CHARACTER ASSOCIATION OF FIFTEEN ADVANCED POPULATIONS OF *Brassica rapa* BASED ON YIELD AND YIELD CONTRIBUTING CHARACTERS

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BY

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CERTIFICATE

This is to certify that thesis entitled, **"Character Association Of Fifteen Advanced Populations Of Brassica rapa Based On Yield And Yield Contributing Characters"** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE*** *in* ***GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by* ***Md. Azaharul Islam Arif****, Registration No.* ***18-09317*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2020
Place: Dhaka, Bangladesh

(Dr. Md. Harun-Ur-Rashid)
Supervisor

DEDICATED
TO
MY BELOVED
FAMILY

LISTS OF COMMONLY USED ABBREVIATIONS

Full word	**Abbreviation**
Agro Ecological Zone	AEZ
Analysis of variance	Anova
And others	et al.
At the rate	@
Bangladesh	BD
Bangladesh Agricultural Research Institute	BARI
Bangladesh Agricultural University	BAU
Bangladesh Institute of Nuclear Agriculture	BINA
Centimeter	cm
Degree	^0C
Co-efficient of variation	CV
Days after sowing	DAS
Degrees of Freedom	df
Environmental variance	σ_e^2
Et cetera	etc.
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genotypic Coefficient of variation	GCV
Genotypic correlation	r_g
Genotypic variance	σ_g^2
Gram	g
Heritability in broad sense	h^2b
Kilogram	Kg
Meter	m
Milliliter	mL
Mean sum of square	MS
Metric ton	MT
Muriate of Potash	MOP
Number	No.
Percent	(%)
Percentage of Coefficient of Variation	CV%
Phenotypic variance	σ_p^2
Phenotypic Coefficient of variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Species	*sp.*
Square meter	m^2
Standard error	SE
Triple Super Phosphate	TSP
Variety	Var.

Full word	**Abbreviation**
United States Department of Agriculture	USDA
Zinc Oxide	ZnO

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June, 2020 **The Author**

SAU, Dhaka

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ABSTRACT

A field study was conducted to evaluate fifteen advanced populations of *Brassica rapa* to estimate the magnitude of variation, heritability, genetic advance, correlation, and direct and indirect effect of different yield and yield contributing characters on seed yield of *B. rapa*. The experiment was executed following Randomized Complete Block Design (RCBD) with three replications at Sher-e-Bangla Agricultural University, Dhaka- 1207, from November 2018 to March 2019. Significant differences were exhibited among the existing genotypes for all traits used in this experiment. The phenotypic variance was higher than the genotypic variance for every character. The yield and yield contributing parameters such as days to first flowering, days to 50% flowering, days to maturity, 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 per plant showed least phenotypic and genotypic variance except for plant height and number of siliquae per plant. Days to first flowering, days to 50% flowering, days to maturity, and length of siliqua showed the low genotypic, and phenotypic coefficient of variation and number of primary branches per plant and number secondary branches per plant revealed the highest phenotypic and genotypic coefficient of variation. High heritability with low genetic advance and genetic advance in percentage of mean were found with days to first flowering, days to 50% flowering, days to maturity, the number of primary branches per plant and number of secondary branches per plant while moderate heritability with high genetic advance and genetic advance in the percentage of mean were seen in the number of siliquae per plant. However, the root length showed low heritability (15.86). Correlation coefficient analysis revealed that seed yield per plant had a significant positive association with days to maturity (r_g=0.540, r_p=0.356), plant height (r_g=0.517, r_p=0.394), number of siliquae per plant (r_g=0.395, r_p=0.372), length of silique (r_g=0.571, r_p=0.558), and thousand seed weight (r_g=0.823, r_p=0.584). Path analysis revealed both direct and indirect effects on seed yield and also check that seed yield per plant had a direct positive impact on days to first flowering, days to maturity, plant height, root length, number of secondary branches per plant, number of seeds per siliqua and thousand seed weight. The finding of the study, revealed that SAU 2 × BARI 6, F_7S_4, Yellow, BARI 9 × BARI 6, F_7, Yellow and SAU 1 × BARI 15, F_8, 75 days were performed best among the studied genotypes and selected as a potential candidate for varietal releasing a new mustard variety in Bangladesh.

CHAPTER I

INTRODUCTION

The species *Brassica rapa* L., generally called turnip mustard or field mustard, belongs to the Brassicaceae family (Naznin *et al*., 2015). It is a cross-pollinated vegetable and oil-seed crop in Bangladesh. The family consists of 372 genera and 4,060 accepted species (https://en.wikipedia.org/wiki/Brassicaceae). The seeds of *B. rapa* contain 42% oil and 25% protein (Kaul, 2006).

The genus *Brassica* has been categorized into three groups' viz-rape-seed, mustard and cole. The rape seed group includes the diploid *B. rapa*, turnip rape (AA, 2n=20) and amphidiploid *B. napus*, rape (AACC, 2n=38) while the mustard group includes species like *B. juncea* Czern and Coss (AABB, 2n=36), *B. nigra* Koch (BB, 2n=16) and *B. carinata* brown (BBCC, 2n=34) (Yarnell, 1956). In Bangladesh, approximately 70% of the total cultivated mustard is the variety of either *B. rapa or B. napus. B. rapa* shows earliness in flowering and maturity, the lower fiber content in the meal, low content of saturated fatty acid in oil, and fewer siliquae shattering of yellow seed. That's why it is more popular than *B. napus* (Akter, 2016).

Besides economic and commercial value, *Brassica* plays a vital role in daily diet. A chemical compound named Indole-3-Carbinol is found in *Brassica* vegetables, promoting DNA repair in cells and tissues and blocks the cancer tissue. Rapeseed and canola are considered as principal edible oil sources in Bangladesh. Rapeseed oil is required for cooking purpose and body massing, hairdressing, and various types of pickles preparation (Islam *et al*., 2015). It also has several medicinal values. It is considered a high energy food and a carrier for fat-soluble vitamins (A, D, E and K) in the body (Islam, 2016). Rapeseed provides essential fatty acids to the human body, such as linoleic acid and linolenic acid, and contains few saturated fatty acids among vegetable oils (Khan *et al*., 2009). Inadequate intake of fat and oil decreases the availability of' fat-soluble vitamins and caused dietary imbalance and food wastage (Akter, 2010). In a balanced diet, 20-25% of calories arrive from fats and oils, and the average demand of fats and oil is about 37 g/day (Rahman, 1981). It is an essential source of raw materials for industrial use i.e. making soaps, paints, hair oils, lubricants, textile auxiliaries pharmaceuticals, etc. (Naznin *et al*., 2015). For animal feeding and organic manures, oil cake is used (Islam *et al*., 2015).

Rapeseed caught the second position among the essential edible oil sources where soybean is in the first position (FAO, 2019). In 2018-19, the total area of rapeseed in the world was 36.51 million hectares (USDA, 2019). In 2018-19, the edible oil production from significant oilseed crops in the world was 571.94 million metric tons, where rapeseed contributed 71.94 million metric tons (USDA, 2019). About 7,87,025 acres of land was under rape and mustard cultivation during 2015-16 produced about 3,61,909 metric tons of seeds (BBS, 2017). But the production is deficient compared to the developed countries. The above scenario shows that producing high-yielding variety is direct ways to improve production. The primary research thrust in the improvement of oilseed *Brassica* involves developing types with early to medium early maturity, non-shattering ability, a shorter plant with more effective stem, a better harvesting index, responsiveness to good managing, resistance to diseases and pests, and enhance oil and meal quality.

In this context, fifteen advanced lines were produced through inter-varietal crosses. These lines were grown along with seven parental lines of mustard, and the performance was evaluated to find out varieties that may solve mustard's current problems. Thus the study was undertaken to find out the variability, select the desired plant type of early maturity, study the relationship between different traits and the direct and indirect contribution of each trait towards yield in the advanced lines of *B. rapa.* Keeping the above in view, the proposed study with the advanced population of *B. rapa*, was undertaken with the following objectives:

Objectives:

- To estimate correlation and path coefficient of different yield traits of *B. rapa* .
- To compare advanced lines for short duration and yield contributing characters.

CHAPTER II

REVIEW OF LITERATURE

B. species has achieved much importance by a large number of researchers on various aspects of its utilization and production. *B.* species is the most important oil crop in Bangladesh and many countries of the world too. Many studies on the variability, interrelationship, path co-efficient analysis, heritability and genetic advance have been done in many countries. The review of the literature concerning the studies presented under the following heads:

2.1 Genotypic and phenotypic variability

2.2 Heritability and genetic advance in B. sp.

2.3 Correlation analysis

2.4 Path co-efficient analysis

2.1 Genotypic and phenotypic variability:

For initiating a successful breeding program, genetic variability is a prerequisite to develop high yielding varieties. There are a good number of pieces of literature concerning the variability in the *B.* species. Some of those are discussed here.

Sikarwar *et al.* (2017) experimented with assessing the genetic variability in 21 diverse genotypes of yellow sarson (*B. rapa* Var. yellow sarson) for ten yield and its contributing characters. Analysis of variance for the design of the experiment showed highly significant differences for all the characters. High phenotypic co-efficient of variation (PCV) and genotypic coefficient of variation (GCV) were found for the number of secondary branches per plant followed by seed yield per plant, the number of primary branches per plant and number of siliqua on the main raceme. Days to flowering, plant height and length of siliqua showed low PCV and GCV.

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

An experiment was conducted by Afrin *et al.* (2016) to study variability among the fifteen F4 population considering different morphological attributes of B. rapa. The presence of highly significant variation was found among the genotypes for almost all of the characters studied.

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

Research work was carried out by Begum (2015) using 31 BC1 F_5 genotypes of B. napus to study the variability. The finding showed significantly variable genotypes for most of the characters. Comparatively, phenotypic variances were higher than the genotypic variances for most of the studied characters. The high GCV value was observed for the number of secondary branches, number of primary branches, number of siliqua per plant, thousand seed weight and seed yield per plant with broad base heritability.

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

Parveen *et al.* (2015) conducted an experiment to study on genetic variability using 15 rape seed genotypes. The result suggested that the phenotypic variance for all the characters was considerably greater than the genotypic variance indicating little influence of environmental factors on their expression

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

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

Shaukat *et al.* (2015) evaluated on eight *B. napus* genotypes to find out genetic variability. They reported highly significant differences among genotypes for primary branches per plant through analysis of variance.

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

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

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

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

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

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

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

A field experiment was conducted by Mili (2014) using 66 F_5 genotypes of *B. napus* L. to study the variability. For most of the characters, she observed significantly variable genotypes and higher phenotypic variances than the genotypic variances. For all of the studied characters, higher PCV was found than the GCV.

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

Abideen *et al*. (2013) studied with eight genotypes of *B. napus*. They observed highly significant variations among the genotypes for most of the traits studied. Simultaneously, non-significant differences were found among the genotypes in primary branches per plant and pods per plant.

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

Halder (2013) experimented with studying the variability in eleven advanced lines of *B. rapa*. She found significant variations among the genotypes for all the characters. The phenotypic variance was higher than the genotypic variance for every character. The difference between phenotypic and genotypic variance was minimum in the number of primary branches per plant, length of siliqua, thousand seed weight, seeds per silique, days to 50% flowering and days to 80% flowering.

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

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

Rameeh (2013) studied on twenty-four rapeseed genotypes, including two cultivars and 22 advanced lines based on randomized complete block design with three replications. There were significant genetic differences among the genotypes.

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

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

Alam (2010) executed an experiment by using twenty-six F_4 populations of some inter-varietal crosses of *B. rapa* to study the variation among them. Significant variations were noticed in the number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, days to 50% flowering, length of siliqua, number of seeds per siliqua, 1000 seed weight and least difference between genotypic and phenotypic variances were observed for yield per plant. Plant height, length of siliqua, number of siliqua per plant, days to 50% flowering exhibited low genotypic and phenotypic coefficient of variation.

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

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

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

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

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

To determine the variation in 15 rapeseed cultivars, Baradaran *et al*. (2007) showed Iran's field studies results. The variance analysis showed significant differences between yield and number of siliqua per plant, harvest index, and oil percent. They noticed an essential high PCV and GCV for the number siliqua per plant and 1000 seed weight.

An experiment was conducted by Dash *et al*. (2007) on fifty genotypes of toria, fourteen characters were included in an investigation to estimate genetic variability in toria (*B.*

rapa L. var. toria). Analysis of variance showed considerable variability among 50 toria genotypes for all the fourteen characters under study. PCV was greater than GCV for all the characters. High estimates of GCV and PCV were found in case of secondary branches per plant and leaf area index reflected.

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

A research work was performed by Rashid (2007) to study the variability of forty oleiferous *B.* species. He observed significant variation among the tested genotypes. High GCV value was noticed for days to 50% flowering, days to maturity, plant height and number of siliquae per plant.

2.2 Heritability and genetic advance:

Sikarwar *et al*. (2017) experimented with heritability and genetic advance in 21 diverse genotypes of yellow sarson (*B. rapa* Var. yellow sarson) for ten yield and its contributing characters. Higher estimates of broad-sense heritability were observed for all the characters. High heritability and high genetic advance were noticed for the number of secondary branches per plant, seed yield per plant, length of the main raceme, number of siliqua on the main raceme, number of seeds per siliqua and number of primary branches per plant. High heritability with the moderate genetic advance in the length of siliqua and thousand seed weight whereas, High heritability and the low genetic advance were observed for days to flowering and plant height.

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

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

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

Nazneen *et al*. (2015) experimented with evaluating on thirty-three genotypes of *B. rapa* L. and revealed that the number of siliquae/plant, number of secondary branches/plant and number of primary branches/plant showed high heritability coupled with the high genetic advance in percent of the mean.

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

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

Siddika (2015) executed an experiment on *B. napus* L. with 30 F_2 genotypes. High heritability and high genetic advance in the percentage of mean were exhibited in the number of primary branches per plant, the number of secondary branches per plant, no. of siliqua per plant, number of seeds per siliqua.

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

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

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

An experiment was undertaken by Iqbal *et al*. (2014) using ten indigenous varieties with eight significant yield contributing characters of *B. rapa* in Pakistan. They showed the highest heritability in association with the higher genetic advance in plant height while the seeds per siliqua showed medium heritability and lowered genetic advance.

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

A field experiment was conducted by Mili (2014) using 66 F_5 genotypes of *B. napus* L. to study the heritability. High broad base heritability was observed in the number of secondary branches, thousand seed weight, number of primary branches, number of siliquae per plant and seed yield per plant

An experiment was undertaken by Shakera (2014) utilizing twenty F_3 and F_4 populations produced through inter-varietal crosses, with three check variety of *B. rapa* L. to study heritability and genetic advance and reported that high heritability coupled with low genetic advance and high genetic advance in the percentage of mean was observed in thousand seed weight and yield per plant.

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

Halder (2013) studied eleven advanced lines of *B. rapa*. High heritability and moderate genetic advance and genetic advance in mean percentage were found in days to 50% flowering and days to 80% flowering. In contrast, moderate heritability with high genetic advance and genetic advance in mean percentage was noticed in siliquae per plant and yield per hectare.

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

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

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

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

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

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

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

Saleh (2009) executed a field experiment by using twenty F_2 populations developed through inter-varietal crosses along with three check variety of *B. rapa* L. High heritability and low genetic advance and genetic advance in the percentage of mean were exhibited in days to maturity, length of siliqua, seeds per siliqua and thousand seed weight.

Sheikh *et al*. (2009) studied on the derivation of genetic variability in Ethiopian mustard (*B. carinata*) through interspecific hybridization for quality traits. The result indicated that inter-specific hybridization was utilized to develop the range of genetic variability in mustard for oil and meal quality traits from quality lines of *B. juncea*.

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

An experiment was performed by Hosen (2008) using five parental genotypes of *B. rapa* and their ten F3 progenies including reciprocals to estimate heritability and reported that plant height, days to 50% flowering and number of siliquae per plant exhibited high heritability with high genetic advance and genetic advance in percentage of the mean.

Jahan (2008) executed a field experiment with 10 F4 lines obtained through intervarietal crosses with eight released varieties of *B. rapa* L. to study heritability. High heritability associated with the low genetic advance in percent of mean was observed for days to maturity. On the other hand, plant height and days to 50% flowering showed high heritability coupled with the moderate genetic advance in percent of the mean.

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

An experiment was carried out by Dash *et al*. (2007) on fifty genotypes of toria. To estimate heritability, fourteen characters were included in the investigation. High estimates of broad-sense heritability with high genetic advance as per cent of mean was found for secondary branches per plant, leaf area index and specific leaf weight, reflecting the more significant contribution of the genetic component.

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

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

2.3 Correlation among different characters:

Research work was performed by Kumari *et al*. (2017) to study the correlation among thirteen quantitative and qualitative characters of forty-four genotypes of yellow sarson (*B. rapa* var. yellow sarson). Seed yield per plant exhibited a significant and positive correlation with biological yield. In contrast, the positive but non-significant correlation with siliqua length, harvest-index, seeds per siliqua, days to maturity, 1000-seed weight. In contrast, the non-significant negative correlation with plant height and primary branches per plant, significant and negative correlation coefficient of oil content was observed with siliqua on the main raceme. Oil content showed a negative and non-significant association with plant height length, length of the main raceme and primary branches per plant, while seeds per siliqua and days to 50 percent flowering showed a significant and positive correlation with oil content. 1000 seed weight exhibited a significant positive correlation with siliqua length and seed per siliqua.

Siddique *et al*. (2017) carried out research to estimate correlation using six genotypes of *B. campestris* L. Results revealed that genotype S-9 (check) surpassed all other genotypes for plant height. Correlation results were positively significant among plant stature with pods plant, height with a yield of a single plant, days to flower with seed index, days to flower with a yield of a single plant, pods per plant with seed index, pods per plant with single plant yield, seed index with single plant yield. The relationship between plant height and seeds per pod, branches per plant and ripeness days and pods per plant and seeds per pod was negative and significant.

