-e-Bangla Agricultural University, Dhaka–1207, Department of Genetics and Plant Breeding during November 2019 to March 2020. Nine advanced population of rapeseed (*Brassica rapa* L.) were planted in randomized block design with three replications in plot size of 1.5 × 3 m. The row to row and plant to plant distance was maintained at 30 × 10 cm. The information regarding the materials and methods of this experiment is discussed below

3.1 Experimental site

The location of the experimental site was situated at 23⁰ 77' N latitude and 90⁰ 37' E longitudes with an elevation of 13.03 meters from the sea level (www.distancesfrom.com). The experimental field was situated to the Argo-ecological zone of "The Madhapur Tract", AEZ-28 (www.banglapedia.com). The experimental field was presented in the map of AEZ of Bangladesh in Appendix I.

3.2 Soil and climate

The land topography was medium high with medium fertility level. The soil texture was clay loam and olive gray with common fine to medium distinct dark yellowish-brown mottles. The pH of the soil was 5.48 to 5.62 and organic carbon content is 0.83% (Appendix II). The climate of the locality is subtropical which is characterized by high temperature with high humidity. Heavy rainfall during Kharif season (April-September) and scanty rainfall during Rabi season (October-March) associated with moderate temperature and short-day length. The prevailing records of humidity, rainfall and air temperature during the period of experiment were shown in (Appendix III)

3.3 Experimental materials

The seeds of nine advanced populations of *Brassica rapa* L. were used as experimental materials obtained from the Department of Genetics and Plant Breeding, Sher-e Bangla Agricultural University. The materials used in the experiment is displayed in the following Table 1.

3.4 Methods

3.4.1 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with power tiller and country plough to bring about good tilth. Weeds and other stubbles were eliminated carefully from the experimental plot and leveled properly. The final land preparation was done on 06 November 2019.

3.4.2 Application of manures and fertilizers

The crop was fertilized with Urea, Triple Super Phosphate (TSP), Gypsum, Zinc oxide Muriate of potash (MOP) and Boric acid were applied to the experimental plot at the proper time. As basal dose fertilizer total amount of cow dung, the first half amount of urea, Gypsum, Zinc Oxide TSP, MOP and Boric acid were applied during final land preparation. After that the rest amount of urea was applied as top dressing after 25 days of sowing in the experimental plot. List of manures and fertilizers with doses and procedures of application is shown in following Table 2.

Table 1. Name of the advanced populations of mustard used in the study

Designation	Advanced populations	Source
G1	SAU 1×BARI 15, F ₈ , Yellow	GEPB, SAU
G2	BARI 9×BARI 6, S5F ₁₆ , Brown	GEPB, SAU
G3	BARI 6×BARI 15, F ₇ , Yellow	GEPB, SAU
G4	SAU 2×BARI 6, F ₇ S ₄ , Yellow	GEPB, SAU
G5	BARI 6×BARI 15, F ₁₀ , 75days, Yellow	GEPB, SAU
G6	BARI 9×BARI 6, S5F ₁₆ , Yellow	GEPB, SAU
G7	Yellow special, F ₁₀ , 75 days	GEPB, SAU
G8	TORI 7×BARI 15, F ₇ , Yellow	GEPB, SAU
G9	SAU1×BARI15, F ₈ , Brown	GEPB, SAU

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

Serial No	Fertilizers/ manures	Dose		Procedures of application
		Applied in the plot	Quantity/ha	
1	Cow dung	125 kg	5 ton	As basal
2	Urea	7 kg	250 kg	50% basal and 50% at the time of flower initiation
3	MOP	2 kg	75 kg	As basal
4	TSP	4.5kg	170 kg	As basal
5	ZnO	80g	3kg	As basal
6	Gypsum	4 kg	150 kg	As basal
7	Boric acid	300 kg	10 kg	As basal

3.4.3 Experimental design and layout

Field layout 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 $19\text{m} \times 13\text{m} = 247\text{m}^2$. Each replication size was $19\text{m} \times 3\text{m}$. Distance between replication to replication was 1m. Line to line spacing was 30cm and plant to plant 10 cm. Layout of the experimental design is Shown in the following figure

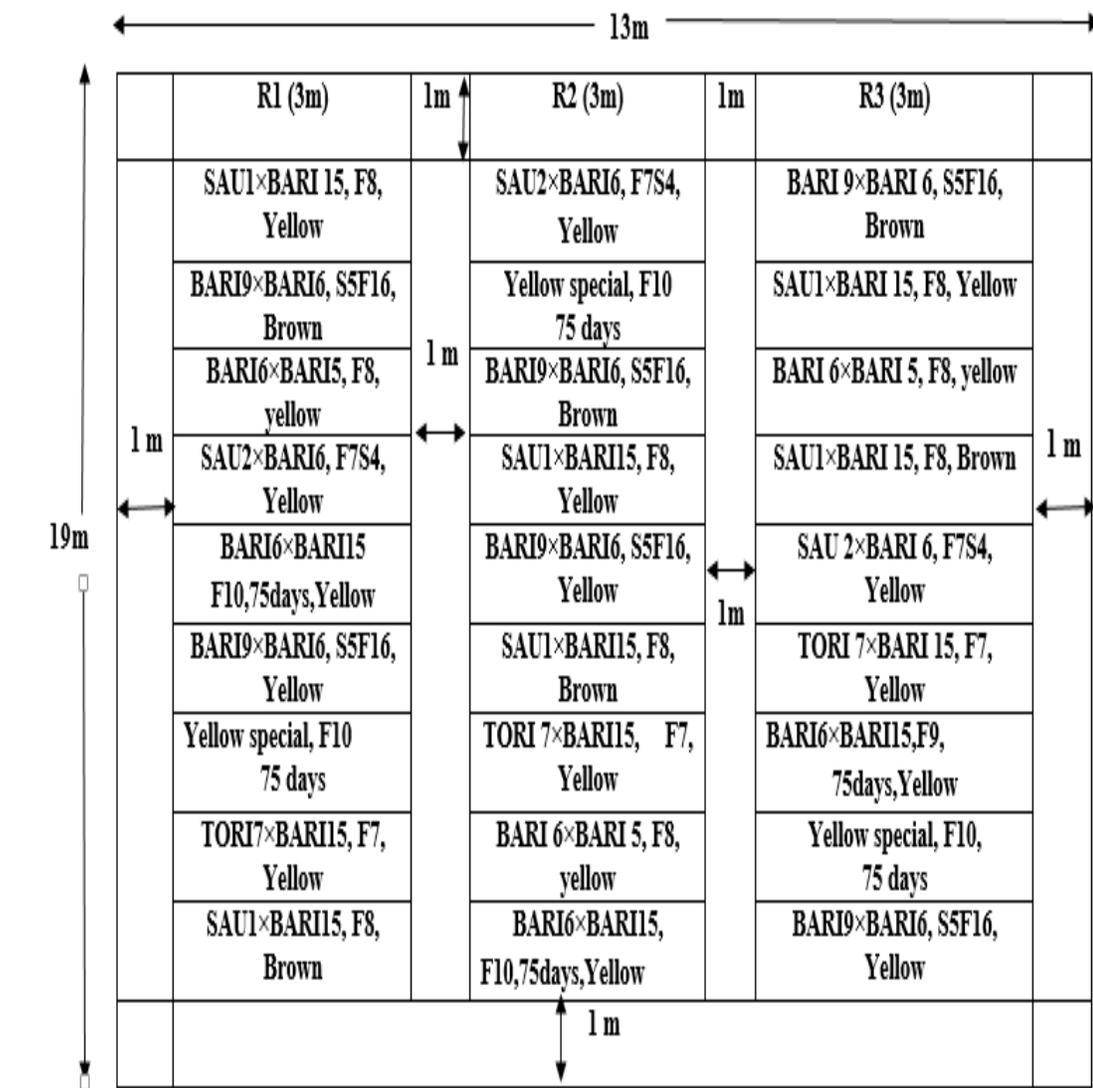


Figure. Layout of the experimental design

3.4.4 Material collection and seed sowing

Seeds of nine advance populations were collected from Department of Genetics and Plant Breeding of SAU. To avoid the unfilled seeds healthy and pure seeds were selected. Seeds were sown in lines in the experimental field on the 8th November, 2019 maintaining a soil depth at about 1.5cm. The seeds were covered with soil carefully after sowing so that no clods were found to suppress the seeds. Germination of seeds was started three to four days after sowing.

3.4.5 Irrigation and drainage

One post sowing irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. After sowing of seeds to maintain moisture condition of the soil and to ensure uniform seed germination sprinkler irrigation was given. Second irrigation was given before the flower initiation (23 DAS). Forty days after sowing third irrigation were given when the pod appeared in the plant. Sixty days after sowing fourth irrigation was given when seeds appeared in the pod. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period.

3.4.6 Intercultural operations, insect and disease control

Several intercultural operations like weeding, thinning was done to ensure normal growth and development of the plants. First weeding was done after 15 days of sowing simultaneously thinning was also done for maintaining 30 cm distance from line to line and 10 cm distance from plant to plant. After 25 days of sowing, second weeding was done. In the field no remarkable disease and pest attack was observed.

3.4.7 Crop harvesting

Harvesting was done from 4th to 15th February, 2020 depending upon the maturity. When 80 % of the plants showed symptoms of maturity i.e., straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. Ten (10) plants were selected at random from of the parental line and 1-11 progenies in each

replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants

On the basis of the maturity harvesting was done from 11th to 22th February, 2020. When 80 % of the plants showed symptoms of maturity i.e., straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. For morphological analysis ten plants were selected at random from the advanced populations of each replication. After those plants were tagged properly and harvested by uprooting. On the basis of different parameters data were recorded from these plants.

3.4.8 Data collection

For studying various genetic parameters and inter-relationships, 13 yield contributing characters were taken such as days to first flowering, days to 50% flowering, days to 80% flowering, days to maturity, plant height, root length, number of primary branches per plant and number of secondary branches per plant, siliquae length, seeds per silique, thousand seeds weight and yield/m².

3.4.9 Data collection method

The procedure of data collection on different traits are described bellow

3.4.9.1 Days to 1st flowering

Days after sowing on which at least one flower opens at any node of the main stem of the treatment rows was considered as days to first flowering.

3.4.9.2 Days to 50% flowering

Days after sowing on which at least 50% flower blooms on 50% plants of the treatment lines were considered as days to 50% flowering.

3.4.9.3 Days to 80% flowering

Days after sowing on which at least 50% flower blooms on 50% plants of the treatment lines were considered as days to 80% flowering.

3.4.9.4 Days to maturity

Days after sowing on which 80% siliquae attained its mature colour were considered as days to maturity.

All the above 4 parameters were selected according to Hans (2010)

3.4.9.5 Plant height (cm)

Data on plant height were recorded during harvesting from 10 randomly selected plants of the treatment rows. Plant height was measured in centimeter (cm) which was starting from the base of the plant to the tip of the longest inflorescence.

3.4.9.6 Root length (cm)

Measurement of root length was started 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 recorded during harvesting from 10 randomly selected plants of the treatment rows.

3.4.9.7 Number of primary branches per plant

The total number of branches that were derived from the main stem of a plant was considered as primary branches and record was taken after counting from 10 randomly selected plants of the treatment rows.

3.4.9.8 Number of secondary branches per plant

The total number of branches derived from the primary branches of a plant was considered as number of secondary branches and record was taken after counting from 10 randomly selected plants of the treatment rows.

3.4.9.9 Number of siliqua per plant

Total number of siliquae of each plant were estimated and considered as the number of siliquae per plant and record was taken after counting from 10 randomly selected plants of the treatment rows.

3.4.9.10 Length of Siliqua

Five representative siliquae were taken randomly from each selected plant and measured in centimeter from the base to the tip of a siliqua without beak.

3.4.9.11 Number of seeds per siliqua

Five siliquae were selected randomly from the sample plants and record was kept after counting the seeds from the siliqua.

3.4.9.12 Thousand seed weight

After harvesting seeds obtained from each treatment were sundried and cleaned. Three sub samples of 1000 pure seeds were taken. Weigh of each sub-sample were taken in grams and the average weight of these three sub-samples was considered as thousand seed weight.

3.4.9.13 Seed yield/ m²

Crops of one square meter randomly selected area were harvested separately. After threshing the seeds were properly sundried and cleaned. Weight of this sundried and cleaned seeds were taken in grams which is considered as seed yield/ m².

3.4.10 Statistical analysis

The recorded data were compiled and analyzed by RCBD design to find out the statistical significance of experimental results by using the “Analysis of variance” (ANOVA) technique with the help of analysis software statistics 10. Analysis of variance was performed by the F test after evaluating the mean values of all the characters. After that the significance of the differences among the treatments was calculated by least significant difference (LSD) test at 5% level of probability. Therefore, phenotypic and genotypic variance was estimated by the formula used by Johnson et al. (1955). Then phenotypic and genotypic coefficient of variation was estimated by the help of the formula of Burton (1952). Then genetic advance was computed by using the formula of Allard (1960) while genetic advance in percentage of mean was measured by using the formula given by Comstock and Robinson (1952). Analysis of path coefficient was done by the outlined method suggested by Dewey and Lu (1959). Phenotypic and genotypic correlation obtained by using the formula of Al-Jabouri et al. (1958). After that heritability in broad sense was calculated by using the formula given by Singh and Chaudhary (1985).

3.4.10.1 Analysis of variance

According to Cochran and Cox (1957), the analysis of variance for different characters was carried out utilizing mean data in order to assess the genetic variability among populations. The level of significance was tested at 1% and 5% using F test. The model of ANOVA was used given 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	σ_e^2
Total	(rp-1)		

Here, p = number of treatments (population) in the experiment

r = number of replications in the experiment

σ_r^2 = variance due to replications in the field

σ_p^2 = variance due to treatments (population)

σ_e^2 = variance due to experimental error

The standard error of mean was computed using the formula:

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

Here, S. E = Standard error of mean

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

r = Number of replications in the field

q = Number of populations in each sub-block

u = Weightage factor q

3.4.10.2 Estimation of Least Significant Differences (LSD)

According to of Gomez and Gomez (1984)

Least Significant Differences were estimated by the formula

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

Where, α = Level of significance

t= tabulated t value with concerned df at same level of significance

s^2 = Error Mean Sum of Square

r = Number of replications

3.4.10.3 Estimation of Phenotypic and Genotypic variance

Estimation of the variability among the populations for traits related to yield per plant in *Brassica rapa L.* were narrated by using the formula given bellow:

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

Here,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error

r = Number of replications

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

Here,

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

σ_e^2 = Environmental variance = Mean square of error

3.4.10.3.1 Estimation of genotypic and phenotypic coefficient of variation

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g \times 100}{\bar{x}}$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p \times 100}{\bar{x}}$$

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

\bar{x} = Population means

Low (0-10%), Moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhava Menon (1973).

