COMPARISON AMONG EIGHT ADVANCED POPULATIONS FOR YIELD AND YIELD CONTRIBUTING TRAITS OF *Brassica rapa* L.

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CERTIFICATE

This is to certify that thesis entitled, **"COMPARISON AMONG EIGHT ADVANCED POPULATIONS FOR YIELD AND YIELD CONTRIBUTING TRAITS OF Brassica rapa L".** *submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by* ***Ahmad Ullah****, Registration No. : 12-05108 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2018
Place: Dhaka, Bangladesh

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DEDICATED TO

MY

BELOVED PARENTS

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SAU, Dhaka ***The Author***

COMPARISON AMONG EIGHT ADVANCED POPULATIONS FOR YIELD AND YIELD CONTRIBUTING TRAITS OF *Brassica rapa* L.

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ABSTRACT

The research was based on the evaluation of eight advanced populations of *Brassica rapa* L. received from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, considering 10 yields and yield contributing traits, using randomized complete block design (RCBD) with three replications during rabi season from 1st November 2017 to February 2018 at GEPB research farm of Sher-e-Bangla Agricultural University. The analysis of variance showed significant variation in all the traits except number of secondary branches per plant and length of siliqua. The phenotypic variances were higher than genotypic variances in all traits except days to 50% flowering, days to 80% maturity, plant height, number of sliliquae per plant, number of seeds per siliqua and yield per plant. High heritability coupled with moderate genetic advance was found in number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight and yield per plant. The correlation studies revealed that yield per plant had highly significant positive relation with number of primary branches per plant, number of siliquae per plant and number of seeds per siliqua. Path analysis showed that thousand seed weight, siliquae per plant had highly significant and positive direct effect on the yield per plant. Among the populations L2 was found as the best populations comparing with the checks and found days to 80% maturity at 78 DAS, number of primary branches/plant (5.02), number of siliqua/plant (120) and yield/plant (7.48 g). By comparing, it might be concluded that populations L1, L2 L4 and L8 had potential for future improvement based on the genetic merit of yield and yield contributing factors.

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SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of variation	CV
Days after sowing	DAS
Degree of Celsius	^oC
Degree of freedom	D.F.
Et cetera	etc.
Food and Agriculture Organization Corporate Statistical Database	FAOSTAT
Genetics and Plant Breeding	GEPB
Genotypic correlation	r_g
Gram	g
Genotypic Coefficient of variation	GCV
Genotypic variation	δ^2g
Genetic Advance	GA
Hectare	ha
Heritability in broad sense	h^2b
Hydrogen ion potentiality	pH
Kilogram	kg
Least significant difference	LSD
Millimeter	mm
Mean Sum of Square	MSS

SOME COMMONLY USED ABBREVIATIONS (CONT'D)

FULL WORD	ABBREVIATION
Muriate of Potash	MP
Milliliter	mL
Milli gram	mg
Meter	m
Metric ton	MT
Number	No.
Per cent	%
Phenotypic variance	$\delta^2 p$
Phenotypic coefficient of variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sixth generation of a cross between two dissimilar homozygous parent	F_6
Sixteenth generation of a cross between two dissimilar homozygous parent	F_{16}
Sher-e-Bangla Agricultural University	SAU
Species	*sp.*
Square meter	m^2
Standard error	SE
Standard deviation	SD
Triple Super Phosphate	TSP
Variety	Var.
Zinc Oxide	ZnO

CHAPTER I
INTRODUCTION

Brassica rapa L. belongs to the family Brassicaceae and commonly known as field mustard or turnip mustard usually cultivated as an oil seed crops. Rapeseed and mustard are the third most important oil crops in the world (FAO-2017). It is widely grown for leafy vegetables in China, Japan and Korea, for vegetable oil in India, China, and Canada, for edible oil in Bangladesh and Indian sub-continents, and used as a fodder crop in Europe. In Bangladesh three major mustard *species Brassica rapa* (2n = 20, AA), *Brassica juncea* (2n = 36, AABB) *and Brassica napus* (2n = 38, AACC) are commonly cultivated. It is believed that *Brassica rapa* was introduced into China through western Asia or Mongolia as an agricultural species. The introduction into Japan could have occurred via China or Siberia. *Brassica rapa* is cultivated in Bangladesh as an oilseed, but no wild forms are known in Bangladesh. It is also cultivated as an oilseed crop in Sweden and Finland, and in Canada. Seven groups of vegetable *Brassica rapa* types are known, and these are: *var. campestris, var. pekinensis, var. chinensis, var. parachinensis, var. narinosa, var. japonica and var. rapa*. Until recently, these groups were considered as separate species because of the wide range of variability they represent and the fact that they evolved in isolation from each other.

Rapeseed is the third leading source of edible oil in the world. Rapeseed oil (RSO) is the most useful of all cooking oils and it contains a significant amount of ω-3 and ω-6 fatty acids. RSO contains mostly of the fatty acid such as oleic, linoleic, linolenic, palmitic and strearic acid (Hui, 1996). The oil content usually makes up about 40-60% of rapeseed. RSO consists 95% of tri-acyl glycerols (TAG) and 5% non-tri-acyl glycerols, known as minor components like free fatty acids, mono and di-acyl glycerols, phospholipids, tocopherols, tocotrienols, flavonoids, other phenolic compounds, pigments, sterols etc.

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

Rapeseed is a crop supplying edible oil as well as for industrial uses. It is not only a high energy food but also a carrier for fat soluble vitamins (A, D, E and K) in the body. Poor intake of fat and oil reduce the availability of fat soluble vitamins and caused dietary imbalance and food wastage. In a balanced diet 20-25% of calories should come from fats and oils and the average need of fats and oil is about 38g per day (Rahman, 1981). It also serves as important source of raw material for different industrial uses such as in making soaps, paints, hair oils, lubricants, textile auxiliaries, pharmaceuticals etc. oil cakes and meals are used as animal feeds and manures.

In 2015-2016, the edible oil production from major oilseed crops in the world is 535 million tons where rapeseed contributes 68 million tons (FAOSTAT, 2017). Total area of mustard and rapeseed in the world is 35.52 million hectares. Global consumption of oils/fats has reached around 211 million tons in 2015-16, up by less than 3 per cent year-on-year and below the average growth of recent years. Production of oils/fats recorded average annual increases of 4–5 per cent during the last three seasons, but the latest crop forecasts for 2015-16 would translate into a 1.6 per cent slide. The year-on-year drop would mainly be on account of lower cottonseed, soybean and rapeseed oil productions (FAOSTAT, 2017).