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

Jamali *et al*. (2016) conducted a research work to study the correlation among yield and yield contributing traits in *B. compestris* L. using six Brassica varieties including three commercial varieties and three candidates selected from the available germplasm. A highly significant positive correlation was observed in plant height, days to 75% flowering, number of pods per plant and seed index vs seed yield per plant. A negative and significant correlation was found in plant height vs seeds per pod, branches per plant vs days to 90% maturity and pods per plant vs seeds per pod.

Begum (2015) experimented with 31 BC_1 F_5 genotypes of *B. napus* L. to study the correlation and found a significant positive correlation between seed yield per plant with the number of primary branches, number of secondary branches, number of siliquae per plant and thousand seed weight.

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

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

Parveen *et al*. (2015) experimented to determine the correlation between yield contributing traits using 15 rapeseed genotypes. The number of primary branches per plant showed a highly significant and positive association with the number of secondary branches per plant and yield per plant whereas days to 50% flowering showed a significant and positive association with seeds per siliqua, 1000 seed weight and yield per plant. Length of siliqua showed a highly significant positive association with siliquae per plant.

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

An experiment was conducted by Sultana (2015) by using sixty-two F_4 genotypes of B. napus L. to study the correlation. A significant positive correlation with seed yield per plant was found with almost all the characters except days to 50% flowering and days to maturity.

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

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

An experiment was conducted by Helal *et al*. (2014) to study the correlation of yield and yield contributing characters in rapeseed. Seed yield and yield contributing characters are correlated significantly and positively with the number of siliqua/plant, thousand seed weight, straw yield, plant height, biological yield and harvest index.

Hussain (2014) experimented with 24 genotypes, including four check varieties of *B. rapa* L. for estimating the character associations. The significant positive correlation was noticed in thousand seed weight, no. of siliquae per plant, no. of primary branches per plant with seed yield per plant.

Mili (2014) carried out research work using 66 F_5 genotypes of *B. napus* L. to study correlation and path coefficient analysis. The significant positive correlation was found in the number of siliquae per plant, siliqua length, number of seed per siliqua and thousand seed weight with seed yield per plant.

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

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

Abideen *et al*. (2013) evaluated on eight genotypes of *B. napus* and the result revealed that positive phenotypic correlation was observed in plant height, pod length and seed yield. A significant positive correlation was also exhibited in seed yield per plant and pods per plant.

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

An experiment using seven parental and twenty-one F_2 progenies of *B. rapa* was executed by Uddin *et al*. (2013) to study correlation among different yield component and revealed that yield per plant had a highly significant positive correlation with the number of primary branches per plant, the number of secondary branches per plant and siliqua per plant at both phenotypically and genotypically and significant positive correlation at genotypically in days to flowering and days to maturity.

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

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

Research work was done by Rameeh (2011) with 36 *B. napus* L. cultivars to determine the associations for yield components in these genotypes. Siliquae per plant was significantly and positively correlated with seed yield with a correlation value of 0.80.

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

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

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

Esmaeeli Azadgoleh *et al*. (2009) observed a significant positive correlation of seed yield with the number of pods per plant, number of pods in sub-branches and number of seeds per pod in *B. napus* L.

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

Basalma (2008) experimented with Ankara conditions utilizing 25 winter oilseed rape cultivars and found the highly positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height was found through correlation analysis during two years. Plant height showed a negative correlation with thousand seed weight, seed yield and oil ratio.

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

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

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

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

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

Kashyap and Mishra (2004) experimented with studying correlation among 11 morphological characters of *B. campestris* Var. Toria using 16 genetically diverse genotypes and reported that seed yield showed a significant and positive correlation with plant height, branches per plant, siliqua per plant, seeds per siliqua and 1000 seed weight. He observed that these characters were also significantly and positively correlated with each other, suggesting the opportunity for their simultaneous improvement through selection.

An experiment was executed by Ali *et al*. (2003) with 25 winter rapeseed and observed that positive flowering duration was significantly correlated with seed yield. Seed yield per plant was negatively and non-significantly correlated with days to maturity and branches per plant. These genotypes seed weight was positively and significantly correlated with harvest index, flower duration and seed yield.

Srivastava and Singh (2002) studied correlation in Indian mustard (*B. juncea* L. Czern and Coss) for ten characters in 24 strains of Indian mustard and two varieties. Findings revealed 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:

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

Kumari *et al*. (2017) studied on different character pairs of yellow sarson (*B. rapa* Var. Yellow Sarson). It was revealed that the path coefficient analysis of biological yield exerted maximum direct effect. In contrast, siliqua length and oil content showed a negative direct effect and days to 50% flowering exerted a negative indirect effect on seed yield.

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

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

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

Parveen *et al*. (2015) conducted an experiment using 15 rapeseed genotypes to determine the path coefficient. Path analysis showed that maximum positive direct effect was found in the case of 1000 seed weight and seeds per siliqua showed the maximum negative direct effect.

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

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

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

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

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

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

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

Tahira *et al*. (2011) experimented with ten wide genetic ranged varieties of *B. juncea* to study the characters relationship. The result reported that plant height and siliquae length exhibited a positive direct effect on seed yield per plant. In contrast, a positive indirect effect of primary branches per plant through plant height and seed per siliquae significantly affected seed yield per plant. Siliqua length contributed a negative indirect effect through plant height, seed per siliquae and thousand-grain weight.

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

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

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

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

Mahmud (2008) executed an experiment with fifty-eight genotypes of *B. rapa*. Path analysis revealed that yield per plant had the highest direct effect on the number of primary branches per plant, number of siliquae per plant, number of secondary branches per plant and number of seeds per siliqua.

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

Parveen (2007) experimented with the F_2 population of *B. rapa*. The path analysis found that the number of seeds per siliqua had the highest direct effect on yield per plant.

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

Kashyap and Mishra (2004) experimented with studying on 11 morphological characters of *B. campestris* Var. Toria using 16 genetically diverse genotypes through Path analysis and indicated that siliquae per plant showed the highest direct effect on seed yield. Other traits such as the number of branches per plant, seeds per siliqua and 1000-seed weight had a high positive effect on yield via other characters.

CHAPTER III

MATERIALS AND METHODS

The present research work was designated as "**Character association of fifteen advanced populations of *Brassica rapa* based on yield and yield contributing characters**'' was carried out in the experimental field of Sher-e-Bangla Agricultural University, Dhaka during Rabi season November 2018 to February 2019. The explicit information regarding the materials and methods of this experiment is discussed below:

3.1 Experimental site:

The experimental site location was located at 23^0 77' N latitude and 90^0 37' E longitudes with an elevation of 13.03 meters from the sea level (www.distancesfrom.com). Agro-ecological zone of "The Modhupur Tract", AEZ-28 (www.banglapedia.com) belongs the experimental field. Photograph showing experimental sites (Appendix I).

3.2 Soil and climate:

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

3.3 Experimental materials:

The Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, provided the healthy and vigorous seeds of fifteen advanced populations and seven parents of *B. rapa* were used as experimental materials. The materials used in the experiment are showed in Table 1 and Table 2.

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

Sl. NO.	**Advanced populations**	**Source**
1.	SAU 2 × BARI 15, F_7, 80 days	GEPB, SAU
2.	SAU 2 × BARI 6, F_6S_4,Yellow	GEPB, SAU
3.	TORI7 × BARI 15, F_6,Yellow	GEPB, SAU
4.	BARI 9 × BARI 6, S_5F_{15}, Brown	GEPB, SAU
5.	Yellow special, 80 days	GEPB, SAU
6.	SAU 1 × BARI 15, F_7, 80 days	GEPB, SAU
7.	SAU 1 × BARI 15, F_7, 75 days	GEPB, SAU
8.	BARI 9 × BARI 6, F_6, Yellow	GEPB, SAU
9.	SAU 1 × BARI 15, F_6E_3 Long	GEPB, SAU
10.	BARI 9 × BARI 6, F_6, Brown	GEPB, SAU
11.	BARI 15 × SS75, F_{10}, 75 days	GEPB, SAU
12.	TORI 7 × BARI 15, F_6, 85 days	GEPB, SAU
13.	BARI 6 × BARI 15, F_9,75 days	GEPB, SAU
14.	BARI 6 × BARI 15, F_6, 85 days	GEPB, SAU
15.	Yellow special, F_9, 75 days	GEPB, SAU

GEPB= Department of Genetics and Plant Breeding

SAU= Sher-e-Bangla Agricultural University

Table 2. Name of the parental lines used in the study:

Sl. NO.	**Parental lines**	**Source**
1.	Tori 7	GEPB, SAU
2.	SS-75	GEPB, SAU
3.	BARI 6	GEPB, SAU
4.	BARI 12	GEPB, SAU
5.	BARI 14	GEPB, SAU
6.	BARI 15	GEPB, SAU
7.	BARI 17	GEPB, SAU

3.4 Methods:

The following specific methods have been used to carry out the experiment:

3.4.1 Land preparation:

The experimental plot was organized by multiple ploughing and cross ploughing followed by laddering and harrowing with a tractor and power tiller to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and levelled properly. The pictorial view of the experimental field during land preparation is presented in plate 1.

Plate 1: The pictorial view of experimental field during land preparation

3.4.2 Application of manures and fertilizers:

At the recommended rate and proper time Urea, Triple Super Phosphate (TSP), Muriate of potash (MOP), Gypsum, Zinc oxide and Boric acid were applied to the field. The first half amount of urea the total amount of cow dung, TSP, MOP, Gypsum, Zinc Oxide and Boric acid were applied during final land preparation as a basal dose. The rest amount of urea was used as a top dressing after 25 days of sowing.

Table 3. List of fertilizers and manures with doses and procedures of application:

Sl. No.	Fertilizers/ manures	Dose		Procedures of application
		Applied in the plot	Quantity/ha	
1.	Cow dung	108 kg	5 ton	As basal
2.	Urea	5.4 kg	250 kg	50% basal and 50% at the time of flower initiation
3.	TSP	3.7 kg	170 kg	As basal
4.	MOP	1.6 kg	75 kg	As basal
5.	Gypsum	3.2 kg	150 kg	As basal
6.	ZnO	64.8 g	3 kg	As basal
7.	Boric acid	216 g	10 kg	As basal

3.4.3 Experimental design and layout:

After finalizing the land preparation, the field layout was done. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 18 m × 12 m = 216 m^2. Each replication size was 18 m × 3 m, and the distance between replication to replication was 1 m. The spacing between line to line was 30 cm, and plant to plant was 10 cm. The layout of the experimental design is presented in figure 1.

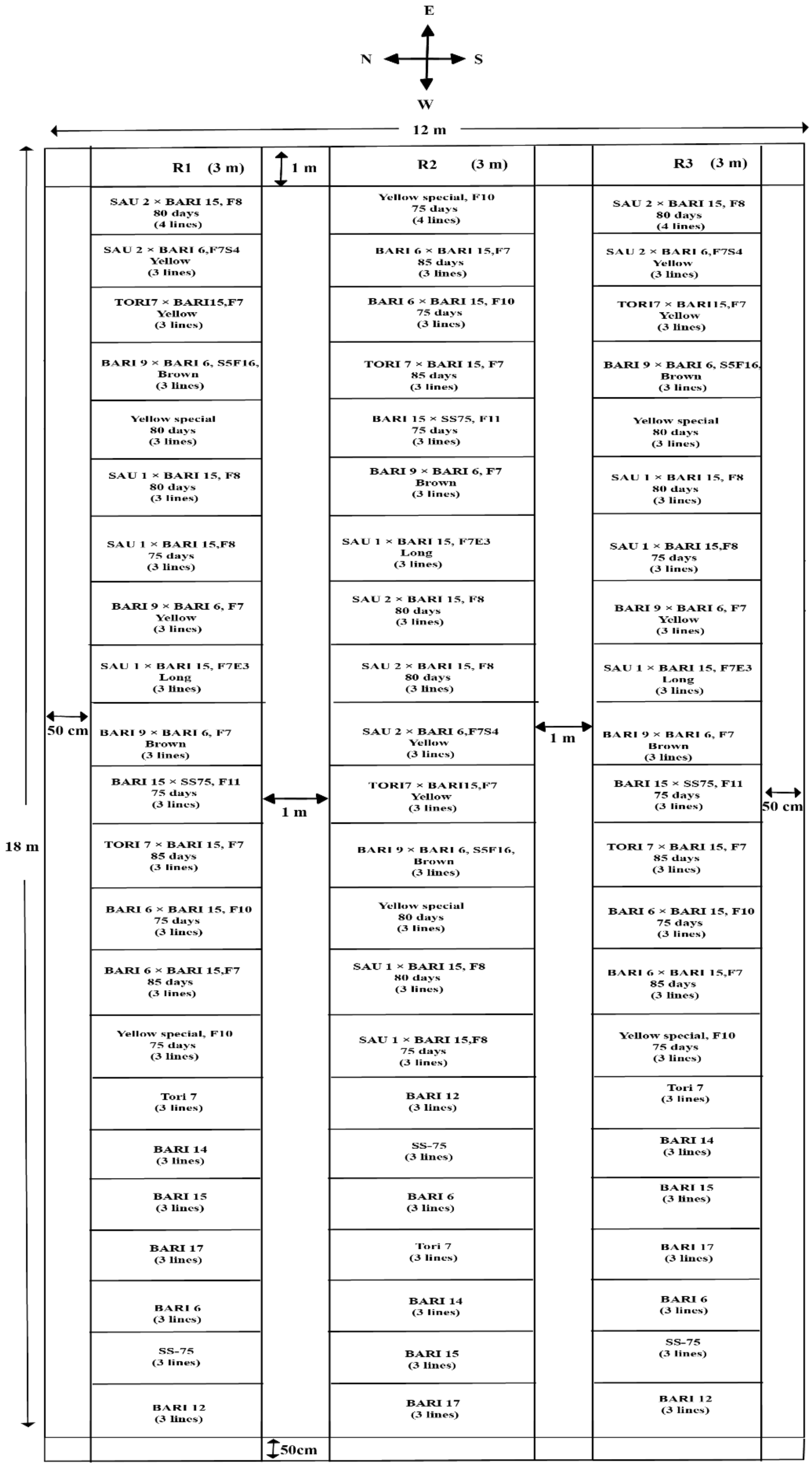

Figure 1. Layout of the experimental design

3.4.4 Seed selection and sowing:

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

3.4.5 Irrigation and drainage:

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

3.4.6 Intercultural operations, insect and disease control:

Various intercultural operations like thinning and weeding were done to ensure the plants average growth and development. After fifteen days of sowing, the first weeding was done. At a similar time, thinning was done for maintaining 30 cm from line to line and 10 cm from plant to plant. After twenty-five days of sowing, the second weeding was done. High dose of Metasystox-R 25EC@0.05% was used to reduce aphid infestation.

3.4.7 Crop harvesting:

Harvesting was done from 15th to 25th February 2019 based on maturity. When 80% of the plants exhibited maturity symptoms, i.e., the straw colour of siliquae, leaves, stems, desirable seed colour in the matured siliqua, the crop was assessed to attain maturity. Ten plants were selected for morphological analysis at random from the advanced populations in each replication. The plants were harvested by uprooting, and then they were appropriately tagged. Data were recorded on different parameters from these plants. A pictorial view of the experimental field at the growth stage, flowering stage and harvesting stage is presented in plate 2, 3, 4 respectively.

Plate 2: The pictorial view of experimental field during growth stage

Plate 3: The pictorial view of experimental field during flowering stage

Plate 4: The pictorial view of experimental field during harvesting period

3.4.8 Data collection:

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

3.4.9 Data collection methods:

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

3.4.9.1 Days to first flowering:

When the genotype of each row showed the 1st flower bloom, days to 1st flowering were counted. Counting should be started from the sowing date to the date of appearance of 1st flower bloom.

3.4.9.2 Days to 50% flowering:

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

3.4.9.3 Days to 80% maturity:

The data were recorded from the date of sowing to siliquae maturity of 80% plants of each entry.

3.4.9.4 Plant height (cm):

Measurement of plant height was done in centimeter (cm) which was starting from the base of the plant to the tip of the most elongate inflorescence. After harvesting, data of plant height was taken.

3.4.9.5 Root length (cm):

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

3.4.9.6 Number of primary branches per plant:

The total number of branches derived from the main stem of a plant was considered primary branches and the record was kept after counting.

3.4.9.7 Number of secondary branches per plant:

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

3.4.9.8 Number of siliquae per plant:

The total number of siliquae of each plant was enumerated and considered as the number of siliquae per plant.

3.4.9.9 Length of Siliqua (cm):

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

3.4.9.10 Number of seeds per siliqua:

All siliquae were collected from the sample plants, and five siliquae were selected randomly. The record was kept after counting the seeds from the siliquae.

3.4.9.11 Thousand seed weight (g):

Ten plants of each cross were selected. A thousand seeds from each entry were counted and weighed in grams

3.4.9.12 Seed yield per plant (g):

Seeds produced by a representative plant were weighted in gram and considered as the seed yield per plant.

3.4.10 Statistical analysis:

The data obtained for different traits were analyzed statistically by using Statistix 10 software (include web address) to find out the significance of the difference among the advanced populations of *B. rapa* . After evaluating all the characters' mean values, analysis of variance was performed by the F test. The significant differences among the treatments were estimated by the least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984). The genotypic and phenotypic variance was estimated by Johnson *et al.* (1955). Genotypic and phenotypic coefficient of variation were counted with Burton's (1952). Heritability in a broad sense was computed by using the procedure given by Singh and Chaudhary (1985). The genetic advance was measured by using the formula of Allard (1960) while the genetic advance in the percentage of mean was computed by Comstock and Robinson (1952). The genotypic and phenotypic correlation was obtained by Al-Jibouri *et al.* (1958). Path coefficient analysis was done by following the outlined method of Dewey and Lu (1959).