3.4.10.3.2 Estimation of heritability in broad sense

$$h_b^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Here, h_b^2 = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Categories:

Low: 0-30%

Moderate: 30-60%

High: >60%

3.4.10.3.3 Estimation of genetic advance

$$\text{Genetic advance} = \frac{\sigma_g^2}{\sigma_p^2} \cdot K \cdot \sigma_p$$

Here,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

σ_p = Phenotypic standard deviation

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

Categories:

Low (<10%)

Moderate (10-20%)

High (>20%)

3.4.10.3.4 Estimation of genetic advance in percentage of mean

$$\text{Genetic advance (GA) in percent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

According to, Johnson *et al.* (1955) there are three categories of genetic advanced are given bellow:

Less than 10% - Low

10-20% -Moderate

More than 20% -High

3.4.10.4 Correlation coefficient analysis

$$\text{Genotypic correlation coefficients } (r_{gxy}) = \frac{Cov_{gxy}}{\sqrt{\sigma_{gx}^2} \sqrt{\sigma_{gy}^2}}$$

$$\text{Phenotypic correlation coefficients } (r_{pxy}) = \frac{Cov_{pxy}}{\sqrt{\sigma_{Px}^2} \sqrt{\sigma_{Py}^2}}$$

Here,

$r_g(xy)$ = Genotypic correlation coefficients of x and y

$r_p(xy)$ = phenotypic correlation coefficients of x and y

Cov_{gxy} = Genotypic covariance of x and y

Cov_{pxy} = Phenotypic covariance of x and y

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

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

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

σ_{py}^2 = Phenotypic variance of the trait y.

The calculated value of 'r' was compared with table 'r' value with n-2 degrees of freedom at 1% and level 5% of significance and n refers to number of pairs of observation.

3.4.10.5 Path coefficient analysis

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

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

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

Where,

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

r's denote simple correlation coefficient

P's denote path coefficient (unknown).

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 on yield y. After calculating the direct and indirect effect of the characters, residual effect (R) was calculated.

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

Here,

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

$$\text{Hence, residual effect, } R = \sqrt{P_{RY}^2}$$

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

r_{iy} = Correlation of the character with yield

Categories

Low (0.10 to 0.19)

Moderate (0.20 to 0.29)

High (0.30 to 1.0)

Very High (>1.00)

Negligible (0.00 to 0.0)

CHAPTER IV

RESULTS AND DISCUSSION

By comparing nine advanced populations of *Brassica rapa* L., we were able to select a population that matured early and produced high yields. As a result, a critical evaluation of genetic variability, phenotypic and genetic coefficients of variation, heritability, genetic advance, genetic advance as a percentage of the mean, correlation coefficient and path coefficient analysis is required to achieve the experiment's goal. On the basis of nine advanced populations data were collected on days to first flowering, days to 50% flowering, days to 80% flowering, days to maturity, plant height, root length, number of primary branches per plant and number of secondary branches per plant, total silique, silique length, seeds per silique, thousand seeds weight and yield per square meter. The data was statistically analyzed and the results are listed 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 studies

4.4 Path coefficient analysis

4.5 Selection

4.1 Mean performance of the populations and genetic variability

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied as days to first flowering, days to 50% flowering, days to 80% flowering, days to maturity, plant height, root length, number of primary branches per plant and number of secondary branches per plant, total silique; silique length, seeds per silique, thousand seeds weight and yield m^2 . The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore, there is a lot of scope for selection for majority of the traits in the genotypes. The ANOVA of all the 13 characters is presented in Table 3.

An estimate of heritability can be used to determine the proportion of variation that is heritable. The fact that all of the characters studied had a narrow gap between PCV and GCV suggested that these traits had little environmental influence. The heritability estimates alone do not indicate the response to selection (Johnson *et al*, 1955). If genetic advance is also estimated, heritability estimates appear to be more meaningful. Additionally, the genetic advance as a percentage of the mean (GAM) was calculated. The extent of variation among the genotypes in respect of thirteen characters was studied and estimate of mean performance were estimated. The mean performance of rapeseed genotypes for various yield components is presented in Table 4. Genotypic and phenotypic coefficients of variation were calculated and presented in Table 5. Heritability, genetic advance and genetic advance in percentage of mean for all the characters were studied and the results are interpreted in Table 6.

Table 3 Analysis of variance of 13 important characters of 9 advanced populations of *Brassica rapa* L.

Source of Variance	Degrees of freedom	Mean sum of square of characters												
		DF (No.)	DFFF (No.)	DEF (No.)	DM (No.)	PH (cm)	RL (cm)	PB (No.)	SB (No.)	TSP (No.)	SL (cm)	SS (No.)	TSW (g)	SY (g/m ²)
Rep	2	3.59	0.26	0.26	0.33	8.02	0.42	0.39	0.03	849.21	0.13	1.52	0.04	0.28
Gen	8	13.04**	26.20**	37.98**	111.92**	74.10**	1.26**	0.81**	2.65**	763.56**	0.55**	22.77**	0.30**	1.83**
Error	16	1.88	2.43	2.43	2.67	15.34	0.28	0.23	0.04	165.70	0.12	3.59	0.06	0.49

** At 1% level of significance

DFF = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering; DM = Days to Maturity; PH = Plant height;

RL = Root length; PB = No. of primary branches; SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;

SS = No. of Seed per siliqua; TSW = Thousand seed weight and SY = Seed yield

Table 4 Mean performance of yield and yield contributing characters of nine advanced populations *Brassica rapa* L.

Advanced populations	DF (No.)	DFFF (No.)	DEF (No.)	DM (No.)	PH (cm)	RL (cm)	PB (No.)	SB (No.)	TSP (No.)	SL (cm)	SS (No.)	TSW (g)	SY(g/m ²)
G1	29.33 ab	33.66 b	37.66 bc	90.33a	103.43b	7.73 bc	5.13cd	1.33 c	74.50cde	4.72d	13.31c	3.63abc	192.05cde
G2	27.00 bc	33.33 b	36.33 bc	86.33b	94.67c	6.46 d	6.10ab	0.96 d	104.53ab	5.44abc	13.50c	3.43abcd	234.3 ab
G3	29.33 ab	32.33 bc	35.33 bc	91.33a	103.77b	8.16 ab	6.30a	0.37ef	81.10cde	4.89cd	14.05bc	3.61abc	194.55bcde
G4	31.00 a	31.66 bc	35.66 bc	92.33a	99.7 bc	8.19ab	5.42bcd	0.13fg	62.97e	5.74a	16.92b	3.36 bcd	187.09de
G5	27.00 bc	30.00 c	32.00e	76.33d	102.3 b	7.09cd	5.83abc	0.20efg	71.00de	4.95bcd	20.28a	3.82a	244.38 a
G6	26.00c	34.00 b	38.00 b	82.33c	97.30bc	7.89abc	6.33a	2.57a	109.93a	5.62a	16.28bc	3.69 ab	231.68 abc
G7	25.00c	30.33c	32.33 de	77.33d	99.77bc	7.64bc	4.97 d	0.50e	75.00cde	4.84cd	15.50bc	3.02de	170.17e
G8	30.00a	40.00a	44.00 a	83.00c	112.30a	8.67a	6.30 a	0.00g	96.32bc	4.60d	20.73a	2.87e	193.21cde
G9	30.00a	32.00 bc	35.00 cd	90.66a	102.73b	7.49bc	5.86abc	2.23b	85.27bcd	5.50ab	14.70bc	3.24cde	222.67abcd
Min	25.00	30.00	32.00	76.33	94.67	6.47	4.97	0.00	62.97	4.60	13.31	2.87	170.17
Max	31.00	40.00	44.00	92.33	112.30	8.67	6.33	2.57	109.93	5.74	20.73	3.82	244.38
Grand Mean	28.30	33.04	36.26	85.56	101.78	7.71	5.81	0.92	84.51	5.15	16.15	3.41	207.79
CV	4.85	4.71	4.30	1.91	3.85	6.92	8.22	20.77	15.23	6.77	11.74	7.03	11.13
LSD (0.05%)	2.38	2.70	2.70	2.83	6.78	0.92	0.83	0.33	22.28	0.60	3.28	0.42	40.02
SE	0.79	0.90	0.90	0.94	2.26	0.31	0.28	0.11	7.43	0.20	1.09	0.14	13.35

Means in the column by the same letter do not differ significantly (LSD 0.05)

DFF = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering; DM = Days to Maturity; PH = Plant height;

RL = Root length; PB = No. of primary branches; SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;

SS = No. of Seed per siliqua; TSW = Thousand seed weight; SY = Seed Yield

Table 5 Estimation of genetic parameters of 9 advanced populations of *Brassica rapa* L.

T	DF (No.)	DFFF (No.)	DEF (No.)	DM (No.)	PH (cm)	RL (cm)	PB (No.)	SB (No.)	TSP (No.)	SL (cm)	SS (No.)	TSW (g)	SY (g/m²)
σ^2g	3.72	7.93	11.85	36.42	19.59	0.33	0.19	0.87	199.29	0.14	6.39	0.08	0.45
σ^2p	5.60	10.35	14.28	39.08	34.92	0.61	0.42	0.91	364.98	0.26	9.99	0.14	0.94
σ^2e	1.88	2.43	2.43	2.67	15.34	0.28	0.23	0.04	165.70	0.12	3.59	0.06	0.49
GCV	6.81	8.52	9.49	7.05	4.35	7.41	7.59	101.13	16.70	7.35	15.66	8.40	10.61
PCV	8.36	9.74	10.42	7.31	5.81	10.14	11.19	103.24	22.61	9.99	19.57	10.96	15.37

DFF = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering; DM = Days to Maturity; PH = Plant height;
 RL = Root length; PB = No. of primary branches; SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;
 SS = No. of Seed per siliqua; TSW = Thousand seed weight and SY = Seed yield

4.1.1 Days to first flowering

Highly significant variations were observed among the genotypes (13.04**) for days to first flowering (Table 3). The highest days to first flowering was observed in G4 (31 days) and the minimum in G7 (25 days) with mean value of 28.30 among 9 genotypes (Table 4). Mean performance of days to first flowering in 9 advanced populations of *Brassica rapa* L. is presented in Figure 1 through line graph.

The phenotypic variance (5.60) was lower than genotypic variance (3.72) and variation between them was lower indicating that environment has little influence for the expression of this trait. Generally, quantitative characters are highly influenced by the environment. The GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) were low with 6.81 and 8.36 percent respectively (Table 5).

4.1.2 Days to 50% flowering

Highly significant variations were observed (Table 3) for the character days to 50% flowering (26.20**). The minimum period for days to 50% flowering was noticed in G5 with 30.00 days indicating that 50% flowers appear earlier than other advanced populations after sowing whereas G8 took longest period 40.00 days and mean value was 33.04 (Table 4). Mean performance for days to 50% flowering in 9 advanced populations of *Brassica rapa* L. is shown in Figure 2 through line graph.

The phenotypic variance (10.35) was slightly higher than genotypic variance (7.93) and variation between them was moderate indicating that environment has moderate influence for the expression of the character. The GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) were low with value of 8.52 and 9.74 percent, respectively (Table 5).

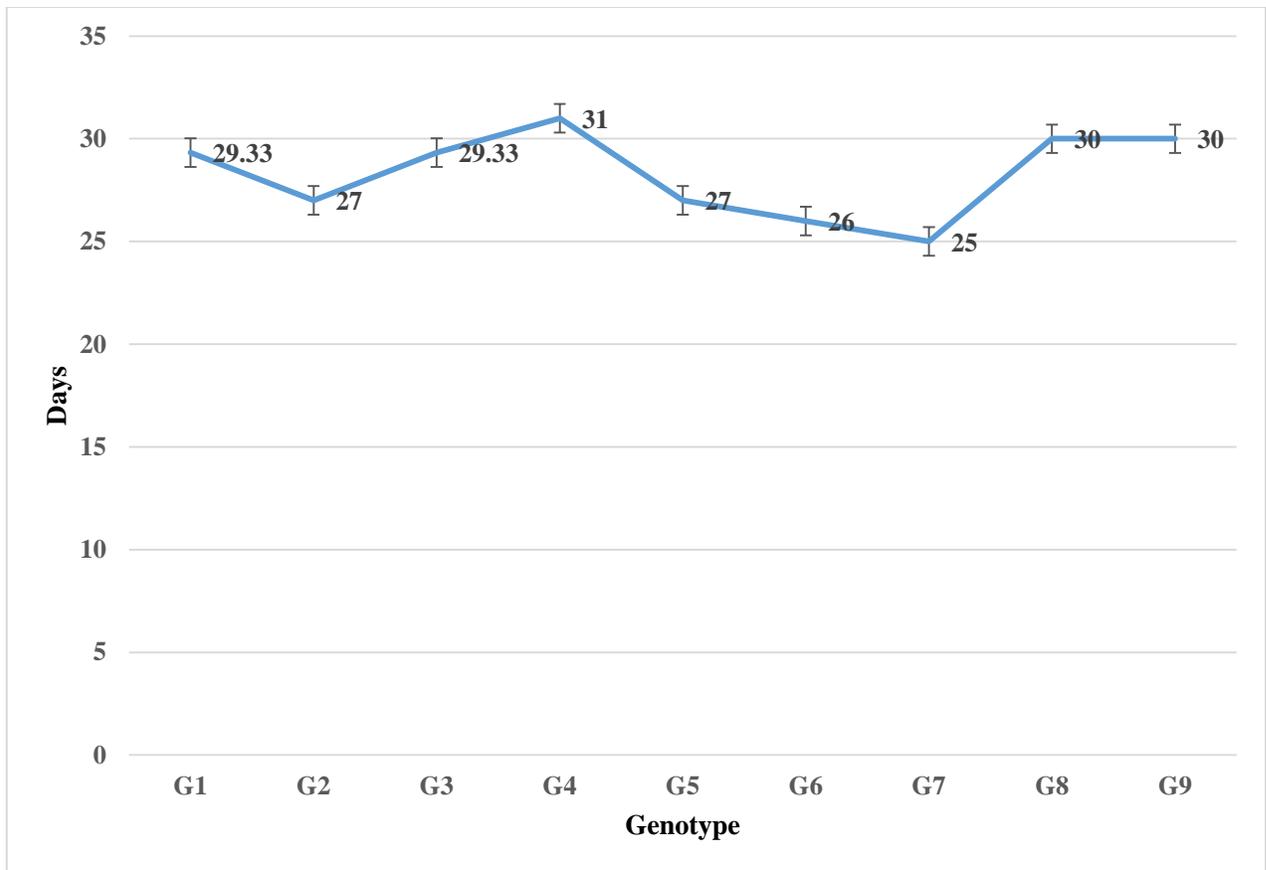


Fig. 1 Days to First Flowering of nine advanced populations of *Brassica rapa* L.