One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be of great importance in planning a successful breeding program. Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations (Shukla *et al*., 2006). Seed yield is a complex character that can be determined by several components reflecting. The present study was undertaken to find out the variability range, to select desired plant type of early maturity, to study the relation between different traits and the direct and indirect contribution of each trait towards yield in the advanced populations of *Brassica rapa* L.

In Bangladesh, it is very important to cultivate oil crops. The cultivated crops are mustard, linseed, sunflower, soybean, sesame, etc. These covers 4.87 lakh ha areas and the production oil is 6.62 lakh MT. This production rate is one-third of our daily requirement. Per capita consumption of edible oil is 11.25 kg per year (FAOSTAT, 2017). Total edible oil consumption is forecast to rise 2.7 per cent in 2015-16 owing to increased population, rising income levels, changing consumer behavior, and increasing oil use as an ingredient in various feeds.

Among all oilseeds *Brassica rapa* occupies 1st position in respect of area and production among the oils crops grown in Bangladesh. Other two major local cultivar, *Brassica juncea* and *Brassica napus* are high yielding but they are not short durable. Though low yielding *Brassica rapa* is widely grown in the country because of their short duration (Islam, 2013). About 901477 MT of edible oil produced in Bangladesh which is very low against requirement (BBS-2015). Singly *Brassica rapa* contributes 359445 MT which represent major oil seed crops in Bangladesh (BBS-2015). This contribution fulfills our requirement approximately 50%. Although short durable variety like Tori-7 of *Brassica rapa* is still popular in Bangladesh because it can fit well into T. aman-Mustard-Boro cropping pattern. But there is lack of improved short durable variety with higher yield. Above scenario indicates we should attempt to develop short durable and high yielding verities of mustard with higher adaptability and stability.

In Bangladesh, the cultivation practice of mustard has been implemented in a span of times. From the last few decades, the cultivation of rice is increasing day by day which is replacing the cultivated area of mustard. For accomplishing the demand, we import around 50% oil from foreign countries. Bangladesh has to spend a huge amount of foreign exchange on imports of edible oils and oilseeds to meet the increasing demand of its population. The value of imports is increasing year after year which is burden for us. As the population of Bangladesh is increasing and economic prosperity has been growing fast, it is now a challenge for accelerating the production of oils. It is essential to reduce the import dependence of it to insulate the domestic market from the volatility of the world market (Hossain, 2013). Farmers usually cultivate the existing low yielding varieties with low input and management. There is no improved short duration variety. They need short duration varieties of T. Aman and Boro rice so that they can successfully cultivate oilseed crops in between two rice crops.

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

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

In this context, different populations were developed through selection of the materials from different segregating generations obtained through inter-varietal hybridization of *Brassica rapa* L. The 8 populations used in this experiment were in F_6 and F_{16} populations. These populations were compared with leading checks of mustard and the performance was evaluated to find out populations that may solve the current problems of mustard.

Therefore, 8 different advanced populations evaluate on the basis of different yield and yield contributing characteristics and the research work was under taken with following objectives:

1) To select promising populations considering early maturity and higher yield
2) To identify short durable *Brassica rapa* with desirable traits and
3) To study the yield and yield contributing characteristics of the populations

CHAPTER II
REVIEW OF LITERATURE

In case of *Brassica rapa* yield and yield contributing traits are complex trait, polygenic in inheritance, more prone to environmental fluctuations than other traits such as branches per plant, seeds per siliqua and thousand seed weight. For better understanding the association between yield and its components characters is of paramount importance for making the best use of these relationships in selection. The path coefficient analysis helps breeders to explain direct and indirect effects, and hence been extensively used in breeding experiments in different crop species. An evaluation is a scientific method, in which the acquired knowledge is tested by observation by setting a standard. It can use quantitative or qualitative data, and often includes both. The analysis of the relationship among the traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. A pertinent literature has been reviewed under mentioned broad heads:

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

2.1 Genotypic and phenotypic coefficient of variation

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

Tyagi *et al.* (2001) evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. Highest variation for plant height of parents and their hybrids was reported. The seed yield per plant exhibited the highest coefficient of variation (41.1%). Genetic variability for 9 traits in 25 genotypes study by Pant and Singh (2001), Analysis of variance revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. The genotypic coefficient of variation estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

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

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

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

Akbar *et al.* (2007) evaluated eight advanced lines of *Brassica junea* in Pakistan and studied variability of different yield components that were under experiment. The highest GCV was found in seed yield per plant followed by plant height, siliqua per plant and thousand grain weights while lowest GCV was in number of primary branches per plant. Rashid (2007) studied variability of 40 oleiferous *Brassica* species. Result revealed that genotypes showed wider variation for morphological characteristics and thus were categorized under three cultivated species - *B. rapa, B. napus and B. juncea* considering genetic parameters. High GCV (Genotypic Co-efficient of Variation) value was observed for days to 50% flowering, days to maturity, plant height and number of siliqua per plant.

Dash *et al.* (2007) conducted an experiment on fifty genotypes of toria with 14 characters to estimate genetic variability for earliness and other yield attributes in toria (*Brassica rapa* L. Var. toria). Analysis of variance revealed considerable variability among 50 toria genotypes for all the fourteen characters under study. For all the characters, PCV was higher than GCV. Secondary branches per plant and leaf area index reflected high estimates of GCV and PCV.

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

Alam (2010) conducted an experiment by using twenty six F4 populations of some inter-varietal crosses of *Brassica rapa* L. to study the variation among them. Higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found plant height, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.Roy *et al.* (2011) conducted an experiment on rapeseed mustard (*Brassica* spp.) and studied variability. The result revealed that significant varietal difference except the number of siliqua on main recyme. The PCV and the GCV was high in secondary branches per plant and number of siliqua per plant.

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

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

Mekonnen (2014) evaluated thirty six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were observed for number of pods per plant, primary and secondary braches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in primary branches per plant. Higher GCV and PCV for seed yield, number of pods per plant, primary and secondary branches which indicated that, it might provide better scope for improvement through selection.