3.4.10.1 Analysis of variance:

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

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

Where, p = number of treatments (population)

r = number of replications

σ_r^2 = variance due to replications

σ_p^2 = variance due to treatments (population)

σ_e^2= variance due to error

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

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

Where, S. E = Standard error of mean

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

r = Number of replications

q = Number of population in each sub-block

u = Weightage factor computed

3.4.10.2 Estimation of Least Significant Differences (LSD):

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

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

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

3.4.10.3 Study of variability parameters:

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

3.4.10.3.1 Estimation of Genotypic variance and phenotypic variance:

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

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

Where,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

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

Where,

σ_p^2= Phenotypic variance

σ_g^2= Genotypic variance

σ_e^2 = Environmental variance = Mean square of error (MSE)

3.4.10.3.2 Estimation of genotypic and phenotypic coefficient of variation:

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

$$\text{GCV} = \frac{\sigma_g \times 100}{\bar{x}}$$

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

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

σ_g= Genotypic standard deviation

σ_p= Phenotypic standard deviation

$\bar{x}$ = Population mean

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

3.4.10.3.3 Estimation of heritability in broad sense:

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

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where, h_b^2=Heritability in broad sense

σ_g^2= Genotypic variance

σ_p^2= Phenotypic variance

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

Categories: Low: 0-30%

Moderate: 30-60%

High: >60%

3.4.10.3.4 Estimation of genetic advance:

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

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

Where,

GA = Genetic advance

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%)

3.4.10.3.5 Estimation of genetic advance in percentage of mean:

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

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

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

Categories:

Less than 10% - Low

10-20% -Moderate

More than 20% High

3.4.10.4 Correlation coefficient analysis:

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

$$r_{gxy} = \frac{\mathrm{Cov}_{gxy}}{\sqrt{\sigma^2_{gx}}.\sqrt{\sigma^2_{gy}}}$$

$$r_{pxy} = \frac{\mathrm{Cov}_{pxy}}{\sqrt{\sigma^2_{px}}.\sqrt{\sigma^2_{py}}}$$

Where,

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

$\mathrm{Cov}_{gxy}, \mathrm{Cov}_{pxy}$ are the genotypic and phenotypic covariance of x and y, respectively.

σ^2_{gx}= Genotypic variance of the trait x and σ^2_{gy} = Genotypic variance of the trait y.

σ^2_{px}= Phenotypic variance of the trait x and σ^2_{py}= Phenotypic variance of the trait y.

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

3.4.10.5 Path coefficient analysis:

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

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3} + \ldots\ldots\ldots\ldots\ldots\ldots.. + P_{yx11}.r_{x1x11}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3} + \ldots\ldots\ldots\ldots\ldots\ldots.. + P_{yx11}.r_{x2x11}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3} + \ldots\ldots\ldots\ldots + P_{yx11}.r_{x3x11}$

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

Where r's denoted simple correlation coefficient and P's indicate path coefficient (unknown).

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

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

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

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

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

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

Where,

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

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$

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

r_{iy}=Correlation of the character with yield

Categories:

Negligible (0.00 to 0.09);

Low (0.10 to 0.19);

Moderate (0.20 to 0.29);

High (0.30 to 1.0);

Very High (>1.00)

CHAPTER IV

RESULTS AND DISCUSSION

The present experiment was conducted regarding genotypic effects and comparative performance among fifteen advanced populations of *B. rapa* generated through inter-varietal crosses and their parent of *B. rapa* to determine the breeding values. The study was also conducted to determine the phenotypic and genotypic variability, coefficient of variation, heritability, genetic advance, correlation and path coefficient to estimate the direct and indirect effect of yield contributing traits on yield. The data were recorded on different characters such as days to first flowering, 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliquae per plant, no. of seeds per silique, silique length (cm), thousand seed weight (g), seed yield per plant (g). The data were statistically analyzed, and thus obtained results are described below under the following headings:

4.1 Mean performance of the populations and genetic variability;

4.2 Heritability, genetic advance and genetic advance in the percentage of the mean;

4.3 Correlation studies;

4.4 Path coefficient analysis; and

4.5 Selection.

4.1 Mean performance of the populations and genetic variability:

Analysis of variance for the experimental design pointed out significant differences for all the characters indicating that the presence of considerable genetic variation among the genotypes for all the traits (Appendix IV). The results are related to the analysis of variance (ANOVA), mean performance, genotypic, phenotypic, environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in a broad sense (h^2_b) and expected genetic advance in percent of the mean (GA) for all the traits. Among the genotypes, almost all characters showed highly significant variation indicating full scope for selection for these characters, i.e., the data revealed substantial variability and thus a high possibility of improvement in most of the traits. Out of the twelve traits studied, plant height, no. of primary branches per plant, no. of secondary branches per plant are considered as growth attributing characters. Days to 1^{st} flowering, days to 50% flowering and days to maturity were considered as earliness attributes. No. of siliquae per plant, length of siliqua, no. of seeds per siliqua and 1000 seed weight were regarded as reproductive traits. Seed yield per plant was the economic trait. Values of mean, range and CV (%) of characters of advanced populations of *B. rapa* are presented in appendix VI and VII. The present study's variability indicated that the potentiality of the materials generated through inter-varietal crosses, i.e., advanced populations for selecting desirable lines for releasing new varieties.

4.1.1 Days to first flowering:

Highly significant variations were observed for the character of days to first flowering at 1% level of significance for fifteen advanced populations (Appendix IV). This finding indicate that there was large genotypic difference among the populations. The minimum duration required for first flowering was found in BARI 9 × BARI 6, F_7, Yellow (27.33 DAS). Though earliest first flowering was seen in BARI 9 × BARI 6, F_7, Yellow, it matured later in 76 DAS. On the contrary, the maximum duration required for first flowering was noticed in BARI 6 × BARI 15, F_{10}, 75 days (34.6 DAS) which matured earlier in 78.67 DAS (Table 4). The mean value for days to first flowering was 30.66 DAS (Appendix VI). In case of parental lines, highly significant variations were observed among advanced populations for the character of days to first flowering (39.89 DAS) (Appendix V). On the contrary, the maximum duration required for first flowering was noticed in SS-75 (36.67 DAS) which matured in 97.33 DAS and minimum duration required for first flowering was found in TORI 7 (28 DAS) which matured in 84 DAS (Table 5). Average of 33.33 was recorded for the trait (Appendix VII).

The phenotypic variance (5.48) was slightly higher than the genotypic variance (3.52) for the advanced populations. The difference between phenotypic and genotypic variance was lower indicating that environment has little influence on the expression of this trait (Table 6). Generally, quantitative characters are highly influenced by the environment. The GCV and PCV were low with 6.12 and 7.63, respectively (Table 6). For the parental lines, the phenotypic variance (14.42) was slightly higher than genotypic variance (12.73) 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 moderate with 10.71 and 11.39 percent respectively (Table 7).

4.1.2 Days to 50% flowering:

Considerable variations were observed for the character of days to 50% flowering (20.18) for fifteen advanced populations. (Appendix IV). The minimum period for 50% flowering was noticed in BARI 9 × BARI 6, F_7, Yellow with 32.67 DAS. In contrast, BARI 6 × BARI 15, F_{10}, 75 days took the most prolonged period for 50% flowering with 41 DAS (Table 4). It was obtained on YSK-S501 × SS-2 in *B. rapa* by Singh *et al.* (2020). Mean value of 37.13 DAS was observed for the trait (Appendix VI). On the other hand, significant variations were observed for the character of days to 50% flowering (76.08) for parental lines (Appendix V). The minimum period for days to 50% flowering was noticed in Tori 7 with 34 DAS which is similar to BARI 9 × BARI 6, S_5F_{16}, Brown (34.67 DAS) and BARI 9 × BARI 6, F_7, Brown (34.00 DAS). The maximum period for days to 50% flowering was SS-75 with 46.33 DAS and BARI 9 × BARI 6, F_7, Yellow with 32.67 DAS which takes less time for days to 50% flowering than Tori 7 with 34 DAS (Table 5). Mean value (41.24 DAS) was recorded for the trait (Appendix VII).

The phenotypic variance (8.5) was higher than genotypic variance (5.84) and the difference between them was lower, indicating that environment has little influence for the expression of this trait. The GCV and PCV were low with 6.51 and 7.85, respectively and difference between them was lower indicating that there was less influence of environment on the expression of the character (Table 6). Sikarwar *et al.* (2017) reported that days to 50% flowering showed low PCV and GCV value. Phenotypic variance was recorded (33.97) which was higher than genotypic variance (28.68) for parental lines indicating that there is little influence in the expression genes for this trait. The value of GCV and PCV was very low 6.05 and 6.59 percent, respectively for days to 80% maturity (Table 7).

4.1.3 Days to maturity:

Days to maturity showed highly significant variations (61.53) for fifteen advanced populations at 1% level of significance, indicating that large variations are present among the tested genotypes (Appendix IV). The SAU 1 × BARI 15, F_8, 75 days and BARI 9 × BARI 6, F_7, Brown required minimum period of days to mature (75.00 DAS). In comparison, the maximum number of days for maturity was observed in the population SAU 2 × BARI 6, F_7S_4, Yellow (91.00 DAS) which gave the highest yield (7.84 g) among the genotypes (Table 4). It was observed in M-27 × Din-2 in *B. rapa* L. by Chowdhury *et al*. 2004. Mean value for days to maturity was recorded as 80.73 days (Appendix VI). In case of parental lines, days to maturity showed highly significant variations (61.53) at 1% level of significance (Appendix V). The BARI 14 required a minimum number of days to mature (81.00 DAS) which is similar to SAU 1 × BARI 15, F_7E_3 long. The maximum number of days to maturity was observed in SS-75 (97.33 DAS), which gave the highest yield (4.47 g) among the parental lines (Table 5). Moreover, the SAU 1 × BARI 15, F_8, 75 days and BARI 9 × BARI 6, F_7, Brown which takes less period for days to maturity than BARI 14 with 81 DAS. Average of 88.48 DAS was observed for the trait (Appendix VII). Mean performance of days to maturity in fifteen advanced populations of *B. rapa* with seven parental lines is presented in figure 4 through a bar graph.

The phenotypic variance was recorded (22.64) which was higher than genotypic variance (19.45) and the difference between them was lower indicating that there is little influence in the expression genes for this trait (Table 6). The value of GCV and PCV was very low 6.12 and 7.63, respectively for days to maturity and difference between GCV and PCV was lower indicating that there was less environmental effect on the expression of the character (Table 6). Naznin *et al*. (2015) showed low PCV (5.60) and GCV (5.29) for this trait. Phenotypic variance was recorded (33.97) which was higher than genotypic variance for parental lines (28.68) indicating that there is little influence in the expression genes for this trait. The value of GCV and PCV was very low 6.05 and 6.59 percent, respectively for days to maturity (Table 7).

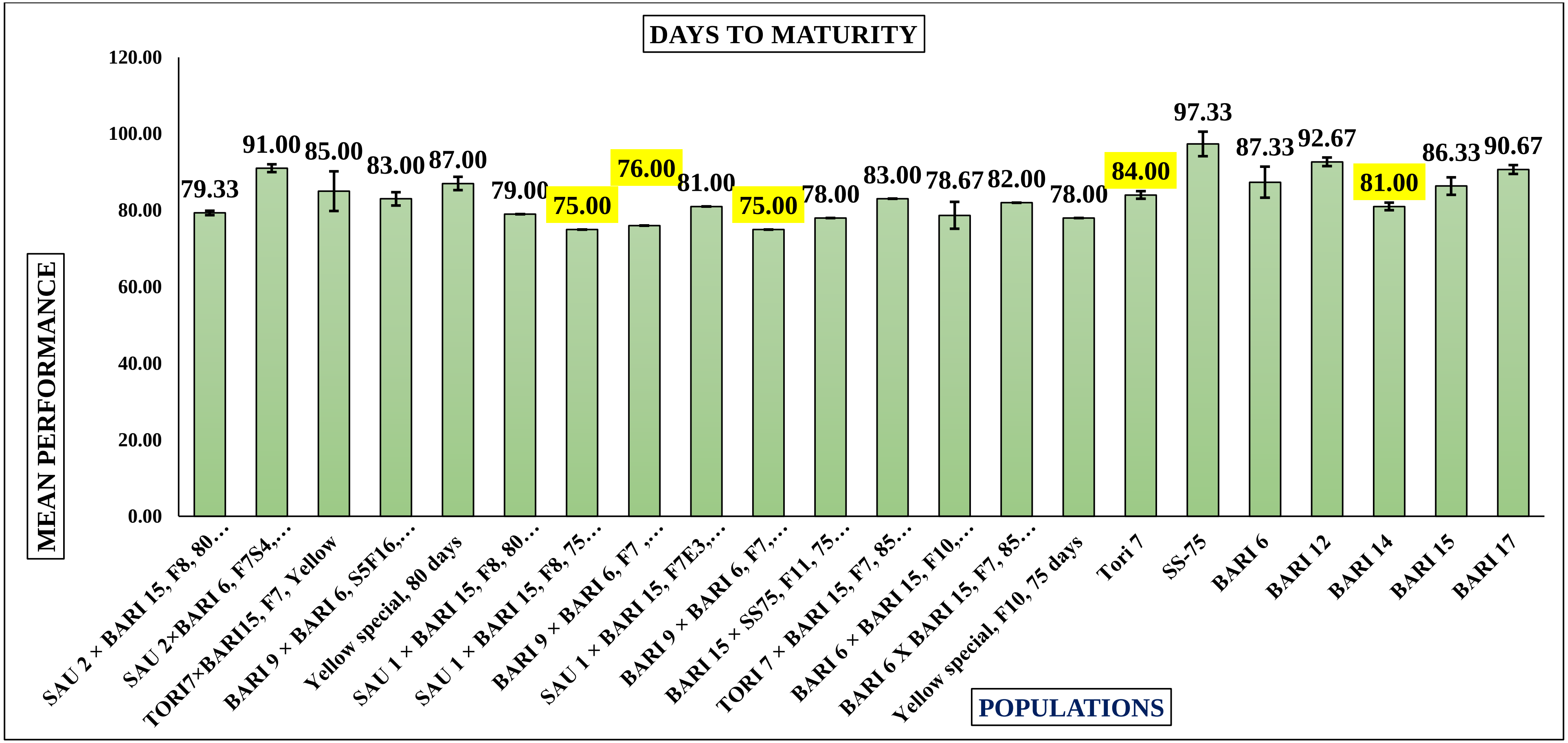

Figure 2. Mean performance of days to maturity of fifteen advanced populations of *Brassica rapa* with seven parental lines

4.1.4 Plant height (cm):

Highly significant variations (258.61) were observed for this trait at 1% level of significance, which indicates the presence of large variations among the tested genotypes (Appendix IV). The same findings were also reported by Ali *et al.* (2002) who showed significant differences for plant height. Plant height was found highest in TORI 7 × BARI 15, F_7, 85 days with (117.75 cm) and the lowest plant height was found in BARI 9 × BARI 6, S_5F_{16}, Brown (87.52 cm) (Table 4). Mean value was 104.43 for the trait (Appendix VI).

Plant height was also observed among the parental lines highest SS-75 with (113.87 cm) which was less than TORI 7 × BARI 15, F_7, 85 days with (117.75 cm). The lowest plant height was observed among the parental lines Tori 7 (88.64 cm) (Table 5). Mean value (97.45 cm) was observed for the trait (Appendix VII).

Phenotypic variance (118.42) was observed higher than genotypic variance (70.09) for plant height (Table 6). High environmental influence was found on the expression of the concerned trait due to higher difference between phenotypic and genotypic variance. Naznin *et al*. (2015) showed higher phenotypic variance (42.06) than the corresponding genotypic variance (29.87) in case of plant height indicated that there was a substantial environmental effect on this trait. Ara *et al.* (2010) also observed the same finding. The plant height exhibited low GCV and medium PCV of 8.02 and 10.42, respectively (Table 6). Jahan (2008) showed low GCV (5.73) and low PCV (8.19) for the trait. Phenotypic variance (110.33) was observed higher than genotypic variance (49.50) for parental lines indicating that high environmental influence on the expression of the concerned trait. Naznin *et al*. (2015) showed moderate phenotypic variance (42.06) than the corresponding genotypic variance (29.87) in case of plant height. Ara *et al.* (2010) also observed the same finding. The plant height exhibited low GCV and medium PCV of 7.22 and 10.78 per cent, respectively (Table 7).

4.1.5 Root length (cm):

Root length showed no significant differences in this character of fifteen advanced populations (2.63) (Appendix IV). The maximum length of the root was found in Yellow special, F_{10}, 75 days (13.38 cm) whereas minimum in BARI 9 × BARI 6, F_7, Brown (10.05 cm) (Table 4). Mean value was recorded as 11.66 for the trait. Among the parental lines, maximum root length was found in SS-75 (13.38 cm) which is similar to the Yellow special, F_{10}, 75 days whereas minimum in BARI 14 (9.08 cm) (Table 5) and mean value was 10.76 (Appendix VII).

Little difference was found between phenotypic variance (1.99) and genotypic variance (0.32) indicated that there was less influence of environment on the expression of the concerned character (Table 6). Low GCV and moderate PCV of 4.83 and 12.12 were observed respectively and the difference between them was higher indicating that there was the considerable influence of environment on the expression of the character (Table 6). Little difference between phenotypic variance (3.32) and genotypic variance (2.04) for parental lines indicated that there was less environment effect on this character. Moderate GCV and moderate PCV of 13.26 and 16.93 were observed, respectively (Table 7).