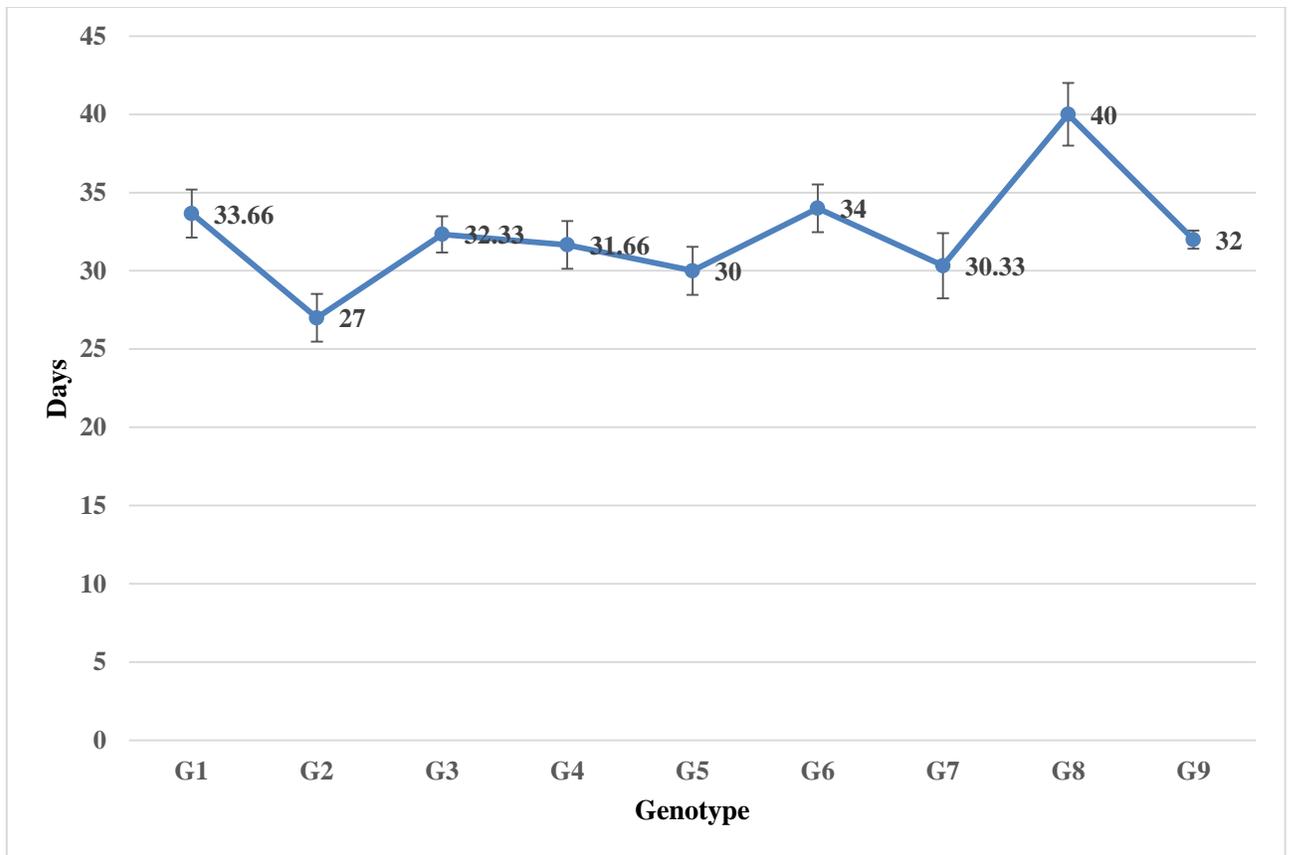


Fig. 2 Days to 50% Flowering of nine advanced populations of *Brassica rapa* L.

4.1.3 Days to 80% flowering

Analysis of variance (Table 3) revealed that highly significant differences among the genotypes were exist for days to 80% flowering (37.98**). The highest days to 80% flowering was recorded in G8 (44 days), minimum in G5 (32 days) and the mean value was 36.26 (Table 4). Mean performance for days to 80% flowering in 9 advanced populations of *Brassica rapa* L. is shown in Figure 2 through line graph.

Phenotypic variance (14.28) was slightly higher from the genotypic variance (11.85) that indicated moderate environmental effect over the trait. Moderate PCV (10.42%) and low GCV (9.49%) values indicated that influence of environment were lower on this character (Table 5).

4.1.4 Days to maturity

Days to maturity showed highly significant variations (111.92**) indicating that large variations were present among the tested advanced populations (Table 3). The G5 required least number of days to mature (76.33 DAS) indicating that it matured earlier than others followed by G7 (77.33 DAS) and G6 (82.33 DAS) whereas maximum number of days for maturity was observed in the population G4 (92.33 DAS) (Table 5) with mean value 85.56 DAS (Table 4). Mean performance of days to maturity in 9 advanced populations of *Brassica rapa* L. is embellished in Figure 4 through line graph.

Phenotypic variance was recorded as 39.08 which was higher than genotypic variance (36.42) with moderate difference between them indicating moderate environmental influence in the expression of genes for this trait (Table 5). Higher Phenotypic variation than genotypic variation was also observed by Alam *et al*, (2010) The value of GCV (Genotypic Coefficient of variation) and PCV (Phenotypic Coefficient of variation) was very low, 7.05 and 7.31 percent, respectively.

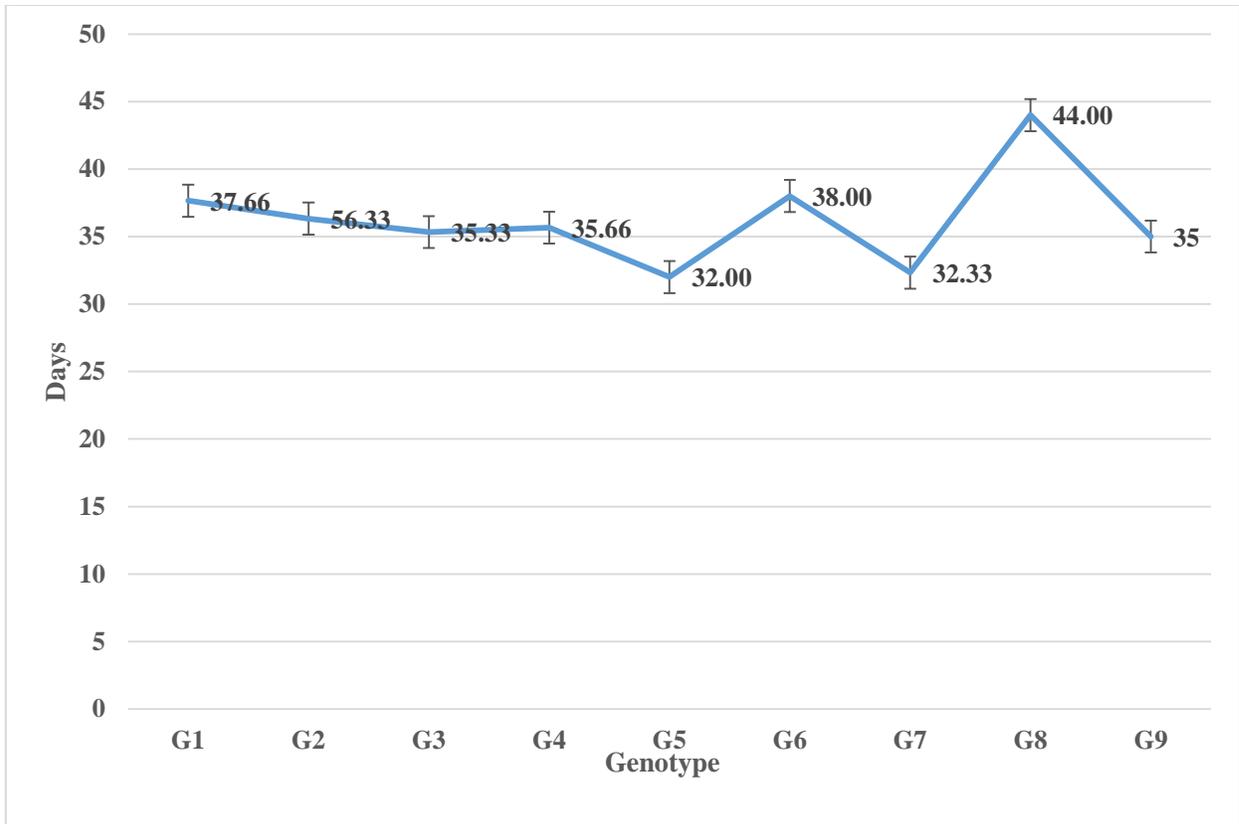


Fig. 3 Days to 80% Flowering of nine advanced populations of *Brassica rapa* L.

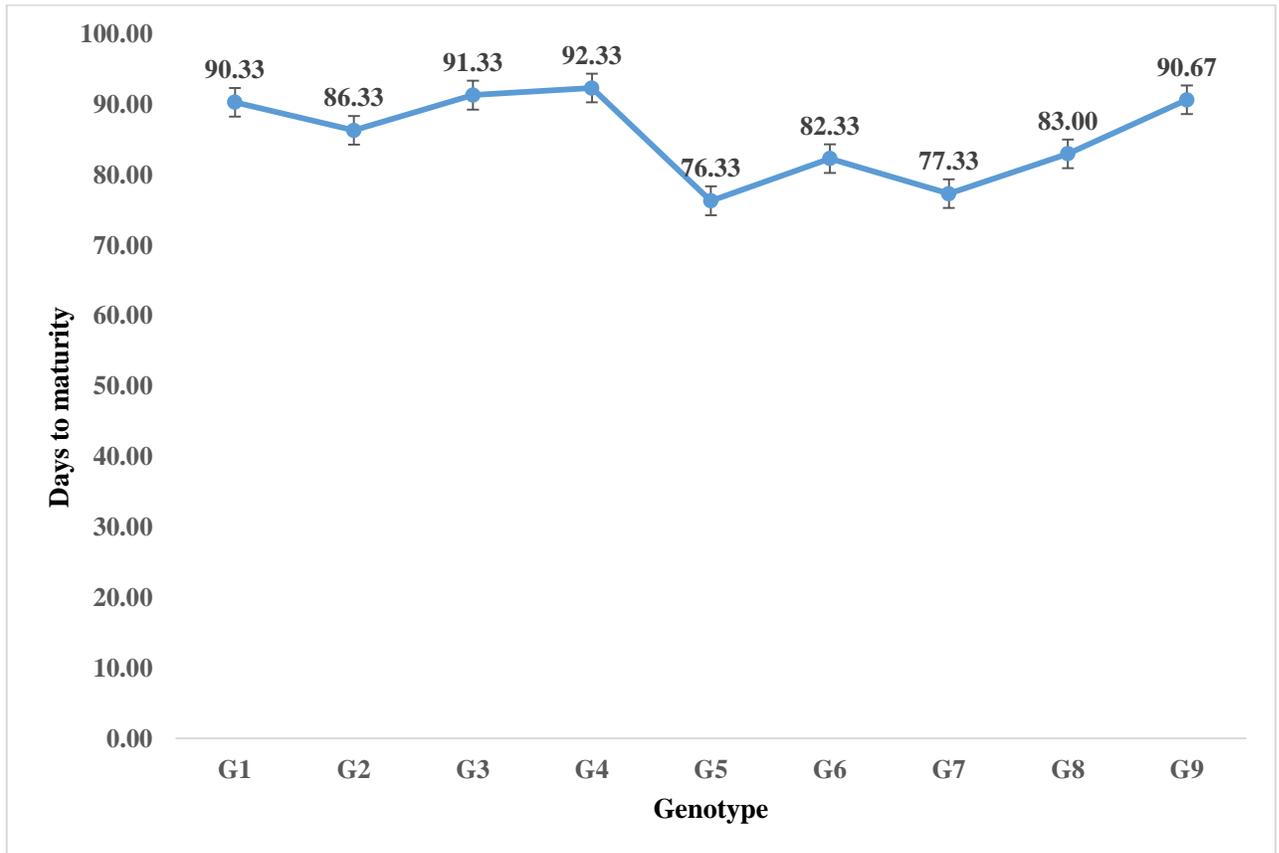


Fig. 4 Days to maturity of nine advanced populations of *Brassica rapa* L.

4.1.5 Plant height

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. From the ANOVA (Table 3), it was found that plant height showed highly significant variations among the genotypes (74.10**). The plant height was maximum in G8 (112.30cm), minimum was observed in G2 (94.67cm) and the mean value was 101.78 cm. among the 9 genotypes (Table 5). Mean performance of plant height in 9 advanced populations of *Brassica rapa* L. is presented in figure 5 through line graph.

Phenotypic variance (34.92) was observed higher than genotypic variance (19.59) and variation between them was higher for plant height indicating that environmental influence was high over the genotypes for the expression of the concerned trait (Table 3). Ara *et al.* (2010) also observed the same finding. The high GCV values of this characters suggested that the possibility of improving this trait through selection. The plant height exhibited low genotypic coefficient of variation (GCV) and low phenotypic coefficient of variation (PCV) of 4.35 and 5.81 percent, respectively (Table 4).

4.1.6 Root length:

Table 3 revealed that root length showed highly significant differences among the advanced populations (1.26**). Maximum length of root was found in G8 (8.67cm) whereas minimum in G2 (6.47cm) and mean 7.71cm (Table 4). Mean performance of root length in 9 advanced populations of *Brassica rapa* L. is shown in Figure 6 through line graph.

Phenotypic variance (0.61) was slightly higher than genotypic variance (0.33) having little difference between them indicated that there was less environment effect over genotypes for the expression of character (Table 3). Low genotypic coefficient of variation (GCV) and moderate phenotypic coefficient of variation (PCV) of 7.41 and 10.14 were observed, respectively (Table 5)

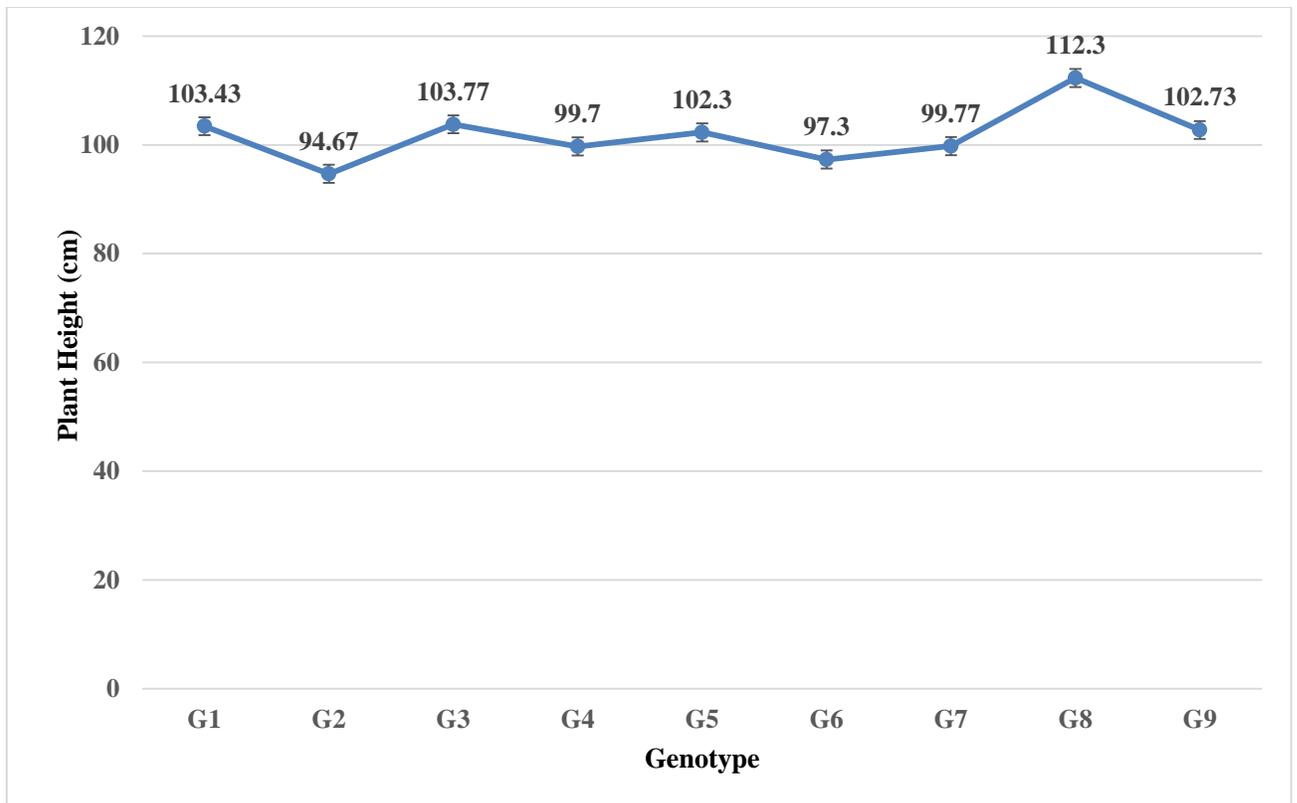


Fig. 5 Plant height of nine advanced populations of *Brassica rapa* L.