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

Iqbal *et al.* (2015) carried out an investigation to study the genetic variability parameters of procured germplasm for various traits *viz*., days to 50% flowering, days to maturity, plant height (cm), no. of primary branches plant^{-1}, no. of secondary branches plant^{-1}, no. of pods plant^{-1}, thousand seed weight (g) and seed yield ha^{-1}. The set of 49 genotypes of brown sarson (*Brassica rapa* Var. Brown sarson) were grown. PCV was higher than corresponding GCV for all the traits studied. High GCV was observed in seed yield plant^{-1}, whereas moderate GCV was revealed in no. of primary branches plant^{-1} and no. of secondary branches plant^{-1}. High values of heritability have been recorded for 50% flowering, days to maturity, no. of primary branches plant^{-1}, no. of secondary branches plant^{-1} and seed yield ha^{-1} (g). Yared and Misteru (2016) studied on sixty four *Brassica* breeding lines for investigated of some morphological characters to identify the extent and nature of genetic variability during 2014 cropping season. Analysis of variance showed the existence of considerable genetic variation among the lines for further selection and hybridization efforts.

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

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

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

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

Heritability studied of yield components in Indian mustard among 12 yield components for 36 genotypes selected from different geographical regions by Ghosh and Gulati (2001). All the characters studied estimates of high heritability except plant height. High heritability, coupled with high genetic advance was observed for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua. This result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection. In a study of heritability in Indian mustard for 10 characters during rabi season in India by Choudhary *et al.* (2003). High heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action.

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

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

Dash *et al.* (2007) conducted an experiment on fifty genotypes of toria with 14 characters to estimate heritability for earliness and other yield attributes in toria (*Brassica rapa* L. Var. toria). High estimates of broad sense heritability coupled with high genetic advance as percent of mean were observed for secondary branches per plant, leaf area index, and specific leaf weight, reflecting greater contribution of genetic component.

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

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

Alam (2010) conducted an experiment by using twenty six F_4 populations of some inter-varietal crosses of *Brassica rapa* L. to study the variation among them. Higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found plant height, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.

Afrin *et al.* (2011) conducted an experiment in *Brassica napus* and studied heritability. The plant height showed highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliquae, number of siliqua per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

Roy *et al.* (2011) conducted an experiment on rapeseed mustard (*Brassica* spp.) and studied heritability. High heritability along with high genetic advance as percent of mean was reported in plant height, seed yield, secondary branches per plant, siliqua per plant and seeds per siliqua. Tahira *et al.* (2011); conducted an experiment with ten wide genetic ranged variety of *Brassica juncea* to study heritability in broad sense and showed siliqua length, plant height and seed yield had high values. Patel and Vyas (2011) experimented with three high yielding varieties and two very low quality varieties and their six generation cross product of *Brassica napus*. The result showed that the heritability in broad sence with high to moderate genetic advance was found in thousand grain weights, seed yield per plant. Moderate to high heritability associated with low genetic advance was recorded in days to maturity and days to flowering

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

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

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

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

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

Salam *et al.* (2017) carried out a research on experimental materials comprised 30 F_1 from a 6 x 6 diallel crosses to estimate the heritability. The highest heritability estimates were observed for the traits erucic acid content followed by plant height, branches per plant, seed yield per plant, siliqua length, days to 50% flowering and harvest index (%). Genetic advance as percentage of mean was observed high for the character number of siliquae per plant, followed by seed yield per plant, days to maturity and plant height.

2.3 Correlation analysis

Analysis of correlation among different traits is important in breeding program. A good number of literatures are available on correlation among characters of *Brassica* sp. Some of these literatures are reviewed here:
Gouping *et al.* (1999) studied on the phenotypic and genotypic correlations of 11 agronomic characters with 14 cultivars of mustard. The results showed that the phenotypic correlations were lower than genetic correlations. The genetic correlation coefficients between flower stalk weight and flower stalk width in diameter, leaves number, blade weight, petiole weight and plant height were highly significant.

Days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. The number of branches per plant and number of siliquae per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight was reported by Malek *et al.* (2000) while studied correlation analysis

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

An experiment conducted by Niraj and Srivastava (2004) on character association studies in Indian mustard of 21 genotypes of *Brassica juncea*. Seed and oil yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

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

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

An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee *et al.* (2006) to study the correlation analysis. The results revealed that yield per plant highest significant positive correlation with number of siliqua per plant. Zahan (2006) studied correlation and reported that yield/plant had highly significant positive association with plant height, length of siliqua, siliquae/plant and seed/siliquae but insignificant negative association with days to 50% flowering, days to maturity.

Tusar *et al.* (2006) studied phenotypic correlation and observed that seed yield per plant was positively and significantly associated with plant height, total dry matter production. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Akbar *et al.* (2007) evaluated eight advanced lines and two check variety of *Brassica junea* in Pakistan and reported that siliqua per plant had strong positive correlation with the seed yield followed by plant height while non-significantly negative correlation with thousand grain weight. But significantly negative correlation was present in siliqua per plant and primary branches per plant

Parveen (2007) conducted an experiment with F2 population of *Brassica rapa* to study the correlation and observed that yield per plant had non-significant positive association with plant height, number of secondary branches per plant, number of seeds per siliquae and number of siliquae per plant, days to 50% flowering and length of siliqua. Rashid (2007) carried out an experiment with 40 oleiferous *Brassica* species to estimate correlation and observed that, highly significant positive association of yield per plant with number of primary branches per plant , number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

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

Singh (2010) studied sixty two F1 and twenty four parental lines of Brassica juncea and observed that positive correlation was present in plant height, primary branches per plant, secondary branches per plant, seed per siliquae, thousand grain weight with seed yield. Afrin *et al.* (2011) studied on *Brassica napus* and found positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliqua per plant. Highest significant positive correlation was found between days to 50% flowering and plant height.

Maurya *et al.* (2012) carried out an experiment with one hundred genotypes of *Brassica juncea* and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50% flowering. Ali *et al.* (2013); conducted an experiment with thirty lines of *Brassica carinata* and observed that highly positive phenotypic correlation for seed yield per plant with plant height and primary branches per plant which was the indication that the traits were the most important contributors to seed yield per plant.

Mokonnen *et al*. (2014) studied *Brassica carinata* and found that seed yield per plant were positively correlated with plant height, days to maturity, secondary branches per plant and thousand seed weight at both genotypic and phenotypic level. There were also found that plant height was strongly and positively correlated with number of pods per plant

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

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

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

2.4 Path co-efficient analysis

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

Srivastava and Singh (2002) reported that number of primary branches per plant, number of secondary branches per plant and 1000 seed weight had strong direct effect on seed yield while working with Indian mustard (*B. juncea* L. Czern and Coss). Results suggested that number of primary branches and 1000 seed weight were vital selection criteria for improvement-in productivity of Indian mustard.