4.1.6 Number of primary branches per plant:

The number of primary branches per plant showed highly significant differences among the genotypes (3.86) at 1% level of significance for fifteen advanced populations (Appendix IV). The maximum number of primary branches per plant was noticed in SAU 2 × BARI 6, F_7S_4, Yellow with (8.10) and the minimum number of primary branches per plant were found in BARI 6 × BARI 15, F_{10}, 75 days with (4.10) (Table 4). Mean value was recorded as 5.15 for the trait (Appendix VI). It was similar to the finding reports of Rashid (2007), Mahmud (2008), Chaudhury *et al*. (2004). Among the parental lines number of primary branches per plant showed highly significant differences (0.83) at 1% level of significance (Appendix V). The maximum number of primary branches per plant was noticed in BARI 12 with (4.80) which is less than SAU 2 × BARI 6, F_7S_4, Yellow with (8.10) among the parental lines. The minimum number of primary branches per plant were found in BARI 17 with (3.40) (Table 4). Mean value was recorded as 4.22 for the trait (Appendix VII).

There was little difference between phenotypic variance (1.51) and genotypic variance (1.17) indicated that there was a less environmental effect on the expression of the character (Table 6). Naznin *et al.* (2015) showed the least differences between the phenotypic variance (1.27) and genotypic variance (0.86) in case of the number of primary branches which was similar to this finding. High GCV and high PCV of 21.03 and 23.89, respectively were observed for this trait, and the difference between them was lower indicating that there was little environmental influence on the expression of the character (Table 6). Akter (2010) reported high PCV (20.28) and low GCV (4.92) for the trait. There was little difference between phenotypic variance (0.45) and genotypic variance (0.19) for parental lines indicated that there was less influence of environment on this character. 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 which was similar to the findings. Moderate GCV and PCV of 10.33 and 15.90 percent were observed, respectively (Table 7).

4.1.7 Number of secondary branches per plant:

Highly significant variations were observed (3.17) for the number of secondary branches per plant at 1% level of significance suggesting that large variations are present among the fifteen advanced populations (Appendix IV). The maximum number of secondary branches per plant was found in BARI 9 × BARI 6, S_5F_{16}, Brown with (3.73) whereas BARI 6 × BARI 15, F_{10}, 75 days with (0.27) having the lowest number of secondary branches per plant. Mean value was recorded for the trait as 1.74 (Appendix VI). Highly significant variations were observed for the number of secondary branches per plant among the parental lines (Appendix V). The maximum number of secondary branches per plant was found in Tori 7 (6.13) which is a good sign for increasing the yield. Tori 7 (6.13) showed more number of secondary branches per plant. But it didn't show good performance in cross materials such as TORI 7×BARI 15, F_7, Yellow (.33) and TORI 7 × BARI 15, F_7, 85 days (1.27). Besides, BARI 15 and SS-75 having no number of secondary branches per plant (Table 5). Average of 1.98 was observed for the trait (Appendix VII).

The genotypic and phenotypic variance were recorded as 0.99 and 1.18 respectively, and the difference between them was lower indicating little environmental influence on the expression of the character (Table 6). High GCV and high PCV of 57.28 and 62.52 per cent were observed, respectively (Table 6) and difference between them was relatively lower indicated that the trait was least influenced by the environment. Sikarwar *et al*. (2017) reported that difference between PCV and GCV was relatively high for the trait. For parental lines, the genotypic and phenotypic variance was recorded as 4.35 and 4.59 respectively. High GCV and high PCV of 109.16 and 112.13 per cent were observed, respectively (Table 7). Sikarwar *et* al. (2017) reported High Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation for number of secondary branches per plant. Naznin *et al.* (2015) showed the same findings.

4.1.8 Length of siliqua (cm):

Highly significant variations were observed among the fifteen advanced populations for this trait (Appendix IV). Siliqua length (cm) was more prolonged (6.54 cm) in SAU 2 × BARI 6, F_7S_4, Yellow followed by SAU 1 × BARI 15, F_7E_3 Long (6.06 cm) while the shorter was found in BARI 9 × BARI 6, F_7, Brown with (5.20 cm) followed by SAU 1 × BARI 15, F_8, 75 days (5.44 cm) and TORI 7×BARI 15, F_7, Yellow (5.45 cm) (Table 4). Mean value of 5.69 cm was observed for the trait (Appendix VI). Highly significant variations were observed among the parental lines for this trait (Appendix V). The longer length of siliqua was (7.56 cm) in BARI 17 while shorter in BARI 15 (5.01 cm) (Table 5). Mean value of 5.85 cm was observed for the trait (Appendix VII). Mean performance of length of siliqua in fifteen advanced populations of *B. rapa* with seven parental lines is presented in figure 9 through a bar graph.

Phenotypic variance (0.17) was higher than genotypic variance (0.08) for the length of siliqua with little difference between them indicating that environment has the least influence for the expression of the trait (Table 6). Low GCV (4.97%) and PCV (7.25 %) values were found in the case of the length of siliqua (Table 6). There was a little difference in the estimates of GCV and PCV for the length of siliqua stated low environment effect in the expression of these traits. The same finding was also reported by Sikarwar *et al. (*2017). For parental lines, phenotypic variance (0.82) was higher than genotypic variance (0.74) for siliqua length with little difference between them indicating that environment has least influence for the expression of the trait. Moderate GCV (14.70%) and moderate PCV (15.48%) values were found in case of siliqua length. There was a little difference in the estimates of GCV and PCV for length of siliqua stated low environment effect in the expression of these traits. The same finding was also reported by Sikarwar *et al. (*2017).

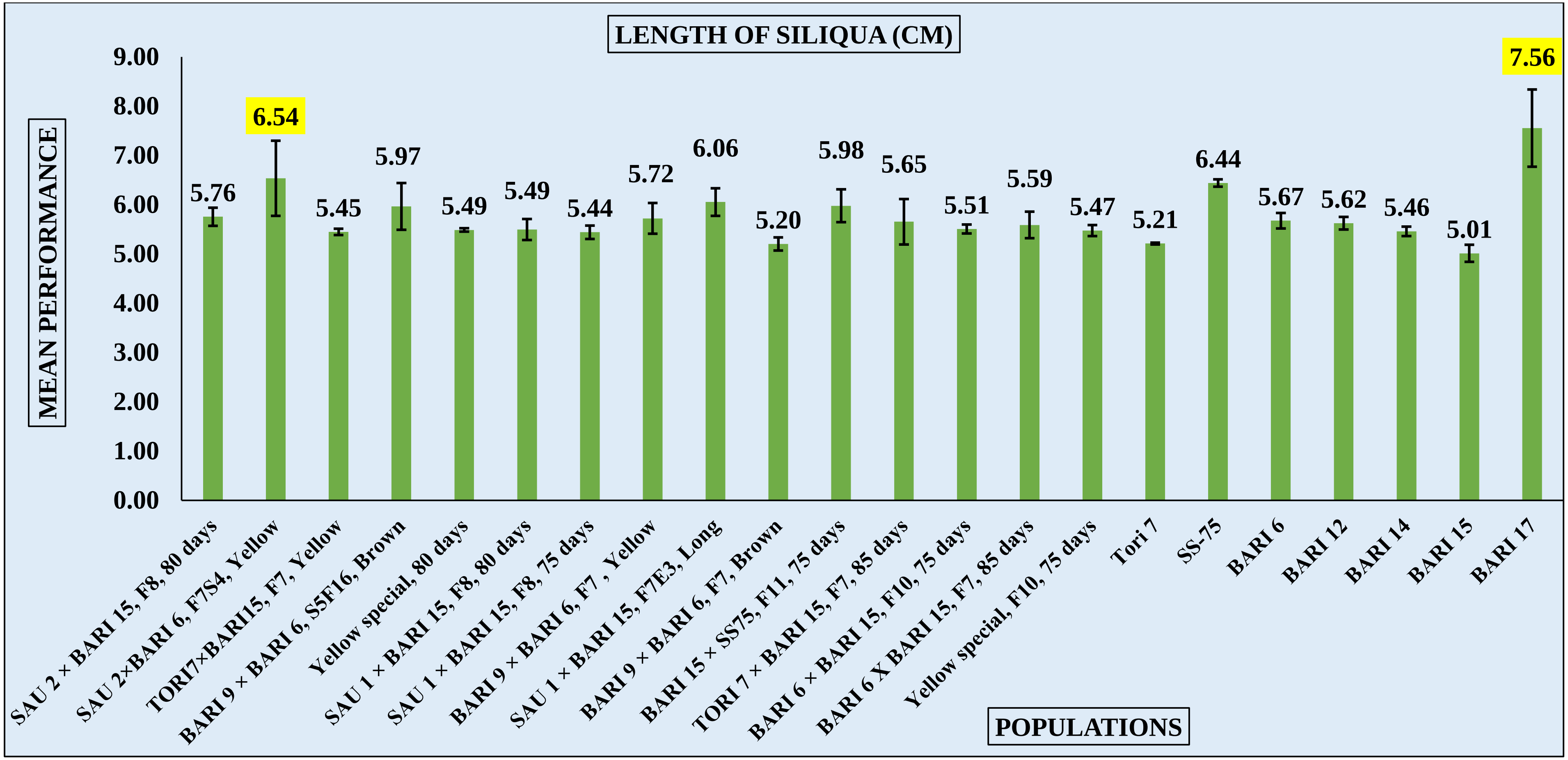

Figure 3. Mean performance of length of siliqua of fifteen advanced populations of *Brassica rapa* with seven parental lines

4.1.9 Number of siliquae per plant:

The number of siliquae per plant was highly significant (1408.31) statistically at 1% level of significance stated that highly significant variations were present among the fifteen advanced populations (Appendix IV). The highest number of siliquae per plant was noticed in population BARI 9 × BARI 6, F_7, Yellow with (168.47). The population TORI 7 × BARI 15, F_7, Yellow showed the lowest number of siliquae per plant (84.47) (Table 4). Average of 126.13 was observed for the trait (Appendix VI). The number of siliquae per plant was highly significant statistically at 1% level of significance stated that highly significant variations were present among the parental lines (Appendix V). The highest number of siliquae per plant was observed in Tori 7 (164) which is less than BARI 9 × BARI 6, F_7, Yellow with (168.47) cross material. The lowest number of siliquae per plant was observed in BARI 15 with (69.50) (Table 5). Mean value of 112.72 was observed for the trait (Appendix VII). Mean performance of the number of siliquae per plant in fifteen advanced populations of *B. rapa* with seven parental lines is presented in figure 10 through a bar graph.

The phenotypic variance (740.75) was higher than the genotypic variance (333.78) and the difference between them was higher (Table 6). This indicates that the environment has a significant influence on this character among the advanced populations. The higher phenotypic coefficient of variation (21.58%) and moderate genotypic coefficient of variation (14.49%) were observed for the trait and the difference between them was higher suggesting that there was the more significant influence of environment on the expression of the character (Table 6). Rashid (2007) reported high genotypic coefficient of variation for the number of siliquae per plant. The phenotypic variance (1496.07) was higher than genotypic variance (1177.42) for parental lines. This indicates less influence of environment on this character. The higher phenotypic coefficient of variation (34.30%) and genotypic coefficient of variation (30.43%) were observed (Table 7) indicating presence of less considerable variability among the populations.

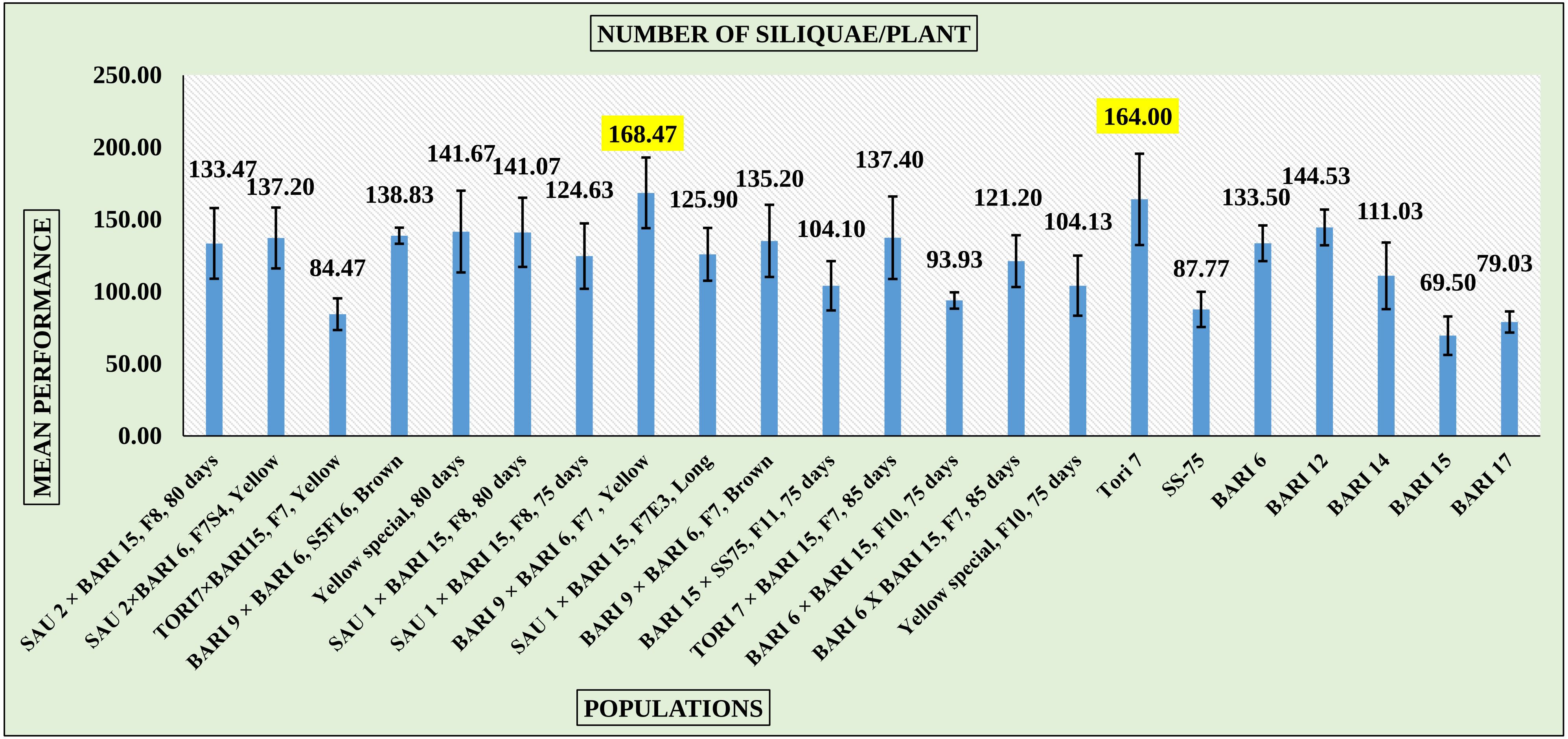

Figure 4. Mean performance of number of siliquae/plant of fifteen advanced populations of *Brassica rapa* with seven parental lines

4.1.10 Number of seeds per siliqua:

The number of seeds per siliqua showed highly significant variations at 1% level of significance, which indicates the presence of large variations among the fifteen advanced populations (Appendix IV). The maximum number of seeds per siliqua was recorded in BARI 6 × BARI 15, F_{10}, 75 days with (24.09) while the minimum number of seeds per siliqua exhibited in population BARI 9 × BARI 6, F_7, Yellow with (13.38) (Table 4). Mean value of 19.37 was found for the trait (Appendix VI). Among the parental lines, the number of seeds per siliqua showed highly significant variations at 1% level of significance (Appendix V). The maximum number of seeds per siliqua was recorded in BARI 17 (22.73) which was less than BARI 6 × BARI 15, F_{10}, 75 days with (24.09). The lowest number of seeds per siliqua exhibited in population BARI 14 with (14.28) (Table 5). Mean value of 17.34 was found for the trait (Appendix VII).

The phenotypic variance was (9.31) higher than genotypic variance was (3.83) with a higher difference between them, indicating that there was very much influence of environment on the character (Table 6). GCV and PCV values were moderate 10.10 and 15.75, respectively, and the difference between them was higher, indicating that there was a considerable influence of environment on the expression of the character (Table 6). Moderate value of the phenotypic coefficient of variation and genotypic coefficient of variation was found by Naznin *et al*. (2015) for number of seeds per siliqua. For parental lines, the phenotypic variance was (12.06) higher than genotypic variance was (9.22) indicating very little influence of environment on the character. Moderate GCV and high PCV values were 17.51 and 20.02 respectively (Table 7).

4.1.11 Thousand seed weight (g):

Thousand seed weight (g) showed significant variations at 5% level of significance among the fifteen advanced populations (Appendix IV). Maximum thousand seed weight (g) was found in SAU 2 × BARI 6, F_7S_4, Yellow (3.87 g) whereas minimum seed weight was recorded in BARI 9 × BARI 6, S_5F_{16}, Brown (2.10 g) (Table 4). Mean value of 2.74 was observed for the trait (Appendix VI). Thousand seed weight (g) showed highly significant variations among the parental lines (Appendix V). Maximum thousand seed weight was found in SS-75 (3.53 g) and minimum thousand seed weight was recorded in Tori 7 (1.72 g) (Table 5). SAU 2 × BARI 6, F_7S_4, Yellow with (3.87 g) was observed more thousand seed weight (g) than SS-75 with (3.53 g). Mean value of 2.34 was observed for the trait (Appendix VII). Mean performance of thousand seed weight (g) in fifteen advanced populations of *B. rapa* with seven parental lines is presented in figure 12 through a bar graph.

The phenotypic variance was higher (0.33) compared to genotypic variance (0.12) with a lower difference between them indicating less environmental effect for this trait (Table 6). Thousand seed weight showed higher PCV (20.97%), but moderate GCV (12.64%) and the difference between them was higher indicating that there was a large environmental effect on the expression of the character (Table 6). High PCV (21.53) and moderate GCV (19.94) were reported by Afrin *et al*. (2016) for thousand seed weight. Phenotypic variance was higher (0.46) compared to genotypic variance (0.42) for parental lines indicating less environmental effect for this trait. Thousand seed weight was found higher PCV (28.88%) and GCV (27.59%) (Table 7).