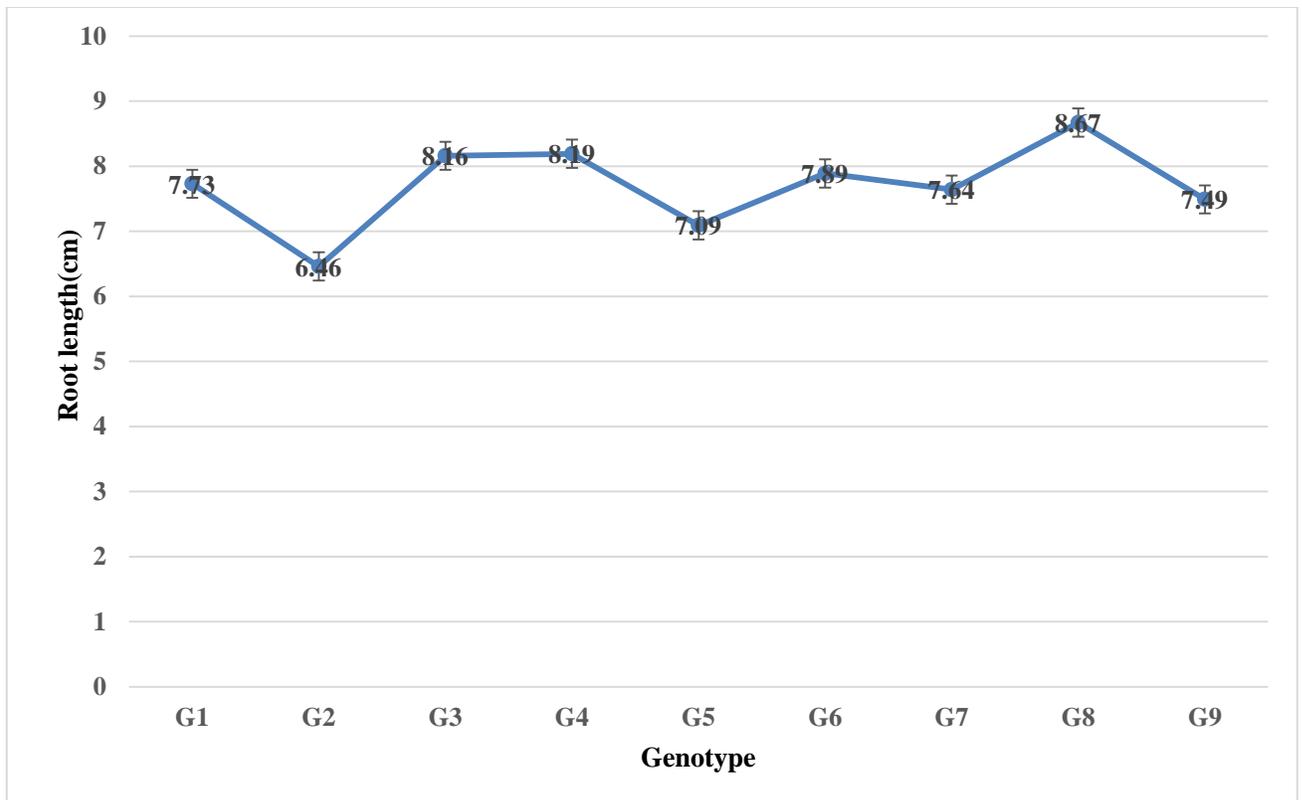


Fig. 6 Root length of nine advanced populations of *Brassica rapa* L.

4.1.7 Number of primary branches per plant

Number of primary branches per plant showed highly significant differences (0.81**) among the advanced populations (Table 3). Maximum number of primary branches per plant was obtained in G6 (6.33) followed by G8 (6.30) and minimum in G7 (4.97) with mean value was 5.81 (Table 4). Mean performance of number of primary branches per plant in 9 advanced populations of *Brassica rapa* L. is embellished in Figure 7 through bar graph.

There was little difference between phenotypic variance (0.42) and genotypic variance (0.19) suggested that there was less influence of environment for the disclosure of this character (Table 4). Hosen, (2008) also agreed to this finding. 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 was similar to this finding. Low genotypic coefficient of variation (GCV) and moderate phenotypic coefficient of variation (PCV) of 7.59% and 11.19% respectively were observed (Table 5).

4.1.8 Number of secondary branches per plant

Highly significant variations were observed (2.65**) for the number of secondary branches per plant suggesting that large variations were present among the tested advanced populations (Table 3). Maximum number of secondary branches per plant was found in G6 (2.57) whereas G8 (0.0) having lowest followed by G4 (0.13) and G5(0.20) with a mean value 0.92 (Table 4). Mean performance of number of secondary branches per plant in 9 advanced populations of *Brassica rapa* L. is embellished in Figure 8 through bar graph.

The genotypic and phenotypic variance were recorded as 0.87 and 0.91 respectively and the difference between phenotypic variance and genotypic variance was low indicating less environmental influence for the exposure of the character. High genotypic coefficient of variation (GCV) and high phenotypic coefficient of variation (PCV) of 101.13% and 103.24% respectively were observed, respectively (Table 5). 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.

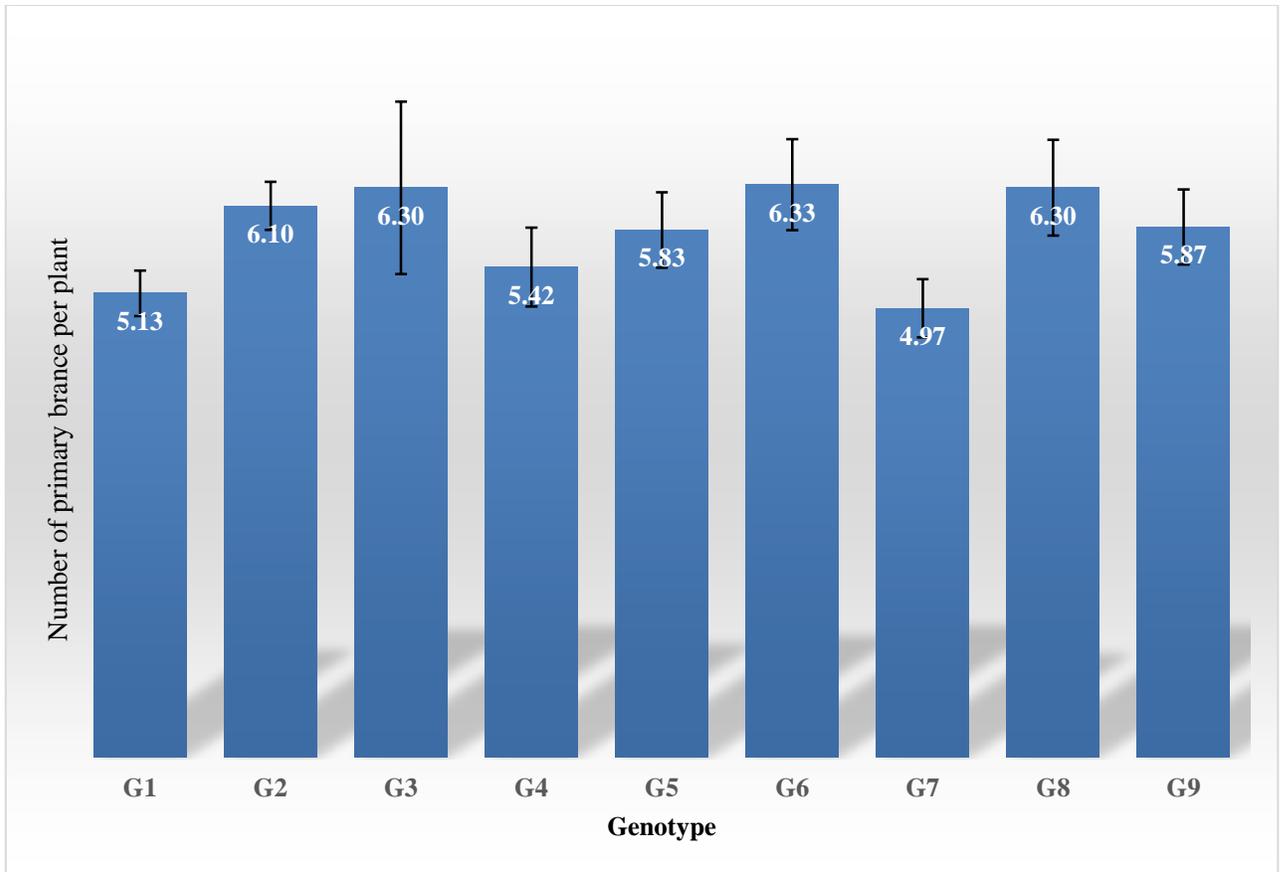


Fig .7 No. of primary branches plant¹ of nine advanced populations of *Brassica rapa* L.

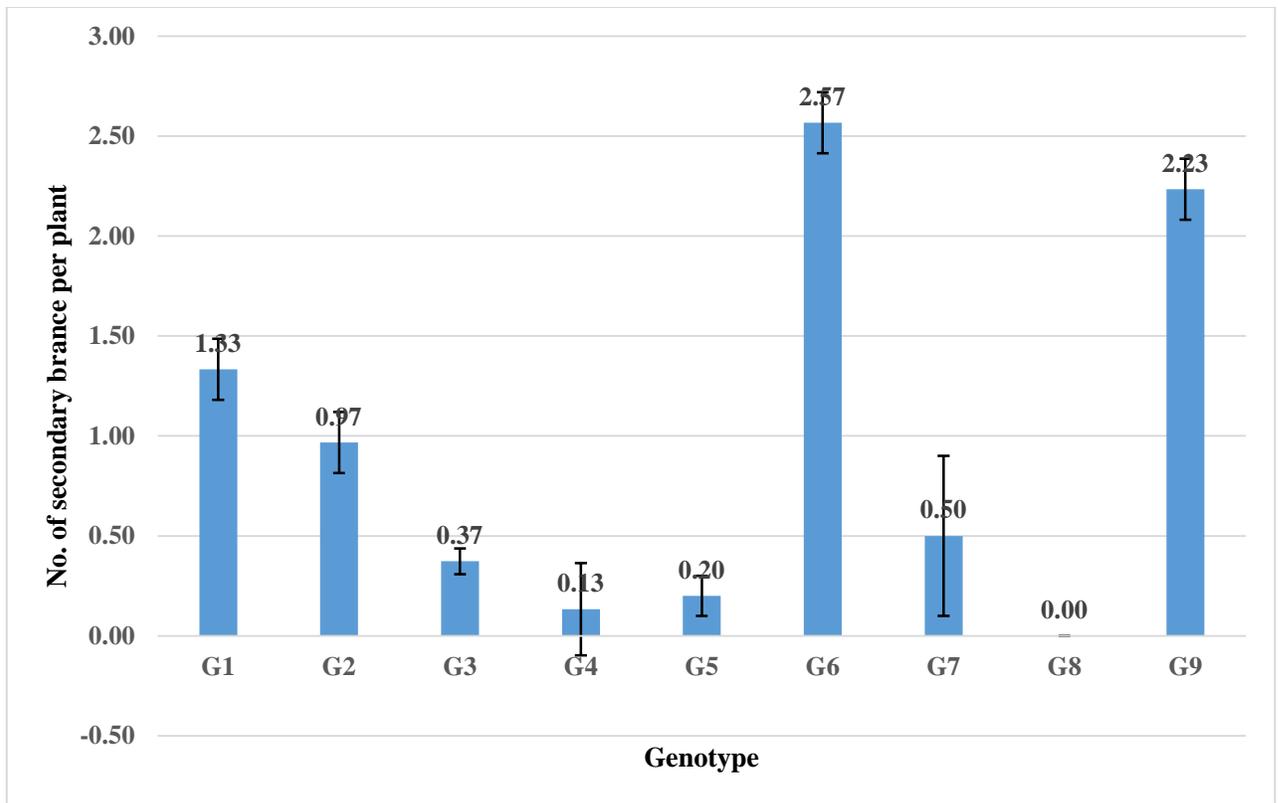


Fig. 8 No. of secondary branches plant¹ of nine advanced populations of *Brassica rapa* L.

4.1.9 Total number of siliquae per plant:

Total siliquae showed highly significant (763.56**) value indicated that there were highly significant variations among the tested advanced populations (Table 3). The highest no. of siliquae was noticed in population G6 (109.93) followed by G2 (104.53) and G8 (96.32). The population G4 showed the lowest total siliquae (62.97). Mean value was 84.51 (Table 4). Mean performance of total siliquae in 9 advanced populations of *Brassica rapa* L. is shown in figure 9 through bar graph.

The phenotypic variance (364.98) was higher than genotypic variance (199.29) (Table 4) having higher difference between them. This indicated large influence of environment for the expression of this character. The higher phenotypic coefficient of variation (22.61%) and moderate genotypic coefficient of variation (16.70%) were observed (Table 5) indicating presence of less considerable variability among the populations.

4.1.10 Siliqua length:

Highly significant variations (0.55**) were observed among the advanced populations for this trait (Table 3). Siliqua length was longer (5.74cm) in G4 followed by G6 (5.62 cm) and G9 (5.50) while shorter in G8 (4.60) followed by G1 (4.72 cm) and G7 (4.84 cm) with a mean value 4.60 cm (Table 4). Mean performance of siliqua length in 9 advanced populations of *Brassica rapa* L. is embellished in figure 10 through bar graph.

Phenotypic variance (0.26) was lower than genotypic variance (0.14) for siliqua length (cm) with little difference between them indicating that environment had least influence for the disclosure of this character (Table 4). Low GCV (7.35%) and low PCV (9.99 %) values were found in case of siliqua length (cm) (Table 5).

There was a little difference in the estimates of GCV and PCV for siliqua length (cm) stated low environment effect in the expression of these traits. Sikarwar *et al.* (2017) also found a little difference in the estimates of GCV and PCV for length of siliqua.