A study was conducted by Tusar *et al.* (2006) to assess the nature and extent of variability of 11 yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Path coefficient analysis revealed that the number of siliqua per plant had the greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliqua per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive direct effect on yield, but its correlation with yield was non-significant and negative.

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica species* to estimate path analysis and observed that yield per plant had the highest direct effect on days to maturity, number of seeds per siliqua, number of siliquae per plant and number of primary and secondary branches per plant. Aytac *et al.* (2008) evaluated on six genotypes of spring rape seed and studied path coefficient and the result stated that plant height, number of siliqua per plant, seeds per siliquae had highest and positive direct effect on yield per plant for all cultivars except cv. Star.

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

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

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

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

Islam *et al.* (2016) studied on 21 F_9 populations which is derived from inter-varietal crosses of *Brassica rapa* L. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliqua, and siliqua length had the positive direct effect on yield per plant and days to 50% flowering, number of secondary branches per plant, and thousand seed weight had the negative direct effect on yield per plant. Kumari *et al.* (2017) reported that the path coefficient analysis of biological yield showed maximum direct effect, while silique length and oil content exerted negative direct effect on seed yield and days to 50 percent flowering exerted negative indirect effect on seed yield.

CHAPTER III

MATERIALS AND METHODS

The investigation entitled to **“**Comparison among eight advanced populations for yield and yield contributing traits of *Brassica rapa* L**.’’** was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. The information regarding the materials and methodology of this experiment is discussed below in detail:

3.1 Experimental site

The experiment was conducted at the Sher-e-Bangla Agricultural University, Dhaka-1207 from November 2017 to February 2018. The experimental area was situated at 23°46'16" N latitude and 90°22'46" E longitude at an altitude of 8.8 meter above the sea level. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28. The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.2 Soil and climate

The soil of the experimental fields was clay loam. The land was medium high and the fertility level was medium. The site was in the subtropical climate zone. Climatic feature of this region was wet summer and dry winter. During the Rabi season, generally the rainfall is very few, the temperature is moderate and the day length is short. The records of air temperature, humidity and rainfall during the period of experiment were noted from the weather station, Sher-e-Bangla Agricultural University, Dhaka 1207.

3.3 Planting materials

The research work was carried out by using 8 advanced lines of *Brassica rapa* which was collected from Sher-e-Bangla Agricultural University, Dhaka. These populations were developed by selecting the materials from different segregating generations obtained through different inter-varietal hybridization of *Brassica rapa* L. The advanced lines which were used in the experiment are shown below in Table 1.

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

Designation	Populations	Sources
L1	BARI Sarisha- 9 X BARI Sarisha-6 F_{16}, S5	GEPB, SAU
L2	BARI Sarisha-6 X Tori-7 F_{16}, S3	GEPB, SAU
L3	BARI Sarisha-9 X F_6 F_{16}, S2	GEPB, SAU
L4	BARI Sarisha- 6 X Tori-7 F_{16}, S2	GEPB, SAU
L5	BARI Sarisha- 9 X BARI Sarisha- 6 F_{16}, S2	GEPB, SAU
L6	BARI Sarisha- 6 X Tori-7 F_{16}, S5	GEPB, SAU
L7	BARI Sarisha- 6 X BARI Sarisha- 15 F_6, S7	GEPB, SAU
L8	BARI Sarisha-6 X Tori-7 F_{16}, S4	GEPB, SAU

3.4 Experimental layout

The field experiment was designed in Randomized Complete Block Design (RCBD) with three (3) replications. The plot size was 201.5 m^2. Row length was maintained as 3.5 m having 0.75 m irrigation channels among the rows. The distance between line to line was 30 cm and plant to plant was 10 cm.

3.5 Field practice

3.5.1 Soil and field preparation

The field was prepared by doing several plough and cross plough followed by laddering and harrowing using power tiller to have fine tilth and optimum level of moisture condition. Weeds and stubbles were removed from the field. During final land preparation, cowdung was applied and leveled the field properly (plate 1).

Plate 1. The experimental field during land preparation.

3.5.2 Fertilizer and manure application

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

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

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

3.5.3 Seed selection and sowing time

Healthy and pure seeds were taken by avoiding the unfilled seeds. Seeds were sown as lines in the experimental field on 1st November, 2017. The seeds were placed at about 1.5 cm depth in the soil. Clods were removed during sowing. Seeds were started to germinate after 3 days of sowing.

3.5.4 Intercultural operations

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

3.5.4.1 Tagging and tying

When the plants are visible after 1 week of germination, then tagging of each population of all replication was done. The field was bound with rope to protect the plants from leaning by using bamboo. Tagging of each population of all replication was done after a week of sowing (Plate 2).

Plate 2. Tagging of each population of entire field

3.5.4.2 Weeding and thinning

Two times weeding and thinning was done according to the requirement of maintaining uninterrupted growth of the crop. The first weeding was done after 14 days of sowing. Thinning was done at the same time for maintaining 30 cm from line to line and 10 cm from plant to plant. Second weeding was done after 21 days of sowing.

3.5.4.3 Irrigation and after care

The experimental plot was lightly irrigated after sowing by using watering canes to bring proper moisture condition of the soil ensuring uniform germination of seeds. Second irrigation was given (20 DAS) before the flower initiation. Third irrigation was given (40 DAS) when the pod appeared. Fourth irrigation was given (60 DAS) when seeds appeared in the pod. Good drainage system was maintained to drain out the excess water. During irrigation, special care was taken of so that the water pressure might not break the shoots of the plants.

3.5.4.4 Pesticide application

Flea beetle and Aphid infection was found during the vegetative and siliqua development stage of the crop. Ripcord-10 EC @ 1mL/liter of water was sprayed to flea beetle and Malathion-57 EC @ 2mL/liter to control aphids. Insecticide was applied in the afternoon to protect the beneficial insect.

3.5.5 Harvesting

Harvesting was started from 2 February to 15 February, 2018 depending upon maturity of the plants. Plants are harvested when 80% showed symptoms of maturity such as, straw color of siliqua, leaves, stem and desirable seed color in the mature siliqua. At maturity, 10 plants were selected for morphological analysis from the populations. The sample plants were harvested by uprooting and tagging was done specifically for analyzing morphological and biochemical traits. Photograph showing the entire view of experimental field during fruiting stage in (Plate 3).