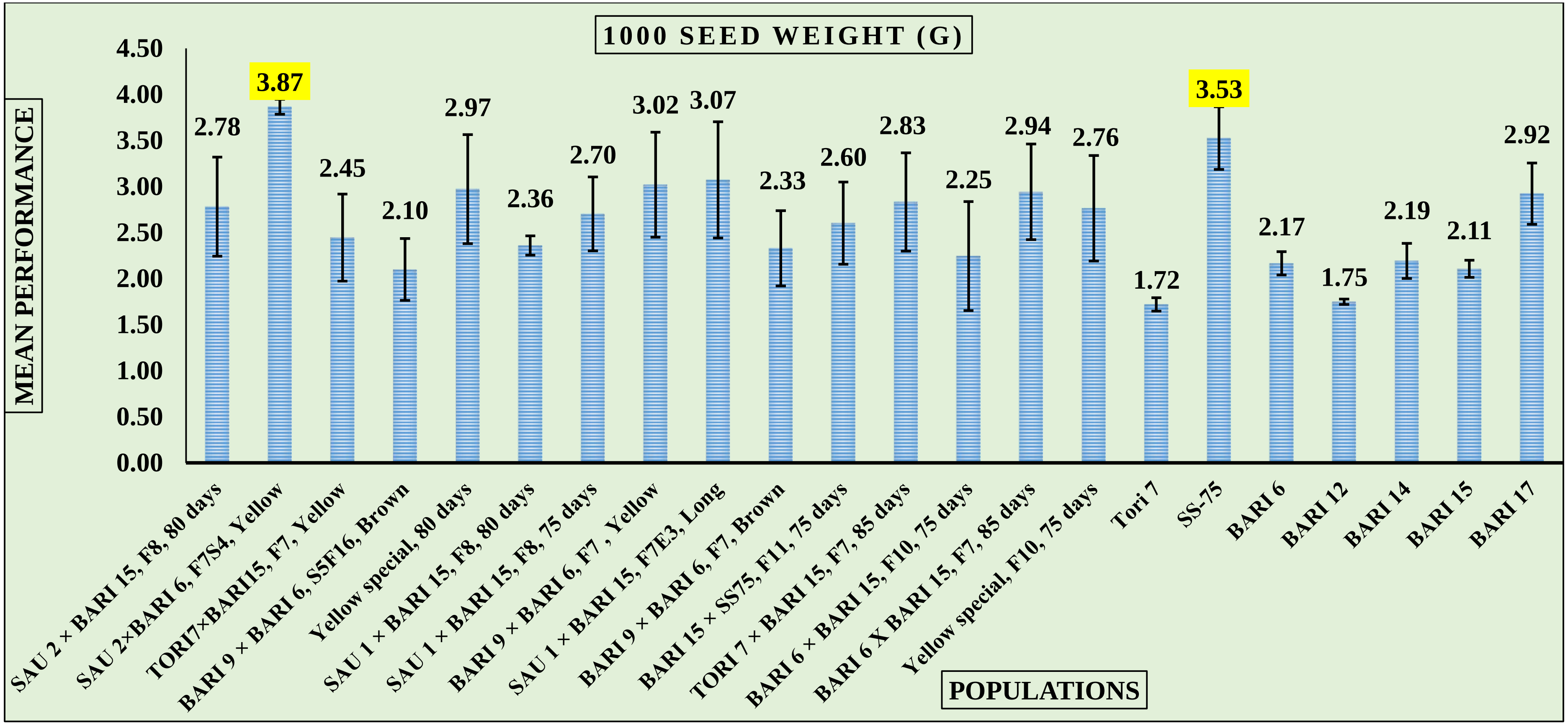

Figure 5. Mean performance of 1000 seed weight of fifteen advanced populations of *Brassica rapa* with seven parental lines

4.1.12 Seed yield per plant (g):

The performance of the genotypes exhibited highly significant variations at 1% level of significance for the trait seed yield per plant (Appendix IV). Highest yield performance per plant was observed in SAU 2 × BARI 6, F_7S_4, Yellow with (7.84 g) and the lowest seed yield per plant was observed in BARI 9 × BARI 6, F_7, Brown with (3.57 g) (Table 4). Mean value of 5.3 g was found for the trait (Appendix VI). Among the parental lines, significant variations were shown at 1% level of significance for the trait seed yield per plant (Appendix V). Highest yield performance per plant was observed in SS-75 with (4.47 g) whereas the lowest yield was observed in BARI 14 with (2.75 g) (Table 5). SAU 2 × BARI 6, F_7S_4, Yellow with (7.84 g) was found more seed yield per plant than SS-75 with (4.47 g). Huq (2006) found the highest seed yield in Agroni × Tori 7, Agroni×BARIsar-6 and Shafal×BARIsar-6 in *Brassica rapa*. Mean value of 3.69g was found for the trait (Appendix VII). Mean performance of seed yield per plant in fifteen advanced populations of *B. rapa* with seven parental lines is presented in figure 13 through a bar graph.

There was little difference between genotypic variance (0.85) and phenotypic variance (1.74) (Table 6) and the difference between genotypic and phenotypic variance was lower, indicating the lower environmental influence for this trait. The similar finding was also reported by Afrin *et al*. (2016). High estimates of PCV (24.94%) and moderate estimation of GCV (17.43%) were marked for this character and difference between them was higher indicating that there was the immense influence of environment on the expression of the character (Table 6). There was little difference between genotypic variance (0.30) and phenotypic variance (0.74) for parental lines indicating the lower environmental influence over genotypes. The similar finding was also reported by Afrin *et al*. (2016), high estimates of PCV (23.31%) and moderate GCV (14.84%) were marked for this character (Table 7).

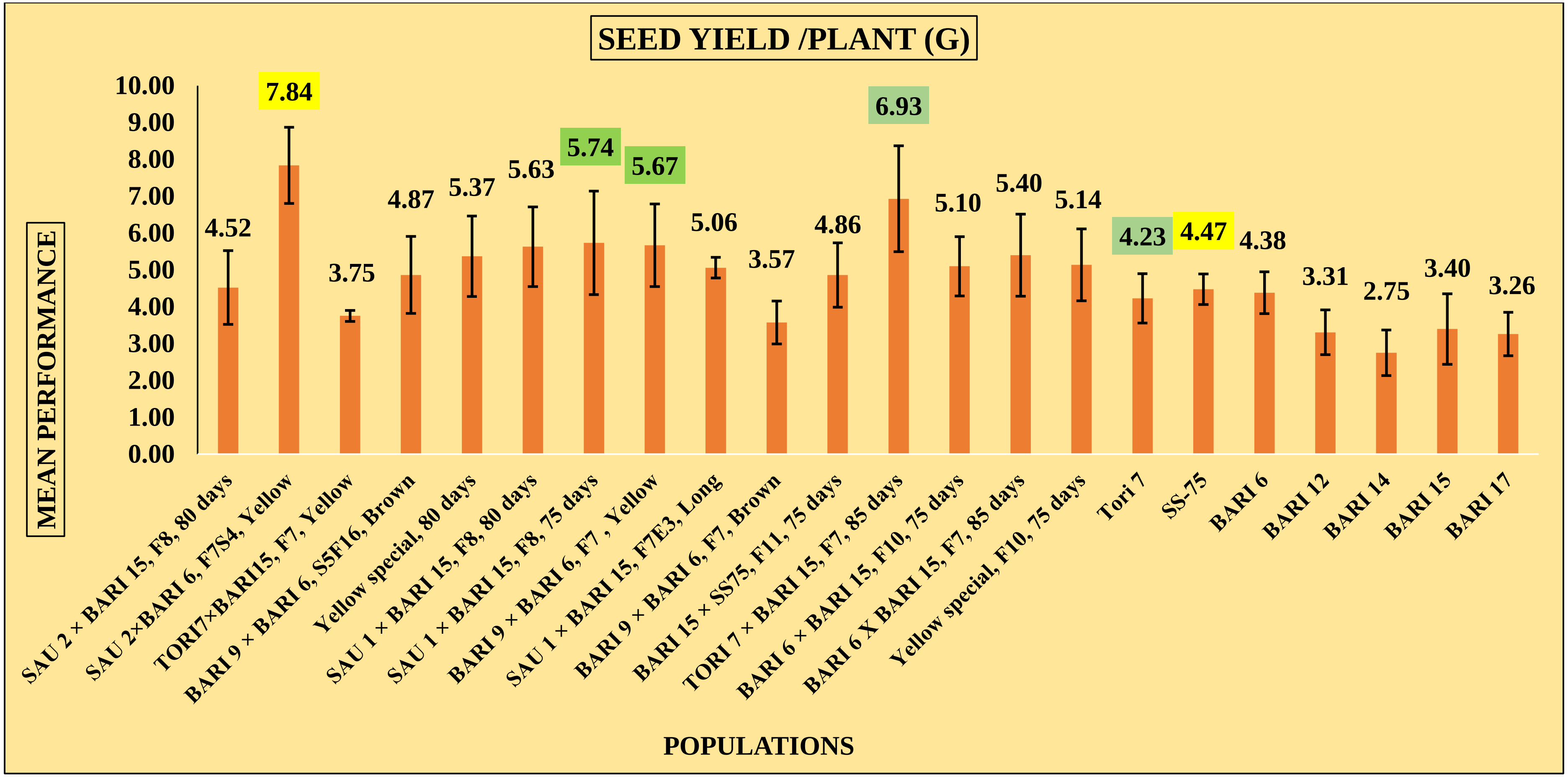

Figure 6. Mean performance of seed yield per plant of fifteen advanced populations of *Brassica rapa* with seven parental line

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

Genotypes	Days to 1st flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Root length (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	Length of siliqua (cm)	No. of siliquae/plant	No. of seeds/ siliquae	1000 seed weight (g)	Seed yield /plant (g)
SAU 2 × BARI 15, F8, 80 days	29.33 d-f	36.00 d-f	79.33 e-g	104.93 c-e	10.47 cd	4.87 b-d	1.90 c-e	5.76 b-e	133.7 bc	16.57 cd	2.78 b-d	4.52 cd
SAU 2×BARI 6, F7S4, Yellow	29.67 c-f	33.00 g	91.00 a	105.26 b-e	12.28 a-c	8.10 a	3.17 a	6.54 a	137.20 a-c	19.82 bc	3.87 a	7.84 a
TORI7×BARI15, F7, Yellow	31.67 bd	39.33 a-c	85.00 bc	103.09 c-f	12.78 ab	7.47 a	0.33 h	5.45 ef	84.47 e	21.29 ab	2.45 b-d	3.75 d
BARI 9 × BARI 6, S5F16, Brown	28.33 f	34.67 e-g	83.00 cd	87.52 h	10.14 cd	4.73 b-d	3.73 a	5.97 b-d	138.83 ab	18.83 bc	2.10 d	4.87 cd
Yellow special, 80 days	32.67 ab	38.00 b-d	87.00 b	104.50 c-f	11.83 a-d	4.97 b-d	2.23 cd	5.49 c-f	141.67 ab	17.93 bc	2.97 bc	5.37 bc
SAU 1 × BARI 15, F8, 80 days	31.33 b-d	37.33 b-e	79.00 fg	105.88 b-e	11.81 a-d	4.93 b-d	1.67 d-f	5.49 c-f	141.07 ab	19.12 bc	2.36 b-d	5.63 bc
SAU 1 × BARI 15, F8, 75 days	31.00 b-e	38.00 b-d	75.00 i	111.68 a-e	11.96 a-d	4.40 b-d	1.57 d-f	5.44 ef	124.63 b-d	19.66 bc	2.70 b-d	5.74 bc
BARI 9 × BARI 6, F7 , Yellow	27.33 f	32.67 g	76.00 hi	100.62 d-g	10.79 b-d	5.00 b-d	2.40 bc	5.72 b-e	168.47 a	13.38 d	3.02 b	5.67 bc
SAU 1 × BARI 15, F7E3, Long	32.00 bc	39.00 a-c	81.00 d-f	116.77 ab	11.88 a-d	5.27 b	1.20 e-g	6.06 ab	125.90 b-d	21.16 ab	3.07 b	5.06 cd

BARI 9 × BARI 6, F7, Brown	28.67 ef	34.00 fg	75.00 i	89.10 gh	10.05 d	5.07 b-d	3.03 ab	5.20 f	135.20 a-c	19.09 bc	2.33 b-d	3.57 d
BARI 15 × SS75, F11, 75 days	29.67 c-f	36.67 c-f	78.00 gh	93.29 f-h	11.57 a-d	4.23 cd	1.50 ef	5.98 bc	104.10 c-e	20.32 a-c	2.60 b-d	4.86 cd
TORI 7 × BARI 15, F7, 85 days	32.3 ab	39.67 ab	83.00 cd	117.75 a	11.93 a-d	5.13 bc	1.27 e-g	5.65 b-f	137.40 a-c	20.03 bc	2.83 b-d	6.93 ab
BARI 6 × BARI 15, F10, 75 days	34.6 a	41.00 a	78.67 f-h	112.00 a-d	12.21 a-d	4.10 d	0.27 h	5.51 c-f	93.93 d-e	24.09 a	2.25 cd	5.10 cd
BARI 6 X BARI 15, F7, 85 days	28.67 ef	37.67 b-d	82.00 de	113.71 a-c	11.76 a-d	4.83 b-d	1.17 fg	5.59 b-f	121.20 b-d	18.63 bc	2.94 bc	5.40 bc
Yellow special, F10, 75 days	32.67 ab	40.00 ab	78.00 gh	100.35 e-g	13.38 a	4.17 cd	0.60 g-h	5.47 d-f	104.13 c-e	20.66 ab	2.76 b-d	5.14 cd
LSD	2.34	2.73	2.99	11.63	2.17	0.98	0.73	0.49	33.74	3.91	0.77	1.59
CV(%)	4.57	4.39	2.21	6.66	11.11	11.37	25.04	5.2	16	12.08	16.87	17.91

Here, the same letter in a Duncan grouping are not significantly different at 5% level of significance.

Table 5. Mean performance of yield and yield contributing characters of seven parental lines of *Brassica rapa* L.

Genotypes	**Days to 1st flowering**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Root length (cm)**	**No. of primary branches /plant**	**No. of secondary branches /plant**	**Length of siliqua (cm)**	**No. of seeds/plant**	**No. of seeds /siliquae**	**1000 seed weight (g)**	**Seed yield /plant (g)**
Tori 7	28.00 c	34.00 c	84.00 de	88.64 b	9.84 cd	4.63 ab	6.13 a	5.21 cd	164.00 a	15.88 b	1.72 d	4.23 ab
BARI 14	30.67 b	37.00 b	81.00 e	95.57 b	9.96 cd	4.23 a-c	1.30 c	5.46 cd	111.03 bc	14.28 b	2.19 c	2.75 c
BARI 15	36.33 a	44.33 a	86.33 d	93.24 b	9.08 d	3.80 b-c	0.00 d	5.01 d	69.50 d	20.76 a	2.11 c	3.40 a-c
BARI 17	36.33 a	45.00 a	90.67 bc	97.47 b	12.21 ab	3.40 c	1.67 c	7.56 a	79.03 d	22.73 a	2.92 b	3.26 bc
BARI 6	35.33 a	45.00 a	87.33 cd	101.62 ab	11.23 bc	4.70 ab	2.23 b	5.68 c	133.50 ab	15.06 b	2.17 c	4.38 ab
SS-75	36.67 a	46.33 a	97.33 a	113.87 a	13.38 a	3.96 a-c	0.00 d	6.44 b	87.7 c-d	17.20 b	3.53 a	4.47 a
BARI 12	30.00 bc	37.00 b	92.67 b	91.72 b	9.62 cd	4.80 a	2.53 b	5.62 c	144.3 a	15.47 b	1.75 d	3.31 a-c
LSD	2.32	2.54	4.09	13.88	2.01	0.91	0.86	0.52	31.76	3.00	0.35	1.18
CV(%)	3.91	3.46	2.6	8	10.52	12.16	25.41	4.95	15.83	9.72	8.34	17.98

Here, the same letter in a Duncan grouping are not significantly different at 5% level of significance.

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

4.2.1 Days to first flowering:

High heritability (64.23%) coupled with low genetic advance (3.10) and moderate (10.10) genetic advance in percent of mean were noted for this character rendering them unfit for improvement through simple selection due to prevalence of non-additive gene action (Table 5). In case of parental lines, high heritability (88.28%) in association with low genetic advance (6.91) and high value (20.72) of genetic advance in percentage of mean were noted for this character rendering them unfit for improvement through simple selection due to prevalence of non-additive gene action (Table 6). Similar result was also reported by Sikarwar *et al.* (2017) for this trait in *B. rapa*.

4.2.2 Days to 50% flowering:

The high heritability of 68.71% with the low genetic advance of 4.13 and moderate (11.11) genetic advance in percent of mean were noted for the character indicating that the character is governed by non-additive gene action and selection may not be rewarding for such trait (Table 5). Saifullah (2010) found high heritability (88.86%) and low genetic advance (2.06) for the trait in *B. rapa.* High heritability of 92.40% with low genetic advance (9.84) and moderate genetic advance in percentage of mean (23.86) were found for the character in case of parental lines indicating the non- additive gene action and selection may not be rewarding for such trait (Table 6).

4.2.3 Days to maturity:

High heritability (85.91%) with low genetic advance (8.42) and moderate genetic advance in percent of the mean (10.43%) indicated the presence of non-additive gene action and selection for such trait might not be recommended (Table 5). Jahan *et al.* (2014) found high heritability along with low genetic advance in percent of the mean for days to maturity in *B. rapa.* In case of parental lines, high heritability (84.43 %) with moderate genetic advance (10.14) and moderate genetic advance in percentage of mean (11.46 percent) indicating the presence of non-additive gene action and selection for such trait may not be recommended (Table 6).