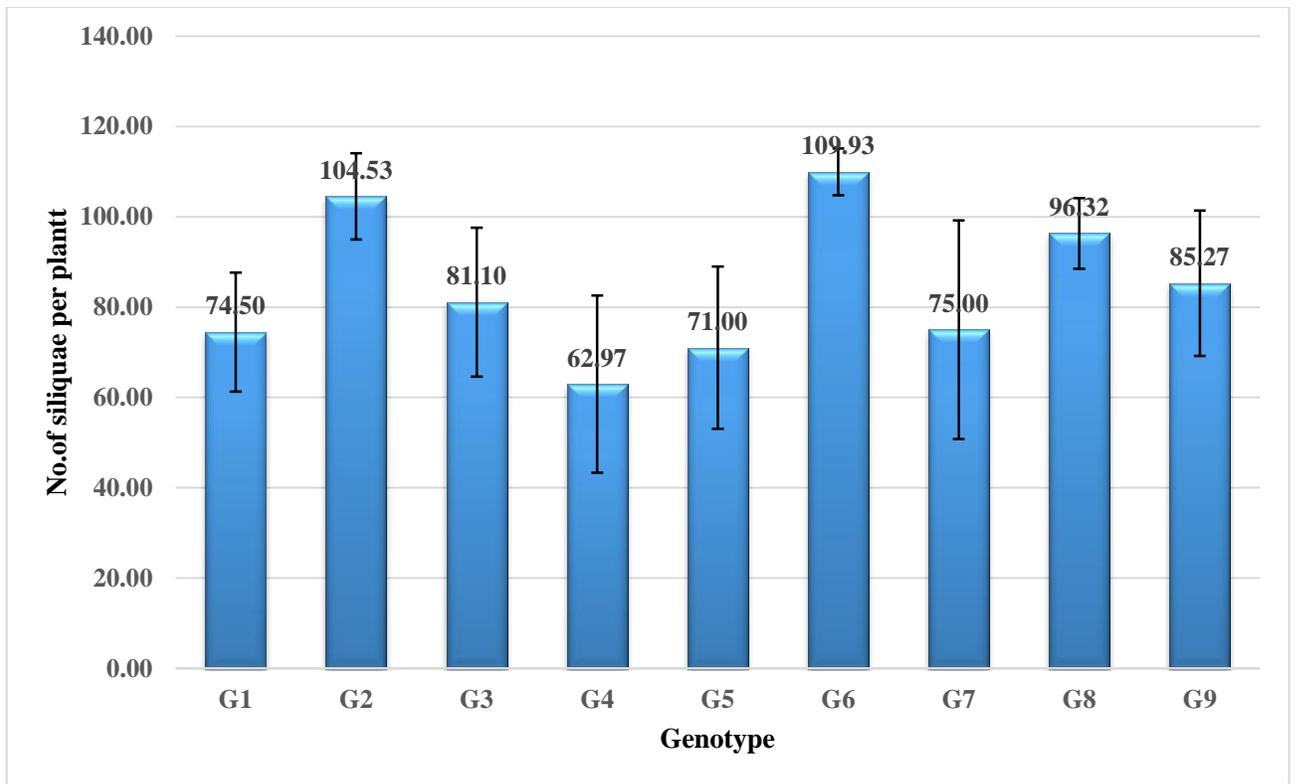


Fig.9 Number of siliques per plant of nine advanced populations of *Brassica rapa* L.

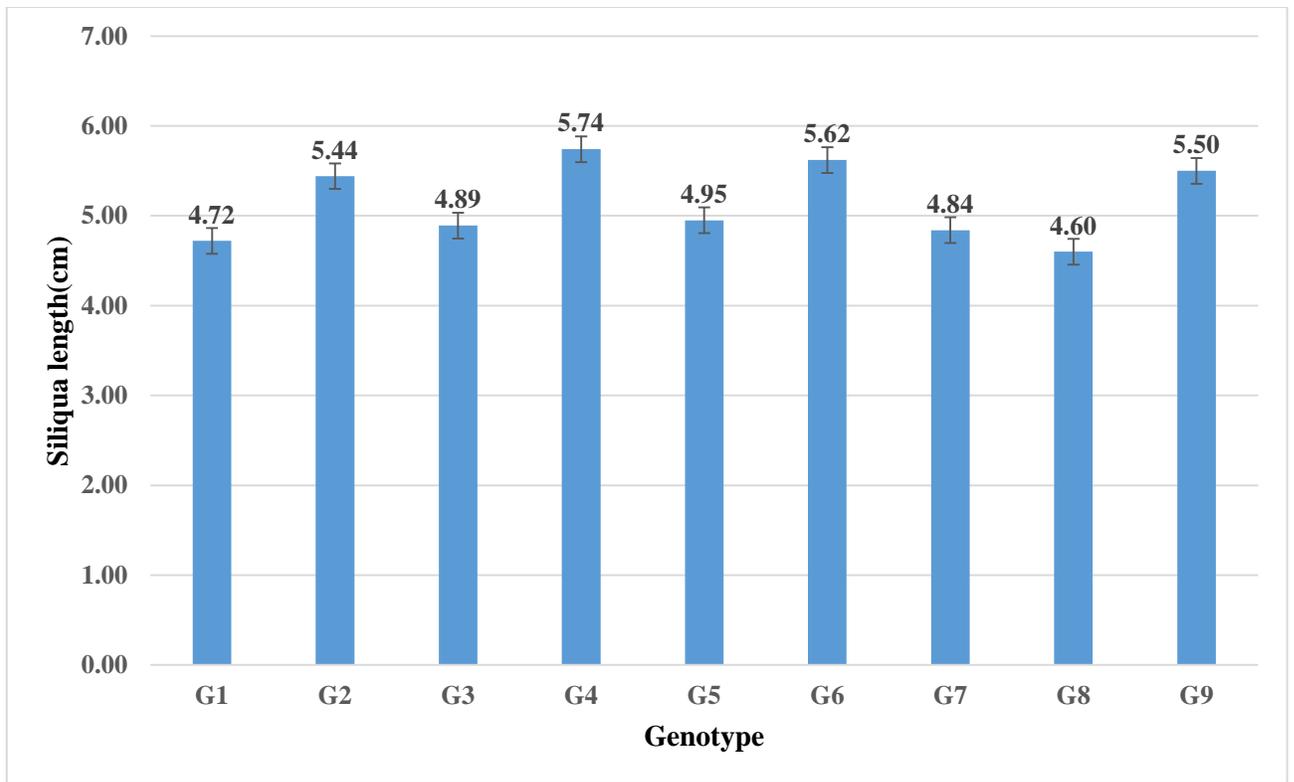


Fig. 10 Siliqua length of nine advanced populations of *Brassica rapa* L.

4.1.11 Seeds per siliqua:

Seeds per siliqua showed highly significant variations (22.77**) which indicated the presence of large variations among the advanced populations (Table 3). The maximum seeds per siliqua was recorded in G8 (20.73). On the contrary, minimum number of seeds per siliqua exhibited in population G1 (13.31). Mean value was 16.15 (Table 4). Mean performance of seeds per siliqua in 9 advanced populations of *Brassica rapa* L. is presented in Figure 11 through bar graph.

The phenotypic variance was (9.99) higher than genotypic variance was (6.39) having moderate difference between them indicating that there was moderate influence of environment on the character (Table 5). Low genotypic coefficient of variation (8.40) and moderate phenotypic coefficient of variation (10.96) were observed (Table 4). There was a little difference in the estimates of GCV and PCV for seeds per siliqua suggested low environment effect in the expression of these traits.

4.1.11 Thousands seed weight:

Thousand seeds weight showed highly significant variations (0.30**) among the tested advanced populations (Table 3). Maximum thousand seed weight was found in G5 (3.82 g) indicating the bigger and higher oil containing seeds followed by population G6 (3.69 g). The lowest thousand seeds weight (g) was found in G8 (2.87 g) and having a mean value 3.41 (Table 4). Mean performance of thousand seed weight in 9 advanced populations of *Brassica rapa* L. is embellished in Figure 12 through bar graph.

There was a little difference between phenotypic and genotypic variance and phenotypic variance was lower (0.14) compared to genotypic variance (0.08) indicating little influence of environment on the expression of character. Moderate PCV (10.96%) and GCV (10.96%) were noted for thousand seed weight (Table 5).

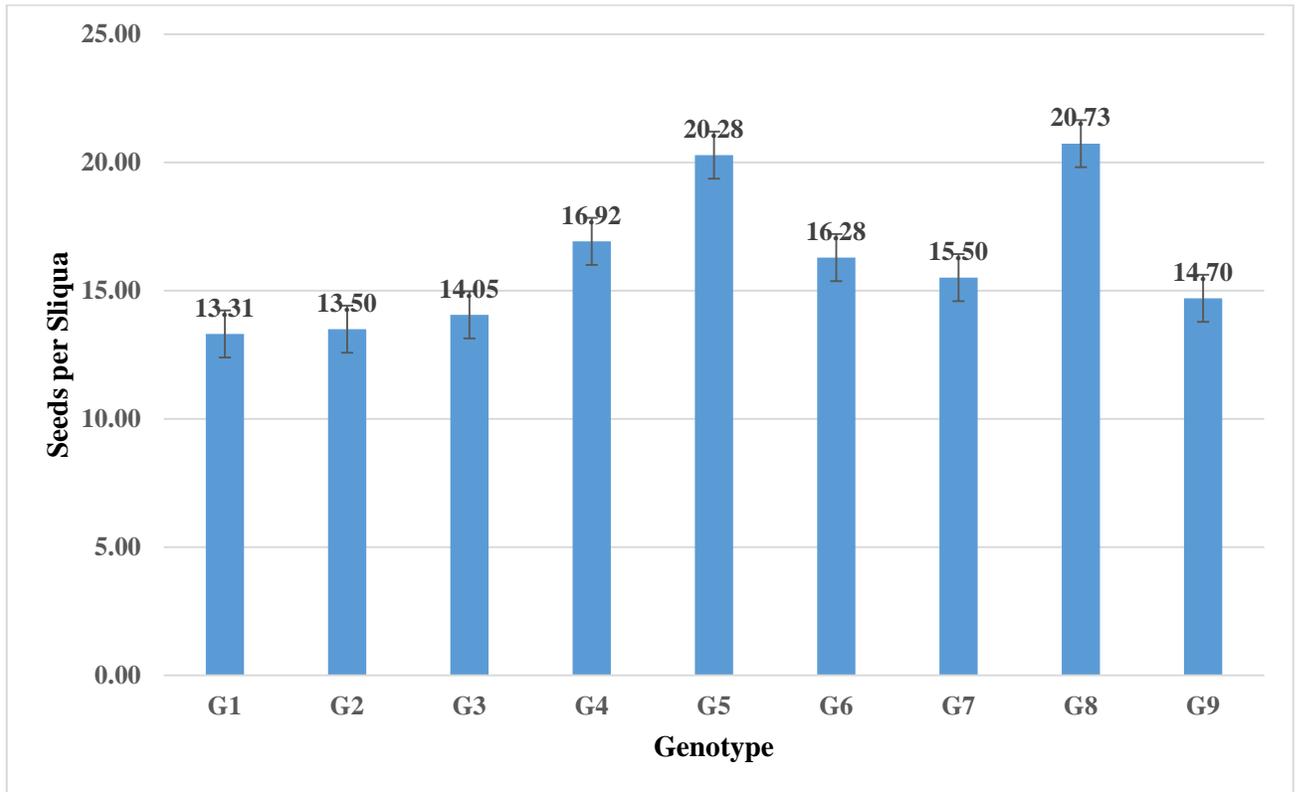


Fig.11 Number of seeds siliqua¹ of nine advanced populations of *Brassica rapa* L.

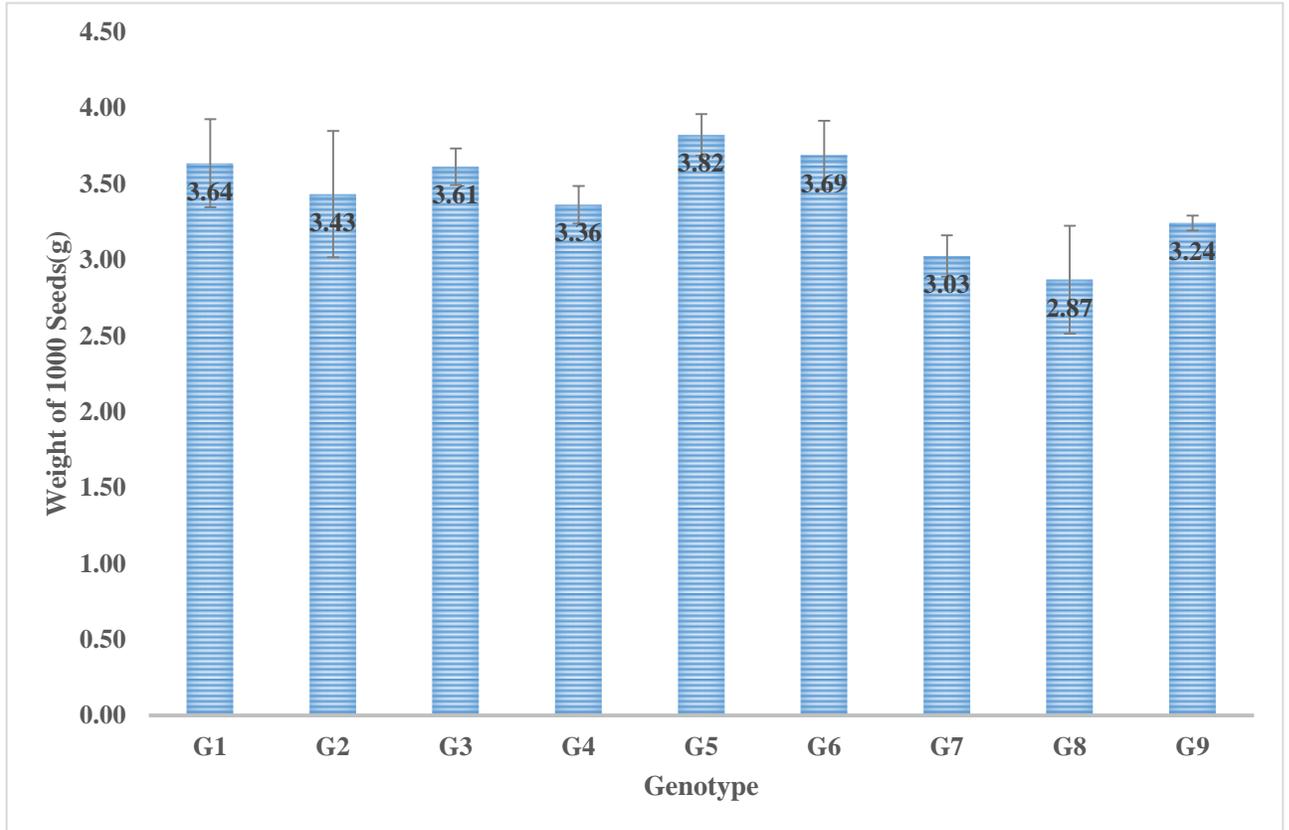


Fig.12 Thousand seeds weight of nine advanced populations of *Brassica rapa* L.

4.1.12 Seed yield / m²

The performance of the advanced populations exhibited highly significant variations (1.83**) for the trait seed yield/ m² (Table 3). Highest yield performance was observed in G₅ (244.38 g/m²) followed by G₂ (234.31 g/m²) and G₆ (231.68 g/m²) whereas lowest yield was observed in G₇ (170.17 g/m²) followed by G₄ (187.09 g/m²). Mean value was 207.79 (Table 5). Mean performance of seed yield per plant in 9 advanced populations of *Brassica rapa* L. is shown in Figure 13 through bar graph.

There was a difference between genotypic variance (0.45) and phenotypic variance (0.94) indicating the least environmental influence over the genotypes. Moderate estimates of PCV (15.37%) and GCV (10.61%) were marked for this character (Table 4).