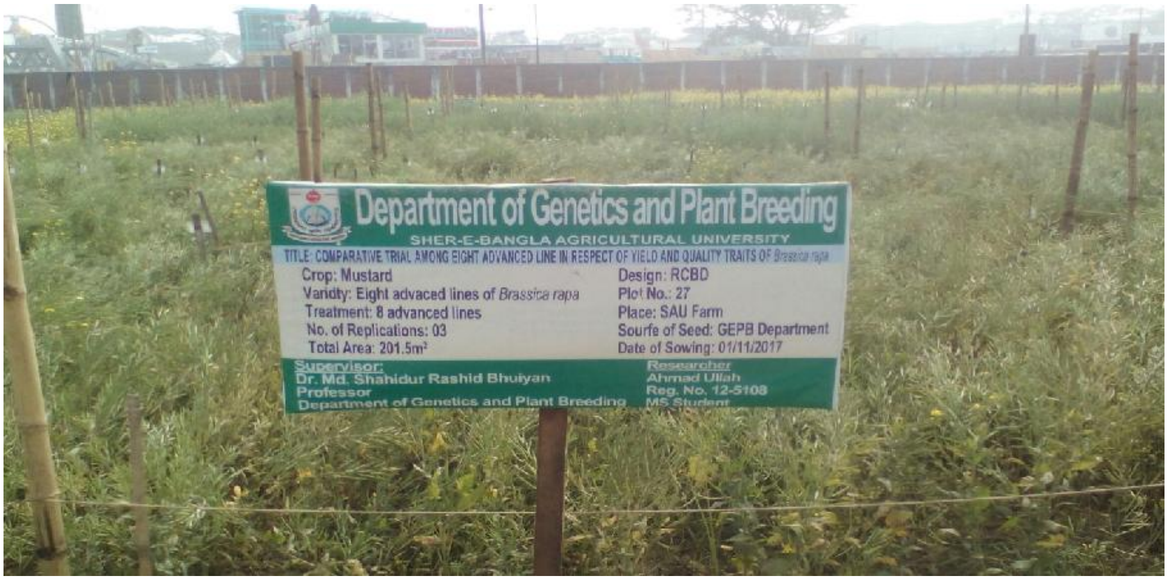

Plate 3. The entire view of experimental field during fruiting stage

3.5.6 Collection of data

To study different genetic parameters and inter-relationships the following ten characters were taken into consideration: 1. plant height, 2. days to 50% flowering, 3. days to 80% maturity, 4. of primary branches/ plant, 5. of secondary branches/ plant, 6. of siliqua/ plant, 7. length of siliqua, 8. of seeds/ siliqua, 9. thousand seed wt., 10. yield/plant.

Plate 4. Photograph showing flowering stage in the experimental at field level

Plate 5. The experimental field view during fruiting stage

Plate 6. Field view at Maturity of stage *Brassica rapa L.*

3.6 Data collection methods

3.6.1 Days to 50% flowering

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

3.6.2 Days to 80% maturity

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

3.6.3 Plant height (cm)

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

3.6.4 Number of primary branches/ plant

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

3.6.5 Number of secondary branches/ plant

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

3.6.6 Number of siliqua/ plant

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

3.6.7 Length of siliqua (cm)

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

3.6.8 Number of seeds/ siliqua

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

3.6.9 Thousand-seed weight (g)

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

3.6.10 Yield/ plant (g)

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

3.7 Statistical analysis

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

3.7.1 Analysis of variance

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

Table 3. ANOVA

Sources of variation	**Degrees of freedom (D.F.)**	**Mean sum of squares (MS)**	**Expected MS**
Replication Population Error	(r-1) (p-1) (p-1) (r-1)	Mr Mp Me	p $б_r^2 + б_e^2$ r $б_p^2 + б_e^2$ $б_e^2$
Total	(rp-1)		

Where,

r = number of replications

p = number of treatments (population)

$б_r^2$ = variance due to replications

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

$б_e^2$ = variance due to error

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

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

Where, S. E = Standard error of mean

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

r = Number of replications

q = Number of population in each sub-block

u = Weightage factor computed

3.7.2 Study of variability parameters in mustard populations

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

3.7.2.1 Genotypic variance and phenotypic variance

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

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

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

3.7.2.2 Co-efficient of variability

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

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

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

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

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

3.7.2.3 Heritability in broad sense (h^2)

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

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

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

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

3.7.2.4 Genetic advance (GA)

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

GA = $h^2_{bs} \times б_p \times$ K

Where,

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

$б_p$ = Phenotypic standard deviation of the trait

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

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

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

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

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

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

3.7.3 Correlation coefficient analysis

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

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

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

Where,

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

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

$б_g^2$ and $б_p^2$ are the genotypic and phenotypic variance of x and y, respectively.

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

3.7.4 Path coefficient analysis

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

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

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

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

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

Where,

r's denote simple correlation co-efficient and P's denote path co-efficient (unknown). P's in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x_1 and y is thus partitioned as follows:

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

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

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

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

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

Where,

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

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

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

Categories

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

High 0.30 to 1.0; Very High >1.00

CHAPTER IV
RESULTS AND DISCUSSION

The experiment was carried out with a view to identify short durable *Brassica rapa* L. with desirable traits by comparing the performance of 8 advanced populations on ten characters of *Brassica rapa* L. The study was also conducted to find out the phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, correlation, path co-efficient to estimate direct and indirect effect of yield contributing traits on yield. The study was also taken to find out the beneficial effect of analyzed acids. The data were recorded on different characters such as days to 50% flowering, days to 80% maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, no. of seeds per siliqua, siliqua length (cm), thousand seed weight (g), yield per plant (g).The data were statistically analyzed by MSTAT-C and OPSTAT and obtained the following results which described below.

- Mean performance and genetic variability
- Correlation analysis
- Path co-efficient analysis
- Selection

4.1 MEAN PERFORMANCE AND GENETIC VARIABILITY

The success in any crop improvement program depends on the ability of the breeder to define and assemble the required genetic variability, and to select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather, 1949). Therefore, it is necessary to have prior information on both PCV and GCV, so that the estimate of heritability that helps the breeder to foretell the expected GA possibly by selection for a character can be enumerated.