4.2.4 Plant height (cm):

Moderate heritability (59.19%), moderate genetic advance (13.27) along with moderate genetic advance in percent of the mean (12.71%) were noted for the character indicating the presence of non-additive gene action and selection for such traits may be restricted for improvement of the crop (Table 5). Afrin *et al*. (2011) showed high heritability with the high genetic advance in the percentage of the mean for this character in *B. rapa.* In case of parental lines, moderate heritability (44.87%), low genetic advance (9.71) along with low genetic advance in percentage of mean (9.96%) were noted for the character in *B. rapa* (Table 6) suggesting the presence of non-additive gene action and selection for such trait may be restricted for the crop improvement.

4.2.5 Root length (cm):

Low heritability (15.86%) along with low genetic advance (0.46) and low genetic advance in percent of the mean (3.96%) was recorded indicating the presence of non-additive gene action. So improvement through selection may not be possible for this trait (Table 5). For parental lines, high heritability (61.41%) along with low genetic advance (2.30) and high genetic advance in percentage of mean (21.41%) were recorded for this trait (Table 6) indicating the presence of non-additive gene action which is responsible for the ineffectiveness of the selection for this trait.

4.2.6 Number of primary branches per plant:

High heritability (77.53%) along with low genetic advance (1.96) and high genetic advance in percentage of the mean (38.15%) was recorded indicating the presence of non-additive gene action which is responsible for the ineffectiveness of the selection for this trait (Table 5). Sultana (2015) reported high heritability (97.43%) and low genetic advance (1.25) for this trait in *B. napus*. For parental lines, moderate heritability (42.22%) along with low genetic advance (0.58) and moderate genetic advance in percentage of mean (13.83%) were recorded for this trait 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 secondary branches per plant:

The high heritability of 83.94% with the low genetic advance of 1.88 and very high genetic advance in percentage of the mean (108.11) was recorded indicating that non-additive gene effect was present, making selection ineffective for this trait (Table 5). Sultana (2015) found high heritability (98.70%) and low genetic advance (1.78) for this trait in *B. napus*. In case of parental lines, high heritability of 94.77% with low genetic advance of 4.18 and very high genetic advance in percentage of mean (218.90) showed that non-additive gene effects were present, making selection ineffective for this trait (Table 6).

4.2.8 Number of siliquae per plant:

Moderate heritability (45.06%), high genetic advance (25.26) and low genetic advance in percentage of mean (20.03) were noted for the character indicated that the heritability is due to non-additive gene effect and selection may be ineffective for the trait (Table 5). Moderate heritability (63.18%) with high genetic advance (31.32) and reasonable genetic advance in percentage of mean (33.59%) were found by Afrin *et al*. (2016) in *B. rapa* for number of siliquae per plant. For parental lines, high heritability (78.70%) estimates with high genetic advance (62.71) and high genetic advance in percentage of mean (55.61%) were found for this trait indicated that most likely the heritability is due to additive gene effects and selection may be effective for the trait (Table 6). Naznin *et al*. (2015) showed high heritability (93.16%) with high genetic advance in percentage of mean (37.74%) for number of siliquae/plant which was similar to this finding. Hosen (2008) also agreed to the above result.

4.2.9 Length of siliqua (cm):

Moderate heritability of 47.06%, low genetic advance 0.40 and low genetic advance in percentage of mean of 7.02% were observed for this trait. Moderate heritability in association with low genetic advance suggesting that non-additive gene effect was present and selection may not be recommended for this trait (Table 5). Moderate heritability (73.12%) with low genetic advance (0.55) and low genetic advance in percentage of mean (10.77%) were found by Afrin *et al*. (2016) in *B. rapa* for length of siliqua. High heritability of 90.24%, low genetic advance of 1.68 and high genetic advance in percentage of mean of 28.78% were observed for this trait in case of parental lines (Table 6). High heritability in association with low genetic advance suggesting that non-additive gene effects are present and selection may not be recommended for this trait.

4.2.10 Number of seeds per siliqua:

Moderate heritability (41.14%) with low genetic advance (2.59) and moderate genetic advance in percentage of the mean (13.35%) indicated that non-additive gene action was present. So, selection was ineffective for the improvement of the crop (Table 5). Low heritability (61.65%) along with moderate genetic advance (2.37) and low genetic advance in the percentage of the mean (13.80%) were found by Afrin *et al*. (2016) for the trait in *B. rapa*. High heritability (76.44), low genetic advance (5.47) and high genetic advance in percentage of mean (31.53%) were found for this character in case of parental lines. High heritability with low genetic advance indicates that non-additive gene action is present and so selection is ineffective for the improvement of the crop (Table 6). High heritability values along with high genetic advance in percentage of mean for seeds per siliqua was reported by Mahmud (2008) which was similar to the result.

4.2.11 Thousand seed weight (g):

Moderate heritability (36.36%) in conjunction with low genetic advance (0.43) was noted for this trait, and moderate genetic advance in percent of the mean (15.71%) was also observed. Moderate heritability with low genetic advance suggested that non-additive gene action governs the character. Thus, for crop improvement, selection may be rewarding this trait (Table 5). Saifullah (2010) reported high heritability (65.03%) along with low genetic advance (0.31) in *B. rapa* for this trait. High heritability (91.24%) in conjunction with low genetic advance (1.27) and high genetic advance in percentage of mean (54.28%) were noted for this trait in case of parental lines (Table 6). High heritability with low genetic advance suggests that non-additive gene action governs the character. Thus, for crop improvement, selection may be ineffective for this trait.

4.2.12 Seed yield per Plant (g):

Moderate heritability (48.85%) combined to low genetic advance (1.33) and high (25.09%) genetic advance in percent of the mean indicated the presence of non-additive gene action which makes the selection ineffective for the trait (Table 5). Rameeh (2014) showed high heritability along with high genetic advance for the trait in *B. napus.*

Hence, moderate heritability (40.54%) combined to low genetic advance (0.72) and moderate (19.47%) genetic advance in percent of mean were found for this trait (Table 6) suggesting the presence of non-additive gene action which makes the selection ineffective for the trait in case of parental lines.

Table 6: Estimation of some genetic parameters of 15 advanced populations of *Brassica rapa*

Parameters	Days to 1st flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Root length (cm)	No. of primary branches /plant	No. of secondary branches /plant	No. of seeds /plant	Length of siliqua (cm)	No. of seeds /siliquae	1000 seed weight (g)	Seed yield /plant (g)
Genotypic variance	3.52	5.84	19.45	70.09	0.32	1.17	0.99	333.78	0.08	3.83	0.12	0.85
Phenotypic variance	5.48	8.5	22.64	118.42	1.99	1.51	1.18	740.75	0.17	9.31	0.33	1.74
Genotypic coefficient of variance	6.12	6.51	5.46	8.02	4.83	21.03	57.28	14.49	4.97	10.10	12.64	17.43
Phenotypic coefficient of variance	7.63	7.85	5.89	10.42	12.12	23.89	62.52	21.58	7.25	15.75	20.97	24.94
Heritability (%)	64.23	68.71	85.91	59.19	15.86	77.53	83.94	45.06	47.06	41.14	36.36	48.85
Genetic advance	3.10	4.13	8.42	13.27	0.46	1.96	1.88	25.26	0.40	2.59	0.43	1.33
Genetic advance in percentage of mean	10.10	11.11	10.43	12.71	3.96	38.15	108.11	20.03	7.02	13.35	15.71	25.09

Table 7: Estimation of some genetic parameters of seven parental lines of *Brassica rapa*

Parameters	Days to 1st flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Root length (cm)	No. of primary branches /plant	No. of secondary branches /plant	No. of seeds /plant	Length of siliqua (cm)	No. of seeds /siliquae	1000 seed weight (g)	Seed yield /plant (g)
Genotypic variance	12.73	24.68	28.68	49.50	2.04	0.19	4.35	1177.42	0.74	9.22	0.42	0.30
Phenotypic variance	14.42	26.71	33.97	110.33	3.32	0.45	4.59	1496.07	0.82	12.06	0.46	0.74
Genotypic co-efficient of variance	10.71	12.05	6.05	7.22	13.26	10.33	109.16	30.43	14.70	17.51	27.59	14.84
Phenotypic co-efficient of variance	11.39	12.53	6.59	10.78	16.93	15.90	112.13	34.30	15.48	20.02	28.88	23.31
Heritability (%)	88.28	92.40	84.43	44.87	61.41	42.22	94.77	78.70	90.24	76.44	91.24	40.54
Genetic advance	6.91	9.84	10.14	9.71	2.30	0.58	4.18	62.71	1.68	5.47	1.27	0.72
Genetic advance in percentage of mean	20.72	23.86	11.46	9.96	21.41	13.83	218.90	55.61	28.78	31.53	54.28	19.47

4.3 CORRELATION COEFFICIENT:

The correlation coefficient is a numerical measure of some interrelation to detect the direction and strength of the relationship between the relative movements of two or more variables—the values of the correlation coefficient range between -1.0 and 1.0. A calculated number higher than 1.0 or less than -1.0 indicates an error in the measurement of correlation. A correlation of -1.0 exhibits a perfect negative correlation, whereas a correlation of 1.0 shows a perfect positive correlation. A correlation of 0.0 exhibits no relationship between the movements of the two variables. Yield being a target character is governed by polygene and highly influenced by the environment. So, selection based on only yield itself is unavailing. When selection is made to develop any character highly correlated with yield, it affects some other correlated characters simultaneously. Therefore, knowledge regarding the association of character with yield and themselves provide a guideline to the plant breeder to improve through selection vis-à-vis. It gives a clear understanding of the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). The genotypic and phenotypic correlation coefficient of different characters of fifteen advanced populations of *B. rapa* L is presented in Tables 8. It was conspicuous that genotypic correlation coefficients were higher than their analogous phenotypic ones suggested that these traits were strongly correlated genetically and the environment less influenced the phenotypic expression of these traits. A similar result was found by Pankaj *et al*. (2002). In many cases, the phenotypic correlation coefficient was higher than their corresponding genotypic correlation coefficient suggesting that both environmental and genotypic correlation performed in the same direction and finally maximized their expression at the phenotypic level.

Table 8. Genotypic and phenotypic correlation coefficient of fifteen advanced populations and seven parents of *Brassica rapa*

Characters		**DFF**	**DFPF**	**DM**	**PH**	**RL**	**NPB/P**	**NSB/P**	**NS/P**	**LS**	**NS/S**	**TSW**	**SY/P**
DFF	r_g		0.898**	0.154^{NS}	0.557**	0.998**	-0.16^{NS}	-0.756**	-0.688**	-0.327*	0.979**	-0.188^{NS}	0.087^{NS}
	r_p		0.824**	0.116^{NS}	0.464**	0.431**	-0.062^{NS}	-0.565**	-0.380*	-0.170^{NS}	0.477**	-0.058^{NS}	0.056^{NS}
DFPF	r_g			-0.024^{NS}	0.649**	0.992**	-0.326*	-0.963**	-0.822**	-0.503**	0.885**	-0.407**	-0.175^{NS}
	r_p			-0.047^{NS}	0.461**	0.371*	-0.248^{NS}	-0.714**	-0.520**	-0.273^{NS}	0.494**	-0.167^{NS}	-0.075^{NS}
DM	r_g				0.188^{NS}	0.471**	0.753**	0.187^{NS}	-0.027^{NS}	0.661**	0.150^{NS}	0.676**	0.540**
	r_p				0.135^{NS}	0.196^{NS}	0.648**	0.158^{NS}	0.013^{NS}	0.400**	0.122^{NS}	0.354*	0.356*
PH	r_g					0.776**	-0.013^{NS}	-0.687**	-0.237^{NS}	-0.018^{NS}	0.428**	0.432**	0.517**
	r_p					0.357*	0.127^{NS}	-0.415**	0.070^{NS}	0.067^{NS}	0.083^{NS}	0.341*	0.394**
RL	r_g						0.274^{NS}	-0.984**	-0.989**	-0.106^{NS}	0.997**	0.561**	0.544**
	r_p						0.200^{NS}	-0.503**	-0.308*	0.036^{NS}	0.256^{NS}	0.150^{NS}	0.171^{NS}
NPB	r_g							0.166^{NS}	-0.142^{NS}	0.469**	0.071^{NS}	0.633**	0.292^{NS}
	r_p							0.203^{NS}	0.127^{NS}	0.411**	-0.013^{NS}	0.412**	0.258^{NS}
NSB	r_g								0.776**	0.399**	-0.618**	0.161^{NS}	0.140^{NS}
	r_p								0.659**	0.349*	-0.447**	0.149^{NS}	0.215^{NS}
NSP	r_g									0.194^{NS}	-0.943**	0.282^{NS}	0.395**
	r_p									0.185^{NS}	-0.673**	0.341*	0.372*
LS	r_g										-0.227^{NS}	0.810**	0.571**
	r_p										0.138^{NS}	0.456**	0.558**
NSS	r_g											-0.295*	-0.156^{NS}
	r_p											-0.210^{NS}	0.021^{NS}
TSW	r_g												0.823**
	r_p												0.584**
SYP	r_g												
	r_p												

DFF=days to 1st flowering, DFPF=days to 50%flowering, DM= days to maturity, PH=plant height, RL= root length, NPB/P=number of primary branches per plant, NSB/P=number of secondary branches per plant, NS/P= number of siliquae per plant, LS=length of siliqua, NS/S=number of seeds per siliqua, TSW=1000 seed weight, SY/P=seed yield per plant

4.3.1 Days to first flowering:

Days to first flowering showed a highly significant and positive correlation with days to 50% flowering (r_g=0.898, r_p=0.824), plant height (r_g=0.577, r_p=0.464), root length (r_g=0.998, r_p=0.431) and the number of seeds per siliqua (r_g=0.979, r_p=0.477). It also observed that highly significant but negative correlation with the number of secondary branches per plant (r_g=-0.756, r_p=-0.565) and the number of siliqua per plant (r_g=-0.688, r_p=-0.380). Non-significant and positive correlation with days to maturity (r_g=0.154, r_p=0.116) and seed yield per plant (r_g=0.087, r_p=0.056) and non-significant but negative correlation with the number of primary branches per plant (r_g=-0.160, r_p=-0.062) and 1000 seed weight (r_g=-0.188, r_p=-0.058).

4.3.2 Days to 50% flowering:

Days to 50% flowering showed a highly significant and positive correlation with plant height (r_g=0.649, r_p=0.461), root length (r_g=0.992, r_p=0.371) and number of seeds per siliqua (r_g=0.885, r_p=0.494) and also highly significant and negative correlation with the number of primary branches per plant (r_g=-0.326), number of secondary branches per plant (r_g=-0.963, r_p=-0.714), number of siliqua per plant (r_g=-0.822, r_p=-0.520), length of siliqua (r_g=-0.503) and 1000 seeds weight (r_g=-0.407). It also presented non-significant and negative correlation with days to maturity (r_g=-0.024, r_p=-0.047), seed yield per plant (r_g=-0.175, r_p=-0.075), number of primary branches per plant (r_p=-0.248), length of siliqua (r_p=-0.273) and 1000 seed weight (r_p=-0.167). Afrin *et al.* (2011) found a highly significant and positive correlation between days to 50% flowering and plant height.

4.3.3 Days to maturity:

Days to maturity showed a highly significant and positive correlation with root length (r_g=0.471), the number of primary branches per plant (r_g=0.753, r_p=0.648), length of siliqua (r_g=0.661, r_p=0.400), 1000 seed weight (r_g=0.676, r_p=0.354) and seed yield per plant (r_g=0.540, P=0.336). It also presented that non-significant and positive correlation with plant height (r_g=0.188, r_p =0.135), number of secondary branches per plant (r_g=0.187, r_p=0.158), number of seeds per siliqua (r_g=0.150, r_p=0.122), root length (r_p=0.196) and number of seeds per siliqua (r_p=0.013) and also showed that non-significant and negative correlation with the number of siliquae per plant (r_g=-0.027).

Lodhi (2014) reported that days to maturity had a non-significant and positive interaction with yield per plant.

4.3.4 Plant height (cm):

Plant height showed a highly significant and positive correlation with root length (r_g=0.776, r_p=0.357), the number of seed per silique (r_g=0.428), 1000 seed weight (r_g=0.432, r_p=0.341), and seed yield per plant (r_g=0.517, r_p=0.394). It also showed that highly significant and negative correlation with the number of secondary branches per plant (r_g=-0.687, r_p=-0.415) and non-significant and negative correlation with the number of primary branches per plant (r_g=-0.013), number of siliqua per plant (r_g=-0.237) and length of siliqua (r_g=-0.018). It also showed a non-significant and positive correlation with the number of seeds per siliqua (r_p=0.083), number of primary branches per plant (r_p=0.127), number of siliqua per plant (r_p=0.070) and length of siliqua (r_p =0.067).

4.3.5 Root length (cm):

Root length showed a highly significant and positive correlation with the number of seeds per siliqua (r_g=0.997), 1000 seed weight (r_g=0.561), seed yield per plant (r_g=0.544) and highly significant and negative correlation with the number of secondary branches per plant (r_g=-0.984, r_p=-0.503), and number of siliqua per plant (r_g=-0.989, P=-0.308). It also showed that non-significant and positive correlation with the number of primary branches per plant (r_g=0.274, r_p=0.2), number of seeds per siliqua (r_p=0.256), 1000 seed weight (P=0.150), seed yield per plant (r_p=0.171) and length of siliqua (r_p=0.036) and non-significant and negative correlation with length of siliqua (r_g=-0.106).