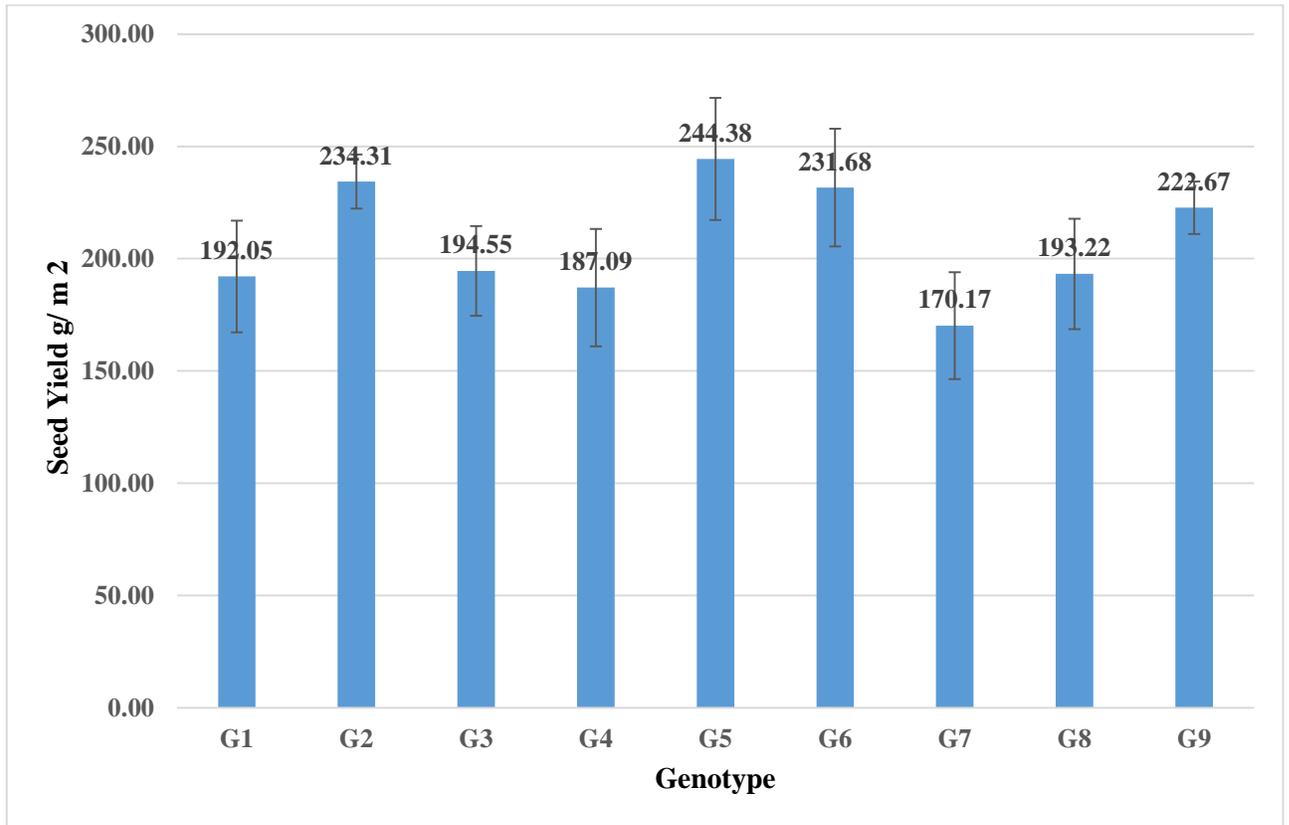


Fig. 13 Seed Yield / m² of nine advanced populations of *Brassica rapa* L

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. Heritability is the principal of transmissibility of characters and as such partition of the total variance into genetic and environmental components. Hence, heritability and genetic advance are essential parameters to study the scope of improvement in various characters via selection. To control traits with high heritability and genetic advance, additive genes are taken into consideration and phenotypic selection would thus be fruitful (Aytac and kinaci, 2009). Heritability, genetic advance and genetic advance in percent of means for yield and yield contributing characters of 9 advanced populations of *Brassica rapa* L. is presented in table 6.

Table 6. Heritability, genetic advance and genetic advance in percentage of means for yield and yield contributing characters of 9 advanced populations of *Brassica rapa* L.

Parameters	Heritability % in broad sense	Genetic Advance	Genetic advance in percentage of mean
DFE	66.36	3.24	11.43
DFFF	76.57	5.07	15.36
DEF	83.01	6.46	17.82
DM	93.18	12.00	14.03
PH	56.09	6.83	6.71
RH	53.48	0.86	11.17
PB	46.01	0.62	10.60
SB	95.95	1.88	204.06
TS	54.60	21.49	25.43
SL	54.07	0.57	11.13
SS	64.02	4.17	25.81
TSW	58.81	0.45	13.28
Y/m ²	47.62	0.95	15.08

DFE = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering;

DM = Days to Maturity; PH = Plant height; RL = Root length; PB = No. of primary branches;

SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;

SS = No. of Seed per siliqua; TSW = Thousand seed weight; SY = Seed Yield

4.2.1 Days to first flowering

High heritability (66.36%) in association with low genetic advance (3.24) and moderate genetic advance in percentage of mean (11.43) were noted for this character was inappropriate for advancement through direct selection due to prevalence of non-additive gene action (Table 6). Similar result was also reported by Sikarwar *et al.*, (2017).

4.2.2 Days to 50% flowering

High heritability (76.57%) with low genetic advance (5.07) and moderate (15.36) genetic advance in percentage of mean were observed for days to 50% flowering (Table 6). High heritability having low genetic advance suggested the prevalence of non-additive gene action and so, improvement through selection might not be so feasible. Afrin *et al.*, (2016) reported high heritability with low genetic advance and moderate genetic advance in percentage of mean for the trait. High heritability with low genetic advance and genetic advance in percentage of mean were also reported by Jahan *et al.* (2014) for the trait.

4.2.3 Days to 80% flowering

High heritability (83.01 %) with low genetic advance of (6.46) (Table 6) and moderate genetic advance in percentage of mean (17.82) were recorded (Table 6). High heritability with low genetic advance stated that the character was controlled by non-additive gene action and selection for such trait may not be effective during crop improvement.

4.2.4 Days to maturity

High heritability (93.18 %) with moderate genetic advance of (12.00) and moderate genetic advance in percentage of mean (14.03) were recorded (Table 6). High heritability with moderate genetic advance stated that the character was controlled by non-additive gene action and selection for such trait may not be effective during crop improvement. Environment was mainly responsible for high heritability (93.18%).

4.2.5 Plant height

Moderate heritability (56.09%), low genetic advance (6.83) along with low genetic advance in percentage mean (6.71%) were noted for this trait (Table 6). Moderate heritability with low genetic advance indicated that non-additive gene governs the character and selection of tallest plant may not be feasible.

4.2.6 Root length

Moderate heritability (53.48%) along with low genetic advance (0.86) and moderate genetic advance in percentage of mean (11.17%) were recorded indicating the presence of non-additive gene action which is responsible for the ineffectiveness of the selection for this trait (Table 6).

4.2.7 Number of primary branches per plant

Moderate heritability (46.01%) along with low genetic advance (0.62) and moderate genetic advance in percentage of mean were recorded (10.60%) indicating the presence of non-additive gene action which restricts the opportunity of betterment by direct selection. (Table 6).

4.2.8 Number of secondary branches per plant

High heritability (95.95) with low genetic advance (1.88) and very high genetic advance in percentage of mean (204.06) for the trait indicating the presence of non-additive gene effect which limits the opportunity of improvement through selection for this trait (Table 6). Afrin *et al*, (2016) reported high heritability and high genetic advance in percentage of mean whereas Akter (2016) reported high heritability with high genetic advance in percentage of mean for the trait.

4.2.9 Total number of siliquae per plant

Moderate heritability (54.60%) with high genetic advance (21.49) and high genetic advance in percentage of mean (25.43) were recorded for the character (Table 6). This showed the prevalence of non-additive gene effect in the inheritance of the trait and during crop improvement, there is a little opportunity of the plant breeders for direct selection.

4.2.10 Siliqua length (cm)

Moderate heritability (54.07%) low genetic advance (0.57) and moderate genetic advance in percentage of mean (11.13%) were noticed for this trait (Table 6) indicating the presence of non-additive gene action and selection may not be effective for further breeding program on the basis of the trait. A trait exhibiting high value of heritability did not basically produce high genetic advance. Afrin *et al*, (2016) reported moderate heritability, low genetic advance for siliqua length (cm)

4.2.11 Seeds per siliqua

High heritability (64.02) with low genetic advance (4.17) and high value of genetic advance in percentage of mean (25.81) were recorded for this trait (Table 6) indicating the presence of non-additive gene action and so selection was not recommended for future breeding program based on the trait. High heritability along with low genetic advance for seeds per siliqua was reported by Begum, (2015).

4.2.12 Thousand seeds weight

Moderate heritability (54.81%) in conjunction with low genetic advance (0.45) was noted for this trait and moderate genetic advance in percentage of mean (13.28%) was also observed (Table 6). High heritability with low genetic advance suggested that non-additive gene action governs the character. Thus, for crop improvement, selection may be ineffective for this trait. Begum, (2015) showed high heritability coupled with low genetic advance for this trait.

4.2.13 Seed yield /m²

High heritability (47.62%) combined to low genetic advance (0.95) and moderate genetic advance in percentage of mean (15.08%) were noted for this trait suggesting the presence of non-additive gene action which made the selection ineffective for the trait (Table 6). High heritability was revealed due to favorable environment. Shakera, (2014) reported high heritability with low genetic advance for this trait.

4.3 Correlation Coefficient

Understanding the interaction of characters among themselves and with the environment has been very useful in plant breeding because yield is the result of the combined effect of several component characters and the environment. Correlation studies, in conjunction with path analysis, provide a better understanding of the relationship between various characters and fruit yield. As a result, selection may be ineffective unless the other contributing factors influence the yield directly or indirectly. When selection pressure is applied to improve any character that is highly associated with yield, it affects a number of other correlated characters at the same time. Hence, knowledge about the association of character with yield and among themselves provides plant breeders with a guideline for making improvements through selection with a clear understanding of the contribution in terms of establishing the association by genetic and non-genetic factors (Dewey and Lu, 1959).

In most cases, the genotypic correlation coefficients (r_g) were greater than the phenotypic correlation coefficients (r_p), indicating a genetic basis for the association. While the phenotypic correlation coefficient was higher than the genotypic correlation coefficient, this indicated that the environment had a suppressing effect on the expression of the characters at the phenotypic level. The depicted of genotypic and phenotypic correlation coefficient among yield and yield contributing characters of *Brassica rapa* L are shown in Table 7 and Table 8.

Table 7. Genotypic correlation coefficient among yield and yield contributing characters of 9 advanced populations of *Brassica rapa* L

Characters	DFF	DFFF	DEF	DM	PH	RL	PB	SB	TS	SL	SS	TSW	SY
DFF													
DFFF	0.357												
DEF	0.438*	0.984**											
DM	0.832**	0.102	0.223										
PH	0.578**	0.713**	0.641**	0.009									
RL	0.583**	0.583**	0.625**	0.279	0.781**								
PB	0.074	0.644**	0.590**	0.032	0.174	0.067							
SB	-0.221	-0.040	0.025	0.168	-0.412*	-0.246	0.184						
TS	-0.374*	0.678**	0.628**	-0.142	-0.153	-0.330	0.803**	0.575**					
SL	0.097	-0.450*	-0.310	0.356	-0.852**	-0.372*	0.251	0.573**	0.226				
SS	0.079	0.363	0.285	-0.581**	0.677**	0.470*	0.424*	-0.511**	-0.093	-0.344			
TSW	-0.104	-0.486**	-0.412*	0.050	-0.626**	-0.491**	0.153	0.308	-0.160	0.239	-0.241		
SY	-0.364	-0.069	-0.100	-0.242	-0.377*	-0.872**	0.737**	0.442*	0.446*	0.575**	0.109	0.722**	

*At 5% level of significance

**At 1% level of significance

DFF = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering; DM = Days to Maturity; PH = Plant height;

RL = Root length; PB = No. of primary branches; SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;

SS = No. of Seed per siliqua; TSW = Thousand seed weight; SY = Seed Yield

Table 8 Phenotypic correlation coefficient among yield and yield contributing characters of 9 advanced populations of *Brassica rapa* L.

Characters	DFF	DFFF	DEF	DM	PH	RL	PB	SB	TS	SL	SS	TSW	SY
DFF													
DFFF	0.307												
DEF	0.370*	0.984**											
DM	0.696**	0.087	0.197										
PH	0.450*	0.484**	0.451*	0.021									
RL	0.376*	0.416*	0.453*	0.158	0.575**								
PB	0.129	0.297	0.292	0.075	0.132	0.123							
SB	-0.167	-0.069	-0.007	0.146	-0.362	-0.182	0.114						
TS	-0.264	0.369*	0.364	-0.123	-0.160	0.049	0.587**	0.431*					
SL	-0.007	-0.131	-0.073	0.284	-0.494**	-0.141	0.048	0.354	0.121				
SS	0.006	0.250	0.204	-0.525**	0.360	0.184	0.034	-0.366	-0.060	-0.097			
TSW	-0.221	-0.428*	-0.374*	0.075	-0.192	-0.237	0.113	0.193	0.033	0.195	-0.151		
SY	-0.077	-0.163	-0.166	-0.172	-0.300	-0.356	0.369*	0.387*	0.461*	0.202	0.165	0.396*	

*At 5% level of significance

**At 1% level of significance

DFF = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering; DM = Days to Maturity; PH = Plant height;

RL = Root length; PB = No. of primary branches; SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;

SS = No. of Seed per siliqua; TSW = Thousand seed weight; SY = Seed Yield

4.3.1 Days to first flowering

Days to first flowering exhibited highly significant and positive correlation with days to 80% flowering ($r_g=0.438$, $r_p=0.370$), days to maturity ($r_g=0.832$, $r_p=0.696$), plant height ($r_g=0.578$, $r_p=0.450$) and root length ($r_g=0.583$, $r_p=0.376$) pointing out a possible increase in days to 80% flowering, days to maturity, plant height and root length by increasing days to first flowering. It showed non-significant and positive correlation with days to 50% flowering ($r_g = 0.357$, $r_p = 0.307$), number of primary branches per plant ($r_g=0.074$, $r_p=0.129$), siliqua length (cm) ($r_g=0.097$) and seeds per silique ($r_g=0.079$, $r_p=0.006$) indicating very little contribution of this trait toward the increase in days to 50% flowering, number of primary branches per plant, siliqua length (cm) and seeds per silique. Correlation of days to first flowering with total siliquae ($r_g = -0.374$) was significant but negative indicating a possible increase in total siliquae by decreasing days to first flowering. It also showed non-significant and negative correlation with number of secondary branches per plant ($r_g= -0.221$, $r_p= -0.167$), total siliquae ($r_p= -0.264$), siliqua length ($r_p= -0.007$), thousand seeds weight ($r_g= -0.104$, $r_p= -0.221$) and yield per plant ($r_g= -0.364$, $r_p= -0.077$). Non-significant association of these traits revealed that the combination between these traits was largely influenced by environmental factors.

4.3.2 Days to 50% flowering

Correlation of days to 50% flowering was highly significant and positive with days to 80% flowering ($r_g=0.984$, $r_p=0.984$), plant height ($r_g=0.713$, $r_p=0.484$), root length ($r_g=0.583$, $r_p=0.416$), number of primary branches per plant ($r_g=0.644$) and total siliquae ($r_g=0.678$, $r_p=0.369$) pointing out a possible increase in days to 80% flowering, root length, number of primary branches per plant and total siliquae by increasing days to 50% flowering. It exhibited non-significant and positive correlation with days to maturity ($r_g=0.102$, $r_p=0.087$), number of primary branches per plant ($r_p=0.297$) and seeds per silique ($r_g=0.363$, $r_p=0.250$) showing very little contribution of this trait toward the increase in days to maturity, number of primary branches per plant and seeds per silique. Significant and negative correlation was observed with siliqua length ($r_g= -0.450$) and thousand seeds weight ($r_g= -0.486$, $r_p= -0.428$) indicating a possible decrease in siliqua length (cm) and thousand seeds weight ($r_g= -0.486$, $r_p= -0.428$) by increasing days to 50% flowering. Mili, (2014) reported that days to 50% flowering had

significant and negative interaction with yield per plant. Association of days to 50% flowering with number of secondary branches per plant ($r_g = -0.040$, $r_p = -0.063$), siliqua length (cm) ($r_p = -0.131$) and yield per plant ($r_g = -0.069$, $r_p = -0.163$) was non-significant and negative. Non-significant association of these traits suggested that the interrelationship between these traits was largely influenced by environmental factors.