Out of the ten characters studied, plant heights, number of primary branches per plant, number of secondary branches per plant were considered as growth attributing characters. Days to 50% flowering and days to 80% maturity were regarded as earliness attributes. Number of siliquae per plant, length of siliqua, number of seeds per siliqua and thousand seed weight were reckoned as reproductive traits. Yield per plant was the economic trait. The analysis of variance of the data on different yield components and yield of 8 populations was significant (Appendix III). The mean performance and range for all the characters were also significant (Table 4). The results are pertained to mean values grand mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GA) for all the ten characters are embellished in (Table 5) . Days to 80% maturity and yield per plant, genotypic and phenotypic variability is shown in Figure 2 and heritability and genetic advance as per cent of mean has shown in Figure 3.

4.1.1 Days to 50% flowering

Significant variance was observed in days to 50% flowering (Appendix III). The maximum duration to days to 50% flowering was found in L7 with 35.667 DAS and the minimum in L2 with 27.33 DAS (Table 4). The mean value was 30.292. Ali *et al*. (2002) found days to 50% flowering for parents and it was ranged from 39 to 46 days. The earliness of 50% flowering of population indicates that the plant matures early. Minimum days to 50% flowering was found in L2 (27.33) indicates that flower came early DAS and it is short durable population.

The phenotypic variance (9.11) was higher than genotypic variance (8.46). High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al*. (1998). Thus, genes controlling this trait experienced less influence of environment on the expression of the character. The GCV (Genotypic co-efficient of variation) and PCV (Phenotypic co-efficient of variation) were low with value of 9.6 and 9.96 per cent, respectively along with high heritability of 92.88% with moderate genetic advance as per cent mean of 19.06%` and low genetic advance (5.77) (Table 5). This moderate value might be due to moderate values for phenotypic variability as the heritability is high for these characters and selection differential is always constant (Nadarajan and Gunasekaran, 2005). Sikawar *et al.* (2017) found that days to flowering showed low PCV and GCV. The flowering trait of the plant was very much sensitive and influenced by the temperature fluctuation which is reflected in the present study. High heritability and low genetic advance indicating that the traits were being exhibited due to favorable influence of environment rather than genotype. Thus, it is indicative that non-additive gene action might be controlling the trait of expression and selection for this trait may not be recommended. In the contrast to the present results, High heritability was being exhibited due to favorable influence of environment rather than genotype. Thus, selection for this trait may not be rewarding. But, Sikarwar *et al*. (2017) reported high heritability and low genetic advance for days to flowering.

4.1.2 Days to 80% maturity

The average of 81.13 days with a range of 78.33 to 87.33 days was recorded for days to 80% maturity. The L2 required least number of days to mature (78.33 days) followed by L1 (79.00 days), whereas maximum number of days to 80% maturity was observed in the population L7 (82.33 days) followed by L5 (83.33 days) (Table 3). The shortest time required for 80% maturity in Tori-7 (81 days) was reported by Ali *et al.* (2002). L2 showed lowest days to maturity (78.33) which indicating that it matures early rather than the other populations.

Days to 80% maturity exhibited low GCV and PCV of 3.61 and 3.84 per cent, respectively along with high heritability of 88.29 per cent, low genetic advance 5.67 and low genetic advance as per cent mean of 6.98 per cent (Table 5).This high heritability with low genetic advance was indicative of non-additive gene action. High heritability is less influenced by the environment. Thus, the selection for improvement of such trait might not be useful. Jahan *et al.* (2014) observed high heritability with low genetic advance in per cent of mean for days to maturity. The genotypic and phenotypic variance was recorded as 3.61 and 3.84, respectively. Genotypic variance was lower than phenotypic variance which means that there is some influence of environment in the expression of genes for this trait. Ara *et al.* (2010) found high heritability with low genetic advance and genetic advance in percentage of mean.

4.1.3 Plant height (cm)

Plant height was observed highest in L7 (107.73 cm) and lowest in L8 (94.56 cm). The mean value was recorded as 101.o6 cm and mean of sum of square was 68.4 indicating significant differences among the populations for this trait (Table 3). The lowest plant height was found in L8 (94.56 cm) which showed least leaning than the other populations.

Genotypic and phenotypic variance was observed 25.29 and 21.96 respectively for plant height with large environmental influence. Ara *et al.* (2010) found the highest difference between genotypic and phenotypic variance in plant height. Naznin *et al.* (2015) also found the similar results. The plant height exhibited low genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 4.61 and 4.95 per cent, respectively (Table 5). High heritability of 86.67 per cent, moderate genetic advance 8.93 along with moderate genetic advance as per cent mean (8.83%) was recorded. High heritability with moderate genetic advance showed that it is controlled by non-additive gene effects and the selection may be ineffective for improvement of *Brassica rapa* L. Jahan *et al.* (2014) found high heritability with moderate genetic advance in per cent of mean for plant height. But, Fayyaz *et al*. (2014) found highest heritability coupled with higher genetic advance in plant height.