4.3.6 Number of primary branches per plant:

The number of primary branches showed a highly significant and positive correlation with length of siliqua (r_g=0.469, r_p=0.411) and 1000 seed weight (r_g=0.633, r_p=0.412). Also, it showed that non-significant and positive correlation with the number of secondary branches per plant (r_g=0.166, r_p=0.203), number of seeds per siliqua (r_g=0.071) and seed yield per plant (r_g=0.292, r_p=0.258). It also showed that non-significant and negative correlation with the number of siliqua per plant (r_g=-0.142) and the number of seeds per siliqua (r_p=-0.013). Rashid (2007) showed that the number of primary branches per plant had a positive and significant association with yield per plant.

4.3.7 Number of secondary branches per plant:

The number of secondary branches showed a highly significant and positive correlation with the number of siliqua per plant (r_g=0.776, r_p=0.659) and length of siliqua (r_g=0.399, r_p=0.349) and highly significant and negative correlation with the number of seeds per siliqua (r_g=-0.618, r_p=-0.447). It also presented that non-significant and positive correlation with 1000 seed weight (r_g=0.161, r_p=0.149) and seed yield per plant (r_g=0.140, r_p=0.215). Naznin (2013) found a significant and positive relation with yield, while Akter (2010) found a negative correlation with the yield.

4.3.8 Number of siliquae per plant:

The number of siliqua per plant showed a highly significant and positive correlation with seed yield per plant (r_g=0.395, r_p=0.372) and highly significant and negative correlation with the number of seeds per siliqua (r_g=-0.943, r_p=-0.673). Naznin *et al.* (2015) reported that number of siliquae/plant had highly significant positive association with seed yield/plant (r_g = 0.7011, r_p = 0.5684). It also showed that non-significant and positive correlation with length of siliqua (r_g=0.194, r_p =0.185) and 1000 seed weight (r_g=0.140). Uddin *et al.* (2013) found that at both phenotypic and genotypic level yield had a highly significant and positive correlation with the number of siliqua per plant

4.3.9 Length of siliqua:

Length of siliqua showed a highly significant and positive correlation with 1000 seed weight (r_g=0.810, r_p=0.456) and seed yield per plant (r_g=0.571, r_p=0.558). Also, it showed non-significant and positive correlation with the number of seeds per siliqua (r_p=0.138). It also presented that non-significant but negative correlation with the number of seeds per siliqua (r_g=-0.227). Saifullah (2010) showed a significant and positive correlation of length of siliqua with yield.

4.3.10 Number of seeds per siliqua

The number of seeds per siliqua showed that significant and negative correlation with 1000 seed weight (r_g=-0.295) and non-significant and negative correlation with seed yield per plant (r_g=-0.156) and 1000 seed weight (r_p=-0.210). It also showed that non-significant and positive correlation with seed yield per plant (r_p=0.021). Significant and negative correlation between the number of seeds per siliqua and yield were found by Naznin (2013).

4.3.11 Thousand seed weight

Thousand seed weight showed a highly significant and positive correlation with seed yield per plant (r_g=0.823, r_p=0.584). Akter (2010) reported a significant and positive correlation of thousand seed weight with yield per hectare at the genotypic level.

4.4 Path co-efficient analysis:

Complex relationships between the dependent variable's various traits can't be figured out through simple correlation. Correlation coefficients exhibit a linear association between variables. But it is not enough to describe these relationships when the causal relationship among variables is necessary. Therefore, it was suggested that path coefficient analysis is the most common statistical method utilized to determine the direct or indirect effects of yield contributing characters on seed yield per plant and measure each component's relative importance on seed yield per plant. Seed yield per plant is considered as a dependent variable and its attributes as independent variables such as days to first flowering, days to 50% flowering, days to maturity, plant height, root length, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, length of siliqua, number of seeds per siliqua, and thousand seed weight. Partitioning of genotypic correlations into direct and indirect effects of important characters by path coefficient analysis of *B. rapa*. is presented in table 9. Residual effects of their independent variables have been denoted as 'R' which have influenced on seed yield per plant to a medium extent.

4.4.1 Days to first flowering:

Path coefficient analysis revealed that days to first flowering had a positive direct effect (0.078) on seed yield per plant. Days to first flowering had a positive indirect effect on seed yield per plant through days to maturity (0.038), plant height (0.073), root length (0.233), number of primary branches per plant (0.111), number of siliqua per plant (0.111), length of siliqua (0.189) and number of seeds per siliqua (0.120) while negative indirect effect was found via days to 50% flowering (-0.075), number of secondary branches per plant (-0.539) and 1000 seed weight (-0.252). It had non-significant positive genotypic correlation (0.087) with seed yield per plant.

4.4.2 Days to 50% flowering:

Days to 50% flowering had a negative direct effect (-0.084) on seed yield per plant. Days to 50% flowering had a positive indirect effect on seed yield per plant through days to first flowering (0.070), plant height (0.085), root length (0.235), number of primary branches per plant (0.225), number of siliquae per plant (0.132), length of siliqua (0.290) and number of seeds per siliqua (0.109) while the negative indirect effect was found via days to maturity (-0.006), number of secondary branches per plant (-0.686) and 1000 seed weight (-0.546). It had non-significant negative genotypic correlation (-0.175) with seed yield per plant.

4.4.3 Days to maturity:

Days to maturity had a positive direct effect (0.249) on seed yield per plant. Days to maturity had a positive indirect effect on seed yield per plant via days to first flowering (0.012), days to 50% flowering (0.002), plant height (0.025), root length (0.091), number of secondary branches per plant (0.133), number of siliqua per plant (0.004), number of seeds per siliqua (0.018), 1000 seed weight (0.907) while the negative indirect effect via number of primary branches per plant (-0.521) and length of siliqua (-0.381). It had a highly significant positive genotypic correlation (0.54) with seed yield per plant.

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

Traits	DFF	DFPF	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Genotypic correlation with yield
DFF	**0.078**	-0.075	0.038	0.073	0.233	0.111	-0.539	0.111	0.189	0.120	-0.252	0.087^{NS}
DFPF	0.070	**-0.084**	-0.006	0.085	0.235	0.225	-0.686	0.132	0.290	0.109	-0.546	-0.175^{NS}
DM	0.012	0.002	**0.249**	0.025	0.091	-0.521	0.133	0.004	-0.381	0.018	0.907	0.54**
PH	0.044	-0.054	0.047	**0.131**	0.150	0.009	-0.489	0.038	0.010	0.053	0.580	0.517**
RL	0.078	-0.083	0.117	0.101	**0.193**	-0.189	-0.815	0.186	0.061	0.145	0.753	0.544**
NPB/P	-0.013	0.027	0.188	-0.002	0.053	**-0.691**	0.118	0.023	-0.270	0.009	0.850	0.292^{NS}
NSB/P	-0.059	0.081	0.047	-0.090	-0.190	-0.115	**0.713**	-0.125	-0.230	-0.076	0.216	0.14^{NS}
NS/P	-0.054	0.069	-0.007	-0.031	-0.191	0.098	0.553	**-0.161**	-0.112	-0.116	0.378	0.395**
LS	-0.026	0.042	0.165	-0.002	-0.020	-0.324	0.284	-0.031	**-0.577**	-0.028	1.088	0.571**
NS/S	0.077	-0.074	0.037	0.056	0.192	-0.049	-0.440	0.152	0.131	**0.123**	-0.396	-0.156^{NS}
TSW	-0.015	0.034	0.168	0.056	0.108	-0.438	0.115	-0.045	-0.467	-0.036	**1.342**	0.823**

Bold figures indicate direct effects

Residual effect: 0.079

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

4.4.4 Plant height (cm):

Plant height had a positive direct effect (0.131) on seed yield per plant. Plant height had a negative direct effect on yield per plant reported by Uddin *et al.* (2013). Plant height had a positive indirect effect on seed yield per plant via days to first flowering (0.044), days to maturity (0.047), root length (0.150), number of primary branches per plant (0.009), number of siliqua per plant (0.038), length of siliqua (0.010), number of seeds per siliqua (0.053) and 1000 seed weight (0.580) while the negative indirect effect through days to 50% flowering (-0.054), number of secondary branches per plant (-0.489). It had a highly significant positive genotypic correlation (0.517) with seed yield per plant.

4.4.5 Root length (cm):

Root length had a direct positive effect (0.193) on seed yield per plant. Root length had a positive indirect effect on seed yield per plant via days to first flowering (0.078), days to maturity (0.117), plant height (0.101), number of siliqua per plant (0.186), length of siliqua (0.061), number of seeds per siliqua (0.145) and 1000 seed weight (0.753) while the negative indirect effect on seed yield per plant through days to 50% flowering (-0.083), number of primary branches per plant (-0.189), number of secondary branches per plant (-0.815). It had a highly significant positive genotypic correlation (0.544) with seed yield per plant.

4.4.6 Number of primary branches per plant:

The number of primary branches per plant had a negative direct effect (-0.691) on seed yield per plant. The number of primary branches per plant had a negative direct effect on yield per plant reported by Islam *et al.* (2013). Number of primary branches had a positive indirect effect on seed yield per plant via days to 50% flowering (0.027), days to maturity (0.188), root length (0.053), number of secondary branches per plant (0.118), number of siliqua per plant (0.023), number of seeds per siliqua (0.009) and 1000 seed weight (0.850) while the negative indirect effect on seed yield per plant via days to first flowering (-0.013), plant height (-0.002) and length of siliqua (-0.270). It had non-significant positive genotypic correlation (0.292) with seed yield per plant.

4.4.7 Number of secondary branches per plant:

The number of secondary branches had a positive direct effect (0.713) on seed yield per plant. The number of secondary branches/plant had a high positive indirect effect on yield observed by Naznin *et al*. (2015). Number of secondary branches had a positive indirect effect on seed yield per plant through days to 50% flowering (0.081), days to maturity (0.047) and 1000 seed weight (0.216) while the negative indirect effect on seed yield per plant via days to first flowering (-0.059), plant height (-0.090), root length (-0.190), number of primary branches per plant (-0.115), number of siliqua per plant (-0.125), length of silique (-0.230) and number of seeds per siliqua (-0.076). It had non-significant positive genotypic correlation (0.14) with seed yield per plant.

4.4.8 Number of siliquae per plant:

The number of siliqua per plant had a negative direct effect (-0.161) on seed yield per plant. Number of siliqua per plant had a positive indirect effect on seed yield per plant via days to 50% flowering (0.069), number of primary branches per plant (0.098), number of secondary branches per plant (0.553) and 1000 seed weight (0.378) while the negative indirect effect on seed yield per plant via days to first flowering (-0.054), days to maturity (-0.007), plant height (-0.031), root length (-0.191), length of siliqua (-0.112) and number of seeds per siliqua (-0.116). It had a highly significant positive genotypic correlation (0.395) with seed yield per plant. Islam *et al.* (2015) observed a negative indirect effect on the number of siliqua per plant.

4.4.9 Length of silique (cm):

Length of silique (cm) had a negative direct effect (-0.577) on seed yield per plant. Length of siliqua had a positive indirect effect on seed yield per plant through days to 50% flowering (0.042), days to maturity (0.165), number of secondary branches per plant (0.284) and 1000 seed weight (1.088) while the negative indirect effect on seed yield per plant via days to first flowering (-0.026), plant height (-0.002), root length (-0.020), number of primary branches per plant (-0.324), number of siliqua per plant (-0.031) and number of seeds per siliqua (-0.028). It had a highly significant positive genotypic correlation (0.571) with seed yield per plant. Islam *et al*. (2016) observed a positive indirect effect of plant height towards yield.

4.4.10 Number of seeds per siliqua:

The number of seeds per siliqua had a positive direct effect (0.123) on seed yield per plant. Number of seeds per siliqua had a positive indirect effect on seed yield per plant through days to first flowering (0.077), days to maturity (0.037), plant height (0.056), root length (0.192), number of siliquae per plant (0.152), length of siliqua (0.131) while the negative indirect effect on seed yield per plant via days to 50% flowering (-0.074), number of primary branches per plant (-0.049), number of primary branches per plant (-0.049), number of secondary branches per plant (-0.440), and 1000 seed weight (-0.396). It had non-significant negative genotypic correlation (-0.156) with seed yield per plant.

4.4.11 Thousand seed weight (g):

Thousand seed weight (g) had a positive direct effect (1.342) on seed yield per plant. 1000 seed weight had a positive indirect effect on seed yield per plant via days to 50% flowering (0.034), days to maturity (0.168), plant height (0.056), root length (0.108) and number of secondary branches per plant (0.115) while the negative indirect effect on seed yield per plant via days to first flowering (-0.015), number of primary branches per plant (-0.438), number of seeds per siliqua (-0.036), number of siliqua per plant (-0.045) and length of siliqua (-0.467). It had a highly significant positive genotypic correlation (0.823) with seed yield per plant. Negative indirect effect for thousand seed weight on yield per plant was reported by Naznin *et al*. (2015).

4.4.12 Residual Effects:

The residual effect (R) of path co-efficient analysis was 0.0795, which reported that the traits under study contributed 92.05% of the seed yield/plant. It is said that there were some other factors that contributed 7.95% to the seed yield/plant that is not included in the present study could have a significant effect on seed yield.

4.5 SELECTION:

SAU 2 × BARI 6, F_7S_4, Yellow

Highest seed yield per plant (7.84 g) was found in SAU 2×BARI 6, F_7S_4, Yellow with the highest number of primary branches/ Plant (8.10), the highest number of secondary branches/plant (3.17), longest length of siliqua (6.54 cm), highest thousand seed weight (3.87g), moderate number of seeds/siliqua (19.82), a moderate number of siliquae/plant (137.20). But SAU 2×BARI 6, F_7S_4, Yellow took highest days to maturity (91 days).

BARI 9 × BARI 6, F_7, Yellow

Moderate seed yield/plant (5.67) was found in BARI 9 × BARI 6, F_7, Yellow with highest number of siliquae/plant (168.47), moderate thousand seed weight (3.02 g), a moderate number of primary branches/ Plant (5.00), highest number of secondary branches/plant (2.40), medium length of siliqua (5.72), short days to maturity (76.00).

SAU 1 × BARI 15, F_8, 75 days

Moderate seed yield/plant (5.74g) was found in SAU 1 × BARI 15, F_8, 75 days with moderate number of siliquae/plant (124.63), a moderate number of seeds per siliqua (19.66), a moderate thousand seed weight (2.70 g) and shortest days to maturity (75.00 days).

Plate 5: Photograph showing branch, siliqua and seeds of SAU 2 × BARI 6, F_7S_4 ,75 days

Plate 6: Photograph showing branch, siliqua and seeds of BARI 9 × BARI 6, F_7, Yellow

Plate 7: Photograph showing branch, siliqua and seeds of SAU 1 × BARI 15, F_8, 75 days

CHAPTER V

SUMMARY AND CONCLUSION

A field study was conducted to evaluate fifteen advanced population of *B. rapa* to estimate the magnitude of variation, heritability, genetic advance, correlation and direct and indirect effect of different yield and yield contributing characters on seed yield. The experiment was executed following Randomized complete block design (RCBD) with three replications in the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka- 1207, from November 2018 to February 2019.

From variability analysis revealed that there were significant variations among all advanced populations of *B. rapa* L. for each character which indicate the considerable variations among the genotypes studied. Among all the advanced populations considering the parental lines BARI 9 × BARI 6, F_7, Yellow was the earliest genotype in respect of days to first flowering compare to the parental lines Tori 7 and the longest days to first flowering was observed in BARI 6 × BARI 15, F_{10}, 75 days. Days to 50% flowering was noticed earlier in BARI 9 × BARI 6, F_7, Yellow compare to the parental lines Tori 7. The longest days to 50% flowering was observed in BARI 6 × BARI 15, F_{10}, 75 days. The SAU 1 × BARI 15, F_8, 75 days and BARI 9 × BARI 6, F_7, Brown required minimum period of days to mature compare to the parental lines BARI 14. The longest period of days to maturity was found in SAU 2 × BARI 6, F_7S_4, Yellow. Plant height was found highest in TORI 7 × BARI 15, F_7, 85 Days which was higher than SS-75. The lowest plant height was found in BARI 9 × BARI 6, S_5F_{16}, Brown. Maximum length of root was found in Yellow special, F10,75 days whereas minimum in BARI 9 × BARI 6, F_7, Brown. Maximum number of primary branches per plant was noticed in SAU 2 × BARI 6, F_7S_4, Yellow which was compared to BARI 12 and minimum number of primary branches per plant was found in BARI 6 × BARI 15, F_{10}, 75 days. Tori 7 was found more number of secondary branches per plant than BARI 9 × BARI 6, S_5F_{16}, Brown and lowest number of number of secondary branches per plant was found in BARI 6 × BARI 15, F_{10}, 75 days. The highest number of siliquae per plant was noticed in population BARI 9 × BARI 6, F_7, Yellow which was more than Tori 7 and lowest number of siliquae per plant. Siliqua length was longer (6.52 cm) in SAU 2 × BARI 6, F_7S_4, Yellow compared to the parental lines BARI 17 while shorter was found in BARI 9 × BARI 6, F_7, Brown. The maximum number of seeds per siliqua was recorded in BARI 17 which was less than BARI 6 × BARI 15, F_{10}, 75 days. The minimum number of seeds per siliqua was recorded in BARI 9 × BARI 6, F_7, Yellow. Maximum thousand seed weight was found in SAU 2 × BARI 6, F_7S_4, Yellow compared to the SS-75 Whereas, minimum seed weight was recorded in BARI 9 × BARI 6, S_5F_{16}, Brown. Highest yield performance per plant was observed in SAU 2 × BARI 6, F_7S_4, Yellow and the lowest seed yield per plant was observed in BARI 9 × BARI 6, F_7, Brown. SAU 2 × BARI 6, F_7S_4, Yellow (7.84 g) was found more seed yield per plant than SS-75 (4.47 g).