4.3.3 Days to 80% flowering

Correlation of days to 80% flowering was highly significant and positive with plant height ($r_g = 0.641$, $r_p = 0.451$), root length ($r_g = 0.625$, $r_p = 0.453$), number of primary branches per plant ($r_g = 0.453$, $r_p = 0.590$) and total siliquae ($r_g = 0.628$) pointing out a possible increase in plant height, root length, number of primary branches per plant and total siliquae by increasing days to 80% flowering. It exhibited non-significant and positive correlation with days to maturity ($r_g = 0.223$, $r_p = 0.197$), number of primary branches per plant ($r_p = 0.292$), number of secondary branches per plant ($r_g = 0.025$), total siliquae ($r_p = 0.364$) and seeds per siliqua ($r_g = 0.285$, $r_p = 0.204$) showing very little contribution of this trait toward the increase in days to maturity, number of primary branches per plant, number of secondary branches per plant, total siliquae and seeds per siliqua. Significant and negative correlation was observed with thousand seeds weight ($r_g = -0.412$, $r_p = -0.374$) indicating a possible decrease in thousand seeds weight by increasing days to 80% flowering. Association of days to 80% flowering with number of secondary branches per plant ($r_p = -0.007$), siliqua length ($r_g = -0.310$, $r_p = -0.073$) and yield per plant ($r_g = -0.100$, $r_p = -0.166$) was non-significant and negative. Non-significant association of these traits suggested that the interrelationship between these traits was largely influenced by environmental factors.

4.3.4 Days to maturity

Correlation of days to maturity with plant height ($r_g = 0.009$, $r_p = 0.021$), root length ($r_g = 0.279$, $r_p = 0.158$), number of primary branches per plant ($r_g = 0.032$, $r_p = 0.075$), number of secondary branches per plant ($r_g = 0.168$, $r_p = 0.146$), siliqua length ($r_g = 0.356$, $r_p = 0.284$) and thousand seeds weight ($r_g = 0.050$, $r_p = 0.075$) was non-significant but positive indicating very little contribution of this trait toward the increase in plant height, root length (cm), number of primary branches per plant, number of secondary branches per plant, siliqua length and thousand seeds weight. It showed non-significant and negative correlation with total siliquae ($r_g = -0.142$, $r_p = -0.123$)

and seed yield ($r_g = -0.242$, $r_p = -0.172$). Significant and negative correlation of days to maturity with was observed with seeds per silique ($r_g = -0.581$, $r_p = -0.525$) stating that when days to maturity decreases, seeds per silique increases.

4.3.5 Plant height

Plant height exhibited highly significant and positive interaction with root length ($r_g = 0.781$, $r_p = 0.575$) and seeds per silique ($r_g = 0.677$) enunciating that increasing plant height results in an increase in root length and seeds per silique. Correlation of plant height with number of primary branches per plant ($r_g = 0.174$, $r_p = 0.132$) and seeds per silique ($r_p = 0.360$) was non-significant and positive revealed that this trait had a very little contribution toward the increase in number of primary branches per plant and seeds per silique. Association of plant height was significant but negative with siliqua length ($r_g = -0.852$, $r_p = -0.494$), thousand seeds weight ($r_g = -0.626$) and Seed yield ($r_g = -0.377$) indicating that a possible decrease of plant height increases siliqua length, thousand seeds weight and seed yield. Non-significant and negative correlation of plant height was observed with number of secondary branches per plant ($r_p = -0.362$), total siliquae ($r_g = -0.153$, $r_p = -0.160$), thousand seeds weight ($r_p = -0.192$) and seed yield ($r_p = -0.300$) indicated that environmental factors largely influenced on the association between these traits.

4.3.6 Root length

Significant and positive correlation of root length was observed with seeds per silique ($r_g = 0.470$) indicating a possible increase in root length causes an increase in seeds per silique. Association of root length with number of primary branches per plant ($r_g = 0.676$, $r_p = 0.123$), total siliquae ($r_p = 0.049$) and seeds per silique ($r_p = 0.184$) was non-significant and positive revealed that the trait showed a very little contribution toward the increase in number of primary branches per plant, total siliquae and seeds per silique. It also exhibited significant and negative correlation with siliqua length ($r_g = -0.372$), thousand seeds weight ($r_g = -0.491$) and seed yield ($r_g = -0.872$). Non-significant and negative correlation was also found with number of secondary branches per plant ($r_g = -0.246$, $r_p = -0.182$), total siliquae ($r_g = -0.330$), siliqua length ($r_p = -0.141$), thousand seeds weight ($r_p = -0.237$) and seed yield ($r_p = -0.356$) indicated that environmental factors largely influenced on the association between these traits.

4.3.7 Number of primary branches per plant

Correlation of number of primary branches per plant with total siliquae ($r_g=0.803$, $r_p=0.587$), seeds per silique ($r_g=0.424$) and yield per plant ($r_g=0.737$, $r_p=0.369$) was significant and positive pointing out a possible increase in total siliquae, seeds per silique and yield per plant by increasing number of primary branches per plant. 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 branching was an important contributor to increase seed yield. It also showed non-significant and positive correlation with number of secondary branches per plant ($r_g=0.184$, $r_p=0.114$), siliqua length ($r_g=0.251$, $r_p=0.048$), seeds per silique ($r_p=0.034$) and thousand seeds weight ($r_g=0.153$, $r_p=0.113$) indicating that it had a very little contribution toward the increase in number of secondary branches per plant siliqua length, seeds per silique and thousand seeds weight.

4.3.8 Number of secondary branches per plant

Highly significant and positive correlation of number of secondary branches per plant was observed with total siliquae ($r_g=0.575$, $r_p=0.431$), siliqua length ($r_g=0.573$) and seed yield ($r_g=0.442$, $r_p=0.387$) enunciating that the traits are less influenced by environment. Naznin *et al.*, (2015) reported that seed yield 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 exhibited non-significant and positive correlation with siliqua length ($r_p=0.354$) and thousand seeds weight ($r_g=0.308$, $r_p=0.193$) whereas significant and negative correlation was observed with seeds per silique ($r_g= -0.511$) indicating a possible increase in seeds per silique by decreasing number of secondary branches per plant. Naznin, (2013) found significant and positive correlation with yield while Akter, (2010) found negative correlation with the yield. It also shown non-significant and negative correlation with seeds per silique ($r_p= -0.366$).

4.3.9 Total number of siliqua per plant

Correlation of total siliquae with seed yield ($r_g=0.446$, $r_p=0.461$) was highly significant and positive expressing that when total siliquae increase, seed yield increases. Ara, (2010) reported that total siliquae had significant and positive effect on seed yield per plant. Naznin *et al.* (2015) also showed highly significant positive association of total siliqua with seed yield/plant. Rameeh, (2011) also confirmed the same finding. It also showed non-significant and positive correlation with siliqua length ($r_g= 0.226$, $r_p=0.121$) and thousand seeds weight ($r_p=0.033$) indicating that it had a very little contribution toward the increase in siliqua length and thousand seeds weight. Non-significant and negative correlation was observed with seeds per siliqua ($r_g= -0.093$, $r_p= -0.060$) and thousand seeds weight ($r_g= -0.160$).

4.3.10 Length of siliqua

Length of siliqua exhibited highly significant and positive correlation with seed yield ($r_g=0.575$) enunciating that a possible increase in length of siliqua increases seed yield. It also showed non-significant and positive correlation with thousand seeds weight ($r_g=0.239$, $r_p=0.195$) and yield per plant ($r_p=0.202$) stated that it had a very little contribution toward the increase of thousand seeds weight and seed yield. Non-significant and negative correlation was observed with seeds per siliqua ($r_g=-0.344$, $r_p=-0.097$).

4.3.11 Number of seeds per siliqua

Correlation of number of seeds per siliqua was non-significant and positive with yield per plant ($r_g=0.109$, $r_p=0.165$). It also exhibited non-significant and negative correlation with thousand seeds weight ($r_g=-0.241$, $r_p=-0.151$) indicating the influence of environmental factors on the association between these traits.

4.3.12 Thousand seed weight

Thousand seed weight exhibited highly significant and positive correlation with seed yield ($r_g=0.722$, $r_p=0.396$) at both genotypic and phenotypic level indicating that an increase in thousand seed weight tends to increase seed yield.

4.4 Path co-efficient analysis

Correlation analysis indicates the pattern of association between component traits and yield, but it does not provide cause and effect relationship. It was developed by Wright (1921) and demonstrated by Deway and Lu, (1959) that the path coefficient analysis technique facilitates the division of correlation coefficients into direct and indirect contributions of various characters on yield. A standardized partial regression coefficient analysis is used in this process. Thus, it measures the direct impact of one variable on another. A breeder would benefit greatly from such information if he or she could identify the important yield traits and use the genetic stock in a planned manner. In path coefficient analysis, the direct effect of a trait on yield of plant and its indirect effect through other characters were computed and the results are presented in Table 9.

Table 9. Partitioning of genotypic correlations into direct and indirect effects of important characters by path coefficient analysis of *Brassica rapa* L.

Character	DFE	DFFF	DEF	DM	PH	RH	PB	SB	TS	SL	SS	TSW	SY
DFE	1.458	0.521	-0.781	-0.673	-0.176	-0.315	-0.006	-0.068	-0.297	0.002	0.030	-0.059	-0.364
DFFF	0.520	1.461	-1.757	-0.083	-0.218	-0.315	-0.055	-0.012	0.538	-0.011	0.135	-0.274	-0.069
DEF	0.638	1.438	-1.785	-0.181	-0.196	-0.338	-0.050	0.008	0.498	-0.007	0.106	-0.232	-0.100
DM	1.213	0.149	-0.398	-0.809	-0.003	-0.151	-0.003	0.052	-0.112	0.008	-0.217	0.028	-0.242
PH	0.843	1.042	-1.144	-0.007	-0.305	-0.422	-0.015	-0.127	-0.122	-0.020	0.252	-0.352	-0.377*
RH	0.849	0.852	-1.116	-0.225	-0.238	-0.540	-0.006	-0.076	-0.261	-0.009	0.175	-0.276	-0.872**
PB	0.107	0.940	-1.054	-0.026	-0.053	-0.036	-0.085	0.057	0.637	0.006	0.158	0.086	0.737**
SB	-0.321	-0.058	-0.045	-0.136	0.126	0.133	-0.016	0.309	0.456	0.014	-0.190	0.173	0.442*
TS	-0.546	0.991	-1.121	0.114	0.047	0.178	-0.069	0.177	0.793	0.005	-0.035	-0.090	0.446*
SL	0.141	-0.657	0.553	-0.288	0.260	0.201	-0.021	0.177	0.180	0.024	-0.128	0.134	0.575**
SS	0.116	0.530	-0.508	0.470	-0.207	-0.254	-0.036	-0.158	-0.074	-0.008	0.373	-0.136	0.109
TSW	-0.152	-0.711	0.735	-0.040	0.191	0.265	-0.013	0.095	-0.127	0.006	-0.090	0.562	0.722**

Bold figures indicate direct effects; Residual effect 0.21

*At 5% level of significance

**At 1% level of significance

DFE = Days to first flowering; DFFF = Days to 50% flowering; DEF = Days to 80% flowering; DM = Days to Maturity; PH = Plant height;

RL = Root length; PB = No. of primary branches; SB= No. of secondary branches; TSP = Total No. of siliquae per plant; SL = Siliqua Length;

SS = No. of Seed per siliqua; TSW = Thousand seed weight; SY = Seed Yield

4.4.1 Days to first flowering

Path coefficient analysis revealed that days to first flowering had positive direct effect (1.458) on seed yield. The trait exhibited positive indirect effect on seed yield via days to fifty percent flowering (0.521), silique length (0.002), seeds per silique (0.030) followed by negative indirect effect via days to 80% flowering (-0.781), days to maturity (-0.673), plant height (-0.176), root length (-0.315), number of primary branches per plant (-0.006), number of secondary branches per plant (-0.068), total silique (-0.297), thousand seed weight (-0.059). Finally, the trait showed negative genotypic correlation with seed yield (-0.364) which was non-significant.

4.4.2 Days to 50% flowering

According to path coefficient analysis, days to 50% flowering exhibited direct positive effect (1.461) towards seed yield per plant. The trait showed positive indirect effect on yield per plant through days to first flowering (0.520), total siliquae (0.538) and seeds per silique (0.135) while negative indirect effect was found toward yield per plant via days to 80% flowering (-1.757), days to maturity (-0.083), plant height (-0.218), root length (-0.315), number of primary branches per plant (-0.055), number of secondary branches per plant (-0.012), silique length (-0.011) and thousand seeds weight (-0.274). Finally, the trait had non-significant and negative association with seed yield per plant that was pointed out by genotypic correlation of co-efficient (-0.069).

4.4.3 Days to 80% flowering

According to path coefficient analysis, days to 50% flowering exhibited direct positive effect (1.461) towards seed yield per plant. The trait showed positive indirect effect on yield per plant through days to first flowering (0.638), days to 50% flowering (1.438), number of secondary branches per plant (0.008), total siliquae (0.498) and seeds per silique (0.106) while negative indirect effect was found toward yield per plant via days to maturity (-0.181), plant height (-0.196), root length (-0.338), number of primary branches per plant (-0.050), silique length (-0.007) and thousand seeds weight (-0.232). Finally, the trait had non-significant and negative association with seed yield per plant that was pointed out by genotypic correlation of co-efficient (-0.100).

4.4.4 Days to 80% maturity

Days to 80% maturity had direct negative effect (-0.809) on seed yield per plant. It showed positive indirect effect on seed yield per plant through days to first flowering (1.213), days to 50% flowering (0.149), number of secondary branches per plant (0.052), siliqua length (cm)(0.008) and thousand seeds weight (0.028) whereas negative indirect effect via days to 80% flowering (-0.398), plant height (cm)(-0.003), root length (cm)(-0.151), number of primary branches per plant (-0.003), total siliquae (-0.112) and seeds per silique (-0.217). Finally, the trait had non-significant and negative genotypic association with seed yield per plant (-0.242).

4.4.5 Plant height

Plant height exhibited direct negative effect (-0.305) on seed yield per plant. Uddin *et al*, (2013) demonstrated that plant height had the negative direct effect on yield per plant whereas Shakera (2014) showed positive direct effect of plant height on yield per plant. Positive indirect effect of the character was observed on seed yield per plant via days to first flowering (0.843), days to 50% flowering (1.042) and seeds per silique (0.252) while indirect negative effect was found via days to 80% flowering (-1.144), days to maturity (-0.007), root length (-0.422), number of primary branches per plant (-0.015), number of secondary branches per plant (-0.127), total siliquae (-0.122), siliqua length (-0.020) and thousand seeds weight (-0.352). Finally, the trait showed significant negative genotypic association with seed yield per plant that was marked by genotypic correlation of coefficient (-0.377).

4.4.6 Root length

According to path coefficient analysis, root length exhibited negative direct effect (-0.540) on seed yield per plant. Besides, positive indirect effect of the character was seen on seed yield/ plant via days to first flowering (0.849), days to 50% flowering (0.852) and seeds per silique (0.175) while negative indirect effect on seed yield per plant via days to 80% flowering (-1.116), days to maturity (-0.225), plant height (-0.238), number of primary branches per plant (-0.006), number of secondary branches per plant (-0.076), total siliquae (-0.261), siliqua length (-0.009) and thousand seeds weight (-0.276). At last, the trait showed highly significant and negative genotypic association (-.872) with seed yield per plant.