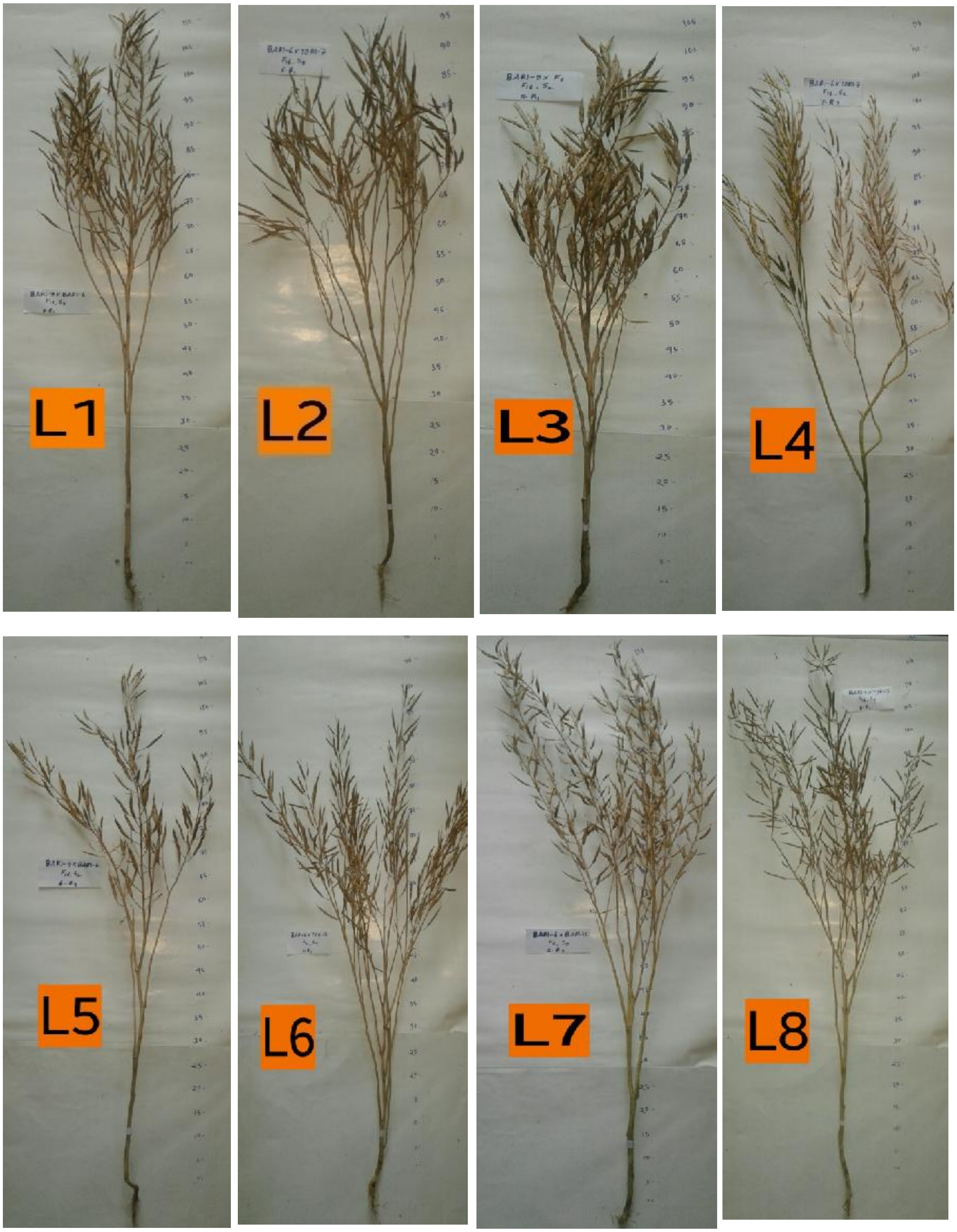

Plate 7. Sowing plant heights and Branches of 8 advanced lines of *Brassica rapa* L.

Plate 8. Length variation in siliqua of different Advanced lines of *Brassica rapa* L.

Table 4. Mean performance of different characters of 8 advance lines *Brassica rapa L.*

A. L.	DF	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Y/P
L1	28.333	79.000	103.567	4.367	1.750	117.727	5.593	14.667	3.633	7.033
L2	27.333	78.333	99.267	5.020	1.450	120.853	5.300	14.527	2.747	7.487
L3	28.667	80.667	100.767	4.800	1.607	122.257	5.690	14.873	3.503	6.940
L4	31.667	79.333	102.567	4.653	1.677	121.783	5.427	14.543	3.133	7.320
L5	33.333	83.333	105.457	4.567	2.273	124.440	6.050	14.433	3.050	6.533
L6	28.333	79.333	94.600	4.123	1.600	100.547	6.383	15.113	2.500	6.013
L7	35.667	87.333	107.733	5.667	1.510	96.543	5.077	11.983	3.137	5.653
L8	29.000	81.667	94.567	4.650	2.067	118.900	6.003	16.223	3.217	7.303
Min.	27.333	78.333	94.567	4.123	1.450	96.543	5.077	11.983	2.500	5.653
Max.	35.667	87.333	107.73	5.667	2.273	124.44	6.383	16.223	3.633	7.487
Mean	30.292	81.125	101.06	4.731	1.742	115.38	5.690	14.545	3.115	6.785