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

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

High heritability with low genetic advance was observed in days to first flowering, days to 50% flowering, days to maturity, number of primary branches per plant and number of secondary branches per plant indicating the non-effective selection of the populations for these traits.

Significant genotypic and phenotypic positive association with seed yield per plant were observed in days to maturity, plant height (cm), number of siliquae per plant, length of siliqua (cm) and thousand seed weight (g) through the correlation analysis.

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

Selection was conducted among SAU 2×BARI 6, F_7S_4, Yellow, BARI 9 × BARI 6, F_7, Yellow and SAU 1 × BARI 15, F_8, 75 days advanced populations of *B. rapa* based on their yield and yield contributing characters. Based on the variability and as per our objectives, the highest seed yield per plant was noticed in SAU 2×BARI 6, F_7S_4, Yellow with highest number of primary branches per plant, number of secondary branches per plant and thousand seed weight (g). Earlier maturity was found in BARI 9 × BARI 6, F_7, Yellow and SAU 1 × BARI 15, F_8, 75 days with moderate seed yield per plant. Moreover, it may be considered as advanced population SAU 2×BARI 6, F_7S_4, Yellow, BARI 9 × BARI 6, F_7, Yellow and SAU 1 × BARI 15, F_8, 75 days were performed best among the studied genotypes and selected as a potential candidate for varietal releasing a new mustard variety in Bangladesh.

CHAPTER VI

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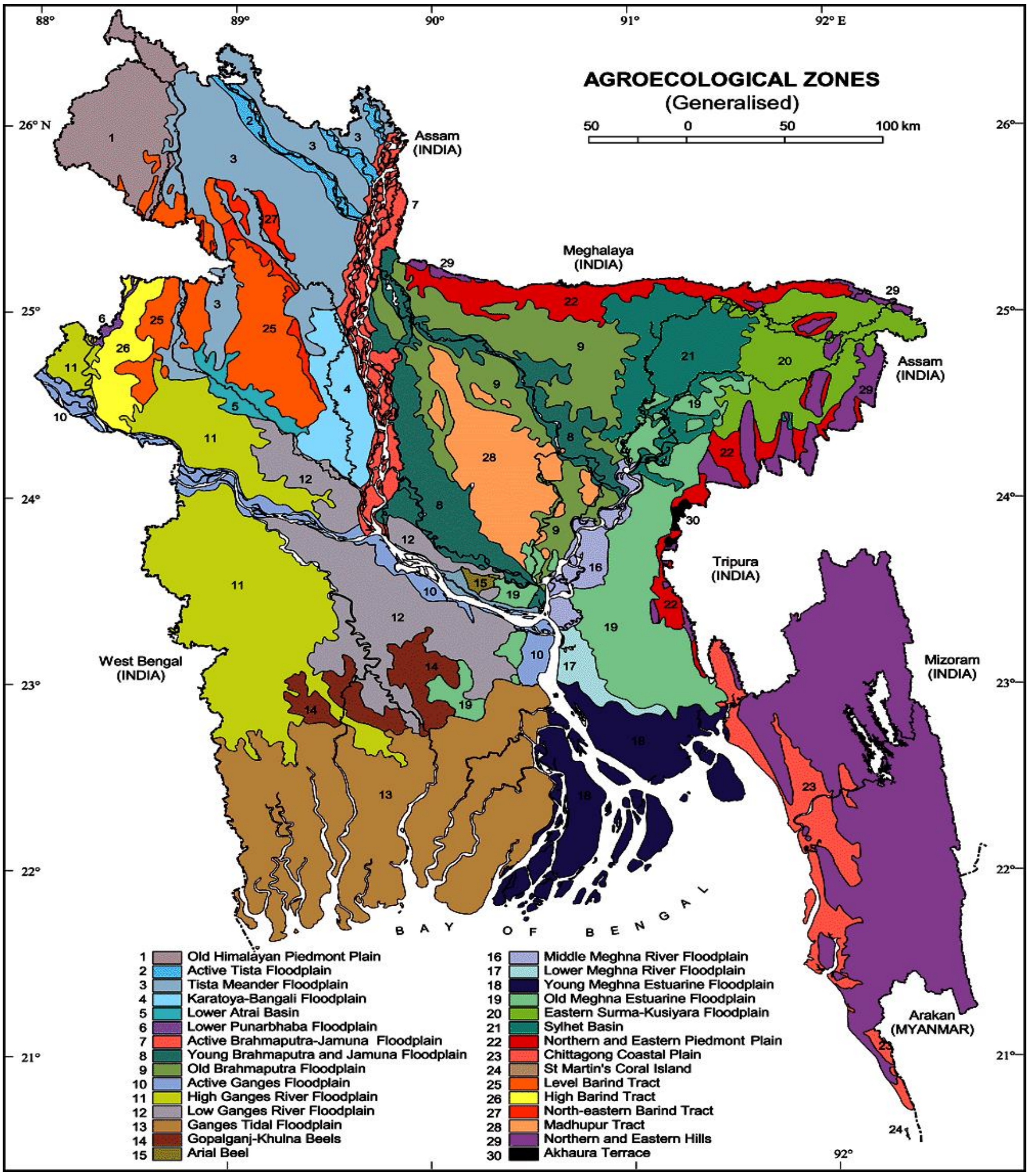
APPENDICES

Appendix I. Map showing the experimental site under the study



🟧 **Legend showing the research site**

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

A. Physical composition of the soil:

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

A. Chemical composition of the soil:

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

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

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

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

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

Appendix IV: Analysis of variance of 12 important character of 15 advanced population of *Brassica rapa* L.

Source of Variation	**Degrees of freedom**	**Mean sum of square of characters**											
		Days to 1st flowering	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Root length (cm)**	**Number of primary Branches /plant**	**Number of secondary branches /plant**	**Length of siliqua (cm)**	**Number of seeds /plant**	**Number of seeds /siliquae**	**1000 seed weight (g)**	**Seed Yield /plant (g)**
Replication	2	1.87	2.07	2.07	48.18	3.13	0.60	0.00022	0.29	851.22	1.4601	0.49	2.25
Genotypes	14	12.52**	20.18**	61.53**	258.61**	2.63^{NS}	3.86**	3.17**	0.33**	1408.31**	16.97**	0.57*	3.44**
Error	28	1.96	2.66	3.19	48.32	1.68	0.34	0.19	0.09	406.97	5.48	0.21	0.89

** Significant at 1% level of significance * Significant at 5% level of significance NS = Non significance

Appendix V: Analysis of variance of 12 important character of 7 parental lines of *Brassica rapa* L.

Source of Variation	**Degrees of freedom**	**Mean sum of square of characters**											
		Days to 1st flowering	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Root length (cm)**	**Number of primary Branches /plant**	**Number of secondary branches /plant**	**Length of siliqua (cm)**	**Number of seeds /plant**	**Number of seeds /siliquae**	**1000 seed weight (g)**	**Seed Yield /plant (g)**
Replication	2	1.48	1.48	4.90	192.32	0.86	0.07	0.51	0.20	301.85	5.59	0.06	0.32
Genotypes	6	39.89**	76.08**	91.32**	209.33*	7.40**	0.83*	13.28**	2.30**	3850.90**	30.50**	1.29**	1.34*
Error	12	1.70	2.03	5.29	60.83	1.28	0.26	0.24	0.08	318.65	2.84	0.04	0.44

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

Appendix VI: Values of mean, range and CV (%) of twelve characters of 15 advanced population of *Brassica rapa* L.

Advanced population	DFF	DFPF	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
SAU 2 × BARI 15, F_8, 80 days												
Mean	29.33	36	79.33	104.93	10.47	4.87	1.9	137.2	6.54	16.57	2.78	4.52
Range	29-30	35-38	79-80	86-123	8-17	3-9	0-16	37-551	4.02-7.18	5.4-27.4	2.2-3.26	1.41-11.63
CV(%)	1.97	4.811	0.73	1.43	9.01	13.37	18.23	15.33	11.65	2.96	19.33	22.14
SAU 2×BARI 6, F_7S_4, Yellow												
Mean	29.67	33	91	105.26	12.28	8.1	3.17	122.9	6.54	19.82	3.87	7.84
Range	29-30	33-33	90-92	84.6-123.8	8.4-17.3	5-12	0-12	69-331	4.1-8.9	8-30	3.82-3.96	4.21-16.39
CV(%)	1.95	0	1.09	7.22	13.05	9.32	19.03	63.52245	11.65	10.54	2.09	13.17
TORI7×BARI15, F_7, Yellow												
Mean	31.67	39.33	85	103.09	12.78	7.47	0.33	84.47	5.47	21.29	2.45	3.75
Range	30-33	39-40	82-91	83-120.6	10.3-17.9	4-11	0-4	47-148	4.36-6.08	11-26	2-2.94	1.75-6.92
CV(%)	4.82	1.47	6.11	6.07	1.41	3.37	17.32	12.98	1.19	2.79	19.28	4.01
BARI 9× BARI 6, S_5F_{16}, Brown												
Mean	28.33	34.67	83	87.52	10.14	4.73	3.73	138.83	5.97	18.83	2.1	4.85
Range	27-30	33-38	82-85		7.2-15	3-8	0-6	85-265				1.68-9.42

CV(%)	5.39	8.33	2.09	66.4-116 7.69	12.67	5.31	27.35	4.03	4.24-8.74 7.93	10.4-25.4 2.31	1.85-2.48 15.93	21.93
Yellow special, 80 days Mean Range CV(%)	32.67 32-33 1.767399	38 38-38 0	87 85-88 1.98	104.5 71.5-135 13.14	11.83 7.2-16.3 11.30	4.97 2-7 9.08	2.33 0-9 12.93	141.67 48-283 20.05	5.49 3.84-7.52 0.65	17.93 9.4-31.4 7.67	2.97 2.3-3.41 19.89	5.37 2.18-8.85 20.26
SAU 1 × BARI 15, F_8, 80 days Mean Range CV(%)	31.33 29-33 6.64	37.33 34-40 8.18	79 79-79 0	105.88 86-139 7.54	11.81 7.5-18.5 6.91	4.93 3-10 20.30	1.67 0-6 15.09	141.07 60-324 16.99	5.49 4.1-7.06 3.91	19.12 9.8-28.2 8.44	2.36 2.24-2.43 4.42	5.63 2.76-12.55 19.18
SAU 1 × BARI 15, F_8, 75 days Mean Range CV(%)	31 29-33 6.45	38 35-40 6.96	75 75-75 0	111.68 91-129 2.69	11.96 8-17.5 13.34	4.4 2-9 17.16	1.57 0-9 19.50	124.63 49-413 18.21	5.44 4.28-6.28 2.47	19.66 11.2-28.8 2.54	2.70 2.35-3.14 14.85	5.75 1.26-15.78 23.78
BARI 9 × BARI 6, F_7, Yellow Mean	27.33	32.67	76	100.62	10.79	5	2.4	168.47	5.72	13.38	3.02	5.67

Range	27-28	32-33	76-76	83-118.2	6.7-16	3-9	0-8	86-365	4.54-7.36	7.2-23.8	2.5-3.63	2.26-12.86
CV(%)	2.11	1.77	0	2.97	13.47	15.62	23.20	14.52	5.41	7.04	18.89	19.77
SAU 1 × BARI 15, F_7E_3 Long												
Mean	32	39	81	116.77	11.88	5.27	1.3	125.9	6.06	21.16	3.07	5.06
Range	31-33	38-40	81-81	96-140	8.4-17	2-16	0-9	56-320	4.22-7.16	6.8-29.2	2.43-3.69	2.78-10.06
CV(%)	3.13	2.56	0	5.85	8.01	20.30	22.05	14.48	4.63	17.13	20.51	5.51
BARI 9 × BARI 6, F_7, Brown												
Mean	28.67	34	75	89.1	10.04	5.07	3.03	135.2	5.20	19.09	2.33	3.57
Range	27-30	33-35	75-75	72-121	7-15.5	3-8	1-7	71-365	4.38-6.3	7.4-27.6	2.05-2.8	1-7.87
CV(%)	5.33	2.94	0	1.68	19.83	3.01	18.16	18.54	2.56	15.47	17.58	16.28
BARI 15 × SS75, F_{11}, 75 days												
Mean	29.67	36.67	78	93.29	11.57	4.23	1.5	104.1	5.97	20.32	2.60	4.86
Range	29-30	35-38	78-78	74-120	8-17	2-9	0-9	33-340	5.06-7.58	8.2-26.8	2.27-3.11	2.14-11.8
CV(%)	1.95	4.17	0	8	9.85	9.83	20	16.45	5.59	7.96	17.13	17.96
TORI 7 × BARI 15, F_7, 85 days												
Mean	32.33	39.67	83	117.75	11.93	5.13	1.27	137.4	5.65	20.03	2.83	6.93
Range	32-33	39-40	83-83			3-8	0-8	75-241				1.71-14.53

CV(%)	1.79	1.46	0	97.5-143 7.21	7.2-16.5 2.23	5.62	16.43	20.86	4.1-6.32 8.18	11.4-27.6 19.86	2.5-3.45 18.86	20.73
BARI 6 × BARI 15, F$_{10}$, 75 days Mean Range CV(%)	34.67 33-36 4.40	41 39-42 4.22	78.67 75-82 4.46	112 91-132 6.97	12.21 5.5-16 2.80	4.1 2-7 6.45	0.26 0-2 21.65	93.93 60-169 6.08	5.51 4.58-6.88 1.62	24.09 10.2-30.6 9.85	2.25 1.61-2.78 26.34	5.10 1.65-12.9 15.75
BARI 6 × BARI 15, F$_7$, 85 days Mean Range CV(%)	28.67 27-30 5.33	37.67 37-38 1.53	82 82-82 0	113.71 93.5-152 5.48	11.76 7-21 16.92	4.83 3-7 7.83	1.17 0-10 17.84	121.2 50-269 14.78	5.58 4.74-7.44 4.80	18.63 8.8-27.8 18.77	2.94 2.36-3.35 17.60	5.41 2.28-10.93 20.06
Yellow special, F$_{10}$, 75 days Mean Range CV(%)	32.67 30-35 7.70	40 39-42 4.33	78 78-78 0	100.35 82-123 5.73	13.38 8.5-22.2 15.02	4.17 2-8 12.31	0.6 0-5 16.67	104.1 44-214 19.97	5.47 4.28-6.9 2.06	20.66 12.6-26.8 14.65	2.76 2.29-3.4 20.72	5.14 2.04-13.52 18.98

CV (%) =Percentage of Co variance

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

Appendix VII: Values of mean, range and CV (%) of twelve characters of 7 parental lines of *Brassica rapa* L.

Parental lines	**DFF**	**DFPF**	**DM**	**PH**	**RL**	**NPB/P**	**NSB/P**	**NS/P**	**LS**	**NS/S**	**TSW**	**SY/P**
Tori 7 Mean Range CV(%)	28 27-29 3.57	34 33-35 2.94	84 83-85 1.19	88.64 76-105 1.76	9.84 7.5-15 5.59	4.63 3-8 10.65	6.13 0-16 19.31	164 87-298 19.25	5.21 3.6-6.7 0.38	15.88 9.8-25 6.56	1.72 1.66-1.8 4.19	4.23 1.03-11.2 15.85
BARI 14 Mean Range CV(%)	30.67 29-33 6.79	37 36-38 2.70	81 80-82 1.23	95.57 78-125 10.78	9.96 5.5-18 5.45	4.23 2-7 18.95	1.3 0-5 20.35	111.03 42-220 20.80	5.46 4.56-6.48 1.74	14.28 8.8-20.6 4.85	2.19 2-2.38 8.67	2.75 1.01-4.88 22.42
BARI 15 Mean Range CV(%)	36.33 36-37 1.59	44.33 44-45 1.30	86.33 85-89 2.67	93.24 77-107 4.36	9.08 5-13.4 7.74	3.8 2-6 18.42	0 0-0 0	69.5 32-120 19.09	5.01 4.2-5.72 3.44	20.76 14.6-28 7.63	2.11 2-2.17 4.41	3.39 1.47-5.08 28.16
BARI 17 Mean Range	36.33 36-37	45 44-46	90.67 90-92	97.47 85-120	12.21	3.4 2-7	1.13 0-8	79.03 40-158	7.56 5.34-8.64	22.73	2.92 2.67-3.3	3.26 1.07-7.74

CV(%)	1.59	2.22	1.27	6.88	6.5-23 7.26	5.88	18.37	9.26	10.37	22.6-29.5 10.66	11.38	18.15
BARI 6												
Mean	35.33	45	87.33	101.62	11.37	4.7	2.23	133.5	5.67	15.06	2.17	4.38
Range	35-36	44-46	85-92	73-156	7.5-15	3-8	0-8	77-231	4.43-7.5	8.76-22.8	2.05-2.3	2.2-7.8
CV(%)	1.63	2.22	4.63	16.48	18.69	3.69	20.68	9.26	2.81	10.55	5.81	12.91
SS-75												
Mean	36.67	46.33	97.33	113.87	13.38	3.97	0	87.77	6.44	17.20	3.53	4.47
Range	35-39	45-48	95-101	90-130	9-18	1-9	0-0	37-160	4.34-8.62	9.6-26.6	3.2-3.88	2.38-7.54
CV(%)	5.68	3.29	3.30	6.07	9.56	1.37	0	13.93	1.13	17.94	9.66	9.28
BARI 12												
Mean	30	37	92.67	91.72	9.62	4.8	2.53	144.53	5.62	15.47	1.75	3.31
Range	29-31	34-39	92-94	76-105	5.2-15	3-7	0-6	49-222	4.3-6.84	8-19.2	1.72-1.78	0.72-5.45
CV(%)	3.33	7.15	1.25	8.38	12.46	0	18.23	8.51	2.29	5.15	1.71	18.28

CV (%) =Percentage of Co variance

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

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