4.4.7 Number of primary branches per plant

Through path coefficient analysis, it was discovered that number of primary branches per plant had negative direct effect (-0.085) on seed yield per plant. Moreover, positive indirect effect was exhibited on seed yield per plant through days to first flowering (0.107), days to 50% flowering (0.940), number of secondary branches per plant (0.057), total siliquae (0.637), siliqua length (0.006), seeds per silique (0.158) and thousand seeds weight (0.086) while negative indirect effect through days to 80% flowering (-1.054), days to maturity (-0.026), plant height (-0.053) and root length (-0.036). Eventually, the trait developed highly significant positive genotypic association with seed yield per plant that was marked by genotypic correlation of coefficient (.737). This result suggested that correlation between yield and this trait was caused by both direct and indirect effects through other component traits.

4.4.8 Number of secondary branches per plant

According to path coefficient analysis, positive direct effect (0.309) of number of secondary branches per plant was observed on 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. Besides, positive indirect effect was noticed in seed yield per plant via plant height (cm)(0.126), root length (0.133), total siliquae (0.456), siliqua length (0.014) and thousand seeds weight (0.173) whereas negative indirect effect via days to first flowering (-0.321), days to 50% flowering (-0.058), days to 80% flowering (-0.045), days to maturity (-0.136), number of primary branches per plant (-0.016) and seeds per silique (-0.190). In the end, the trait showed highly significant positive genotypic association with seed yield per plant that was marked by genotypic correlation of coefficient (.442). This result suggested that correlation between yield and this trait was owing both direct and indirect effects through other component traits.

4.4.9 Total number of siliquae per plant

Number of siliquae per plant exhibited positive direct effect (0.793) on seed yield per plant through path coefficient analysis. Besides this, positive indirect effect was noticed in seed yield per plant through days to 50% flowering (0.991), plant height (0.047), root length (0.178), days to maturity (0.114), number of secondary branches per plant (0.177) and siliqua length (0.005) whereas negative indirect effect was found on days to first flowering (-0.546), days to 80% flowering (-1.121), number of primary branches per plant (-0.069), seeds per siliqua (-0.035) and thousand seeds weight (-0.090). At last, the trait showed significant and positive genotypic association with seed yield per plant that was marked by genotypic correlation of co-efficient (.446). This result suggested that correlation between yield and this trait was caused by both direct and indirect effects through other component traits.

4.4.10 Length of siliqua

Through path coefficient analysis, length of siliqua showed positive direct effect (0.024) on seed yield per plant. On the other hand, positive indirect effect was exhibited in seed yield per plant via days to first flowering (0.141), days to 80% flowering (0.553), plant height (0.260), root length (0.201), number of secondary branches per plant (0.177), total siliquae (0.180) and thousand seeds weight (0.134) followed by negative indirect effect via days to 50% flowering (-0.657), days to maturity (-0.288), number of primary branches per plant (-0.021) and seeds per siliqua (-0.128). In the end, the trait showed highly significant positive genotypic association with seed yield per plant that was marked by genotypic correlation of coefficient (.575). This result suggested that correlation between yield and this trait was caused by both direct and indirect effects through other component traits.

4.4.11 Number of seeds per siliqua

Number of seeds per siliqua had positive direct effect (0.373) on seed yield per plant. Besides, positive indirect effect was noticed in seed yield per plant through days to first flowering (0.116), days to 50% flowering (0.530) and days to maturity (0.470) whereas negative indirect effect was found via days to 80% flowering (-0.508), plant height (-0.207), root length (-0.254), number of primary branches per plant (-0.036), number of secondary branches per plant (-0.158), total siliquae (-0.074), siliqua length (-0.008) and thousand seeds weight (-0.136). Eventually, the trait showed non-significant and positive genotypic association (0.109) with seed yield per plant.

4.4.12 Thousand seed weight

Thousand seed weight had positive direct effect (0.562) on seed yield m^2 . Halder, (2013) observed that thousand seed weight had positive direct effect on seed yield/hectare. Moreover, positive indirect effect on yield per plant through days to 80% flowering (0.735), plant height (0.191), root length (0.265), number of secondary branches per plant (0.095) and siliqua length (0.006) followed by negative indirect effect via days to first flowering (-0.152), days to 50% flowering (-0.711), days to maturity (-0.040), number of primary branches per plant (-0.013), total siliquae (-0.127) and seeds per silique (-0.090) Eventually, the trait showed highly significant positive genotypic relationship (0.722) with seed yield per plant. As direct effect (0.562) is positive and higher than the genotypic correlation of co-efficient, it showed true relationship between them and direct selection for this trait will be recommended for the improvement of yield.

4.4.12 Residual effect

The residual effect (R) of path co-efficient analysis was noted as 0.21 which indicated that the characters under study contributed 79% to the seed yield m^2 . There are some other factors which contribute 21% to the seed yield m^2 . But those factors were not utilized in the present study which could have considerable effect on seed yield.

4.5 Selection

Our study's goals were to find a short-duration, high-yielding population of *Brassica rapa* L. that would work well in the Aman-Mustard-Boro cropping pattern. Mean performance was observed for the majority of the characters in nine advanced populations and three advanced populations G5 (BARI 6 x BARI 15, F₁₁, 75 days), G2 (BARI 9 x BARI 6, S₅F₁₇, Brown), and G6 (BARI 9 X BARI 6, S₅F₁₇, Yellow), were chosen from those populations based on variability and our objectives. Table 10 showed the selection of the most promising populations from different cross combinations of *Brassica rapa* L. based on mean performance:

Table 10. Selection of most promising populations from different cross combinations of *Brassica rapa* L. based on mean performance

Advanced populations	DM (No.)	SB (No.)	TSP (No.)	SL (cm)	SS (No.)	TSW (g)	SY (g/m²)
G5	76.33	0.20	71	4.95	20.28	3.82	244.38
G2	86.33	0.96	104.53	5.44	13.50	3.43	234.31
G6	82.33	2.47	109.93	5.62	16.28	3.69	231.68

DM = Days to Maturity; SB= No. of secondary branches; TSP = Total No. of siliquae per plant;
 SL = Siliqua Length; SS = No. of Seed per siliqua; TSW = Thousand seed weight; SY = Seed Yield

CHAPTER V

SUMMARY AND CONCLUSION

Summary

The current study was carried out to evaluate advanced populations of *Brassica rapa* L. in order to estimate the variability among the characters, namely heritability, genetic advance and genetic advance in percentage of mean, character association, and direct and indirect effect of different considerable traits on seed yield/ m² using nine promising advanced populations of *Brassica rapa* L. The experiment was carried out in the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, from November 2019 to March 2020.

The variability analysis in this study revealed that there were significant differences among all advanced populations of *Brassica rapa* L. for each individual trait. Among all the advanced populations, the highest days to first flowering was taken in G4 (31 days) and the minimum days to first flowering was taken in G7 (25 days). The minimum period for 50% flowering was noticed in G5 with 30.00 DAS whereas G8 took longest period for 50 % flowering with 40.00 DAS. The highest days to 80% flowering was recorded in G8 (44 DAS) whereas the minimum days to 80% flowering was recorded in G5 (32 DAS). The G5 required least number of days to mature (76.33 DAS) whereas maximum number of days for maturity was observed in the population G4 (92.33 DAS). The plant height was maximum in G8 (112.30) and minimum was observed in G2 (94.67). Maximum length of root was found in G8 (8.67) whereas minimum in G2 (6.47). Maximum number of primary branches per plant was obtained in G6 (6.33) and minimum number of primary branches per plant was found in G7 (4.97). Maximum number of secondary branches per plant was found in G6 (2.57) whereas G8 (0.00) having lowest number of secondary branches per plant followed by G4 (0.13). The highest total siliquae were noticed in population G6 (109.93) and the lowest in G4(62.97). Silique length was longer (5.74cm) in G4 while shorter in G8 (4.60 cm). The maximum seeds per siliqua was recorded in G8 (20.73). On the contrary, minimum number of seeds per siliqua exhibited in population G1 (13.31).

Maximum thousand seed weight was found in G5 (3.82 g) and the lowest thousand seeds weight was found in G8 (2.87 g). Highest yield performance was observed in G5 (244.38 g/m²) whereas lowest yield was observed in G7 (170.17 g/m²).

For all of the investigated characters, phenotypic variance was significantly greater than genotypic variance. The differences between genotypic and phenotypic variances were minimal in days to first flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, silique length, thousand seeds weight and seed yield indicating a low environmental influence on them. Days to 50% flowering, days to 80% flowering and root length showed moderate difference between the phenotypic and genotypic variance indicating moderate influence of environment on them. The greatest differences between genotypic and phenotypic variances were found in plant height, total siliquae and seeds per siliqua, indicating that the environment has the most influence over the characters. For all of the studied characters, the phenotypic coefficient of variation was found to be greater than the genotypic coefficient of variation. Low genotypic and phenotypic coefficient of variations were found in days to first flowering, days to 50% flowering, days to maturity, plant height, root length, number of primary branches per plant, silique length and seeds per siliqua while days to 80% flowering, total siliquae, thousand seeds weight and seed yield showed moderate genotypic and phenotypic coefficient of variations and high genotypic and phenotypic coefficient of variations were found in number of secondary branches per plant.

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

Significant and positive genotypic and phenotypic correlation with seed yield was observed in days to number of primary branches per plant, number of secondary branches per plant, total siliquae and thousand seeds weight through the correlation coefficient analysis.

According to the path coefficient analysis, direct positive effect on seed yield was observed by days to first flowering, days to 50% flowering, number of secondary branches per plant, total silique, silique length, seeds per siliqua and thousand seed weight.

On the other hand, negative direct effect on seed yield was found by days to 80% flowering, days to maturity, plant height, root length and primary branches per plant.

Conclusion

Based on the variability and as per our objectives, three advanced populations such as G5 (BARI 6 x BARI 15, F₁₁, 75 days), G2 (BARI 9 x BARI 6, S₅F₁₇, Brown), and G6 (BARI 9 X BARI 6, S₅F₁₇, Yellow) were selected from the 9 advanced populations. Among all the populations, the highest seed yield (244.38 g/m²), short duration (76.33 days) and thousand seed weight (3.82g) was observed in G5 (BARI 6 x BARI 15, F₁₁, 75 days) followed by G2 (BARI 9 x BARI 6, S₅F₁₇, Yellow) and G6 (BARI 9 X BARI 6, S₅F₁₇, Yellow). Therefore, these genotypes may be considered as promising population to release as a variety for having high yield potential.

CHAPTER VI

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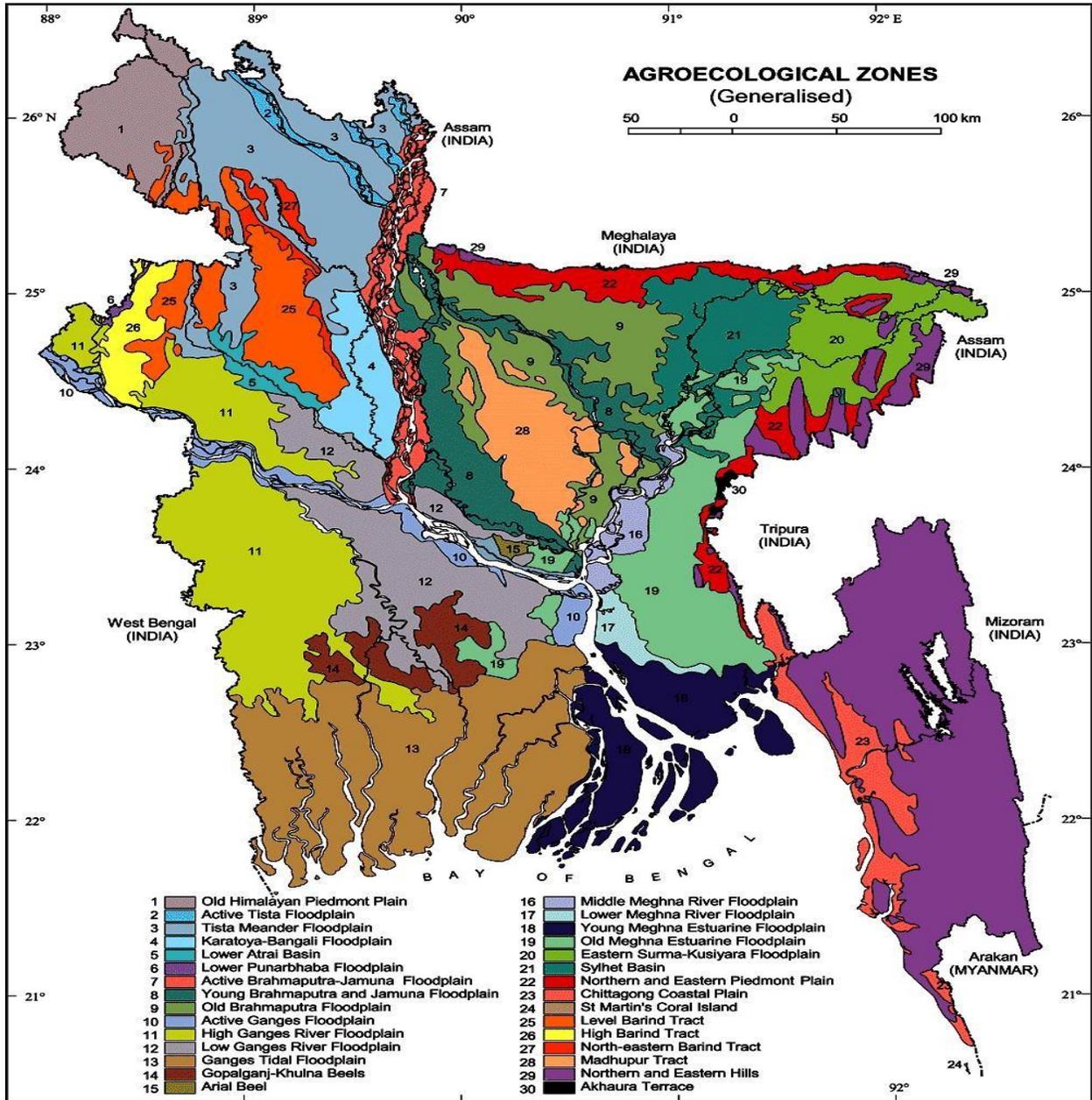
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CHAPTER VII

APPENDICES

Appendix I Map showing the experimental site under the study



Legend showing the research site (AEZ 28 Madhupur tract)

Appendix II Physical and chemical characteristics of soils of the experimental site

A. Physical composition of the soil:

Soil separates	Percentage (%)	Methods
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Textural class	Clay loam	Do

B. Chemical composition of the soil:

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

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

Appendix III Monthly Average temperature, RH, rainfall and sunshine of the experimental site during the period from November,2019 to February,2020.

Month	Air Temperature (⁰ C)		Relative humidity (%)	Total rainfall (mm)	Sunshine (hrs.)
	Minimum	Maximum			
November,2018	18	31	63	12.6	5.8
December, 2018	16	28	61	1.9	7.9
January, 2019	13.0	27	57	3.5	3.9
February, 2019	18	28	58	12.3	5.7

Source:

<https://www.timeanddate.com/weather/bangladesh/dhaka/climate>

Appendix IV The pictorial view of experimental field during seed sowing



Appendix V The pictorial view of experimental plot during Intercultural operations



Appendix VI The pictorial view of experimental plot during irrigation



Appendix VII The pictorial view of experimental plot during harvesting stage