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

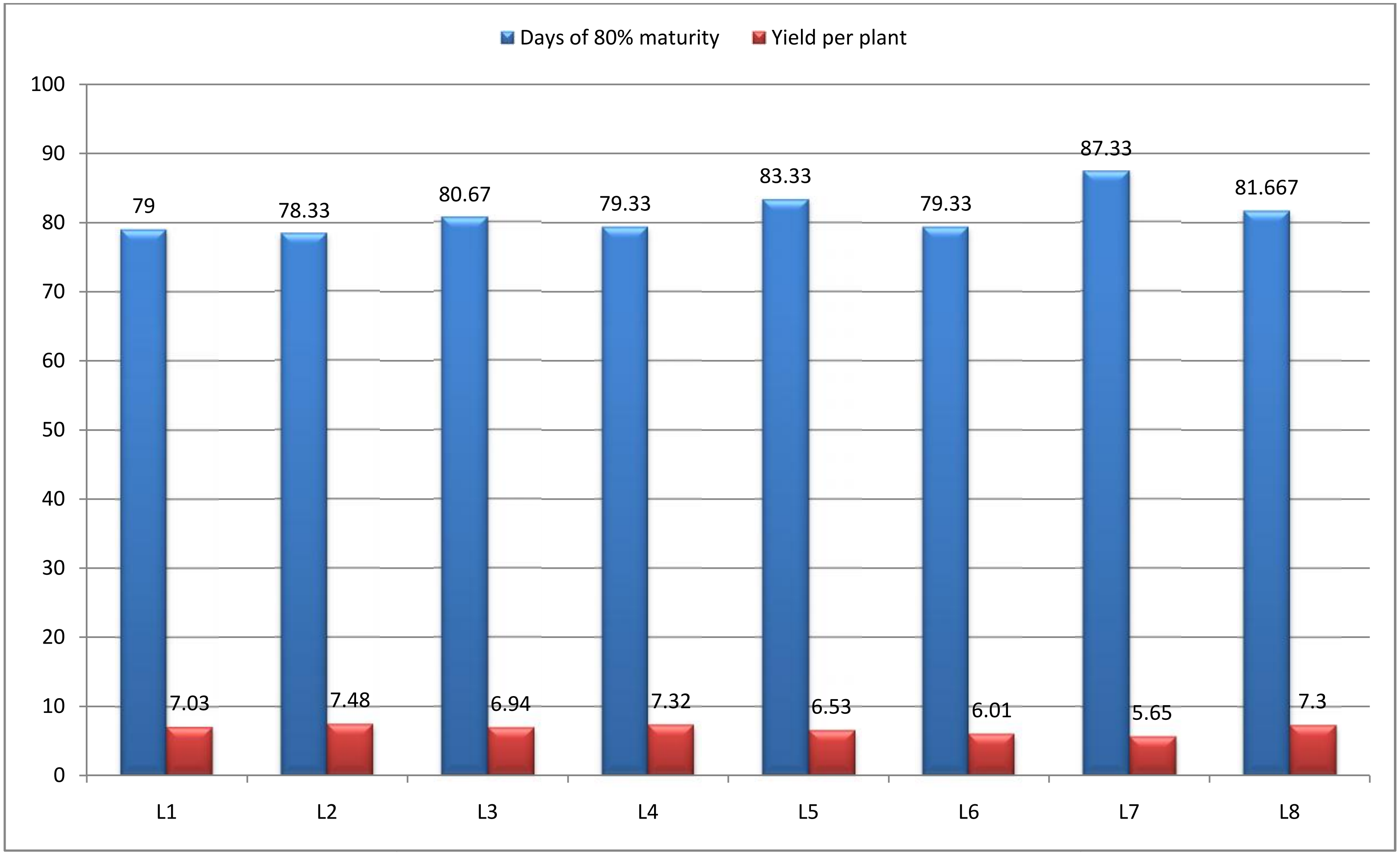

Fig 1. Showing days of 80% maturity and yield per plant of 8 advance populations

Table 5. Estimation of genetic parameters for different characters in *Brassica rapa* advance populations

Traits	$\pm^2$p	$\pm^2$g	$\pm^2$ e	PCV	GCV	h^2	GA (5%)	GA (% mean)
Days to 50% flowering	9.113	8.464	0.649	9.966	9.604	92.880	5.776	19.068
Days 80% maturity	9.677	8.57	1.37	3.841	3.609	88.289	5.667	6.985
Plan height (cm)	25.295	21.96	3.335	4.950	4.608	86.673	8.932	8.838
Primary branches per plant	0.235	0.21	0.025	10.178	9.609	89.123	0.884	18.687
Secondary branches/plant	0.114	0.065	0.049	19.385	14.646	57.086	0.397	22.796
Siliqua per plant	125.256	107.272	17.984	9.701	8.978	85.646	19.748	17.116
Length of siliqua (cm)	0.209	0.177	0.032	8.035	7.401	84.822	0.799	14.041
Seeds per siliqua	1.66	1.278	0.381	8.857	7.773	77.019	2.044	14.052
1000 seeds weight (g)	0.165	0.121	0.044	13.025	11.167	73.504	0.614	19.722
Seed yield per plant (g)	0.806	0.256	0.550	15.516	8.736	31.700	0.586	10.133

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

PCV : Phenotypic coefficient of variation
GCV : Genotypic coefficient of variation

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

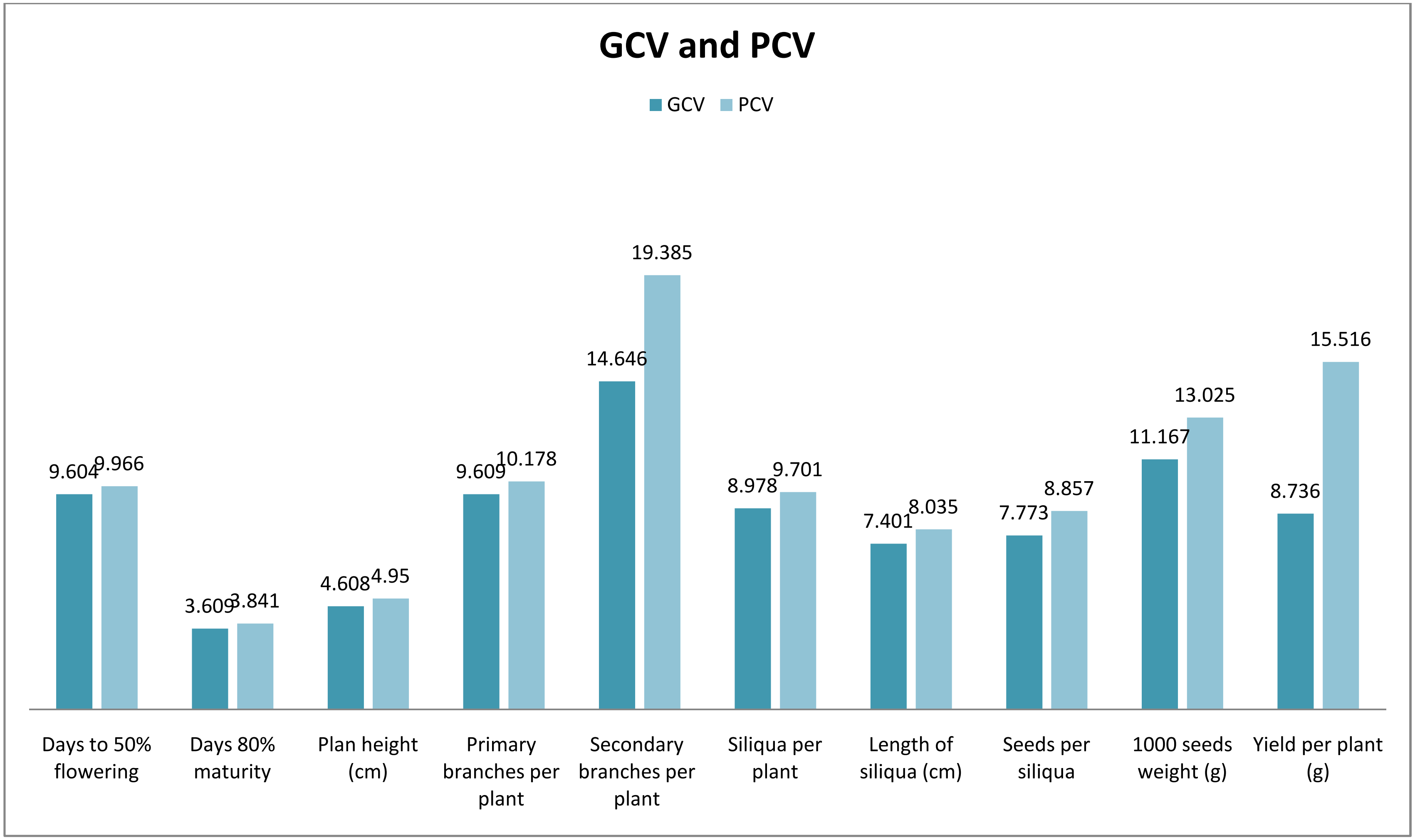

Fig. 2. Genotypic and phenotypic variability of ten character in *Brassica rapa* L.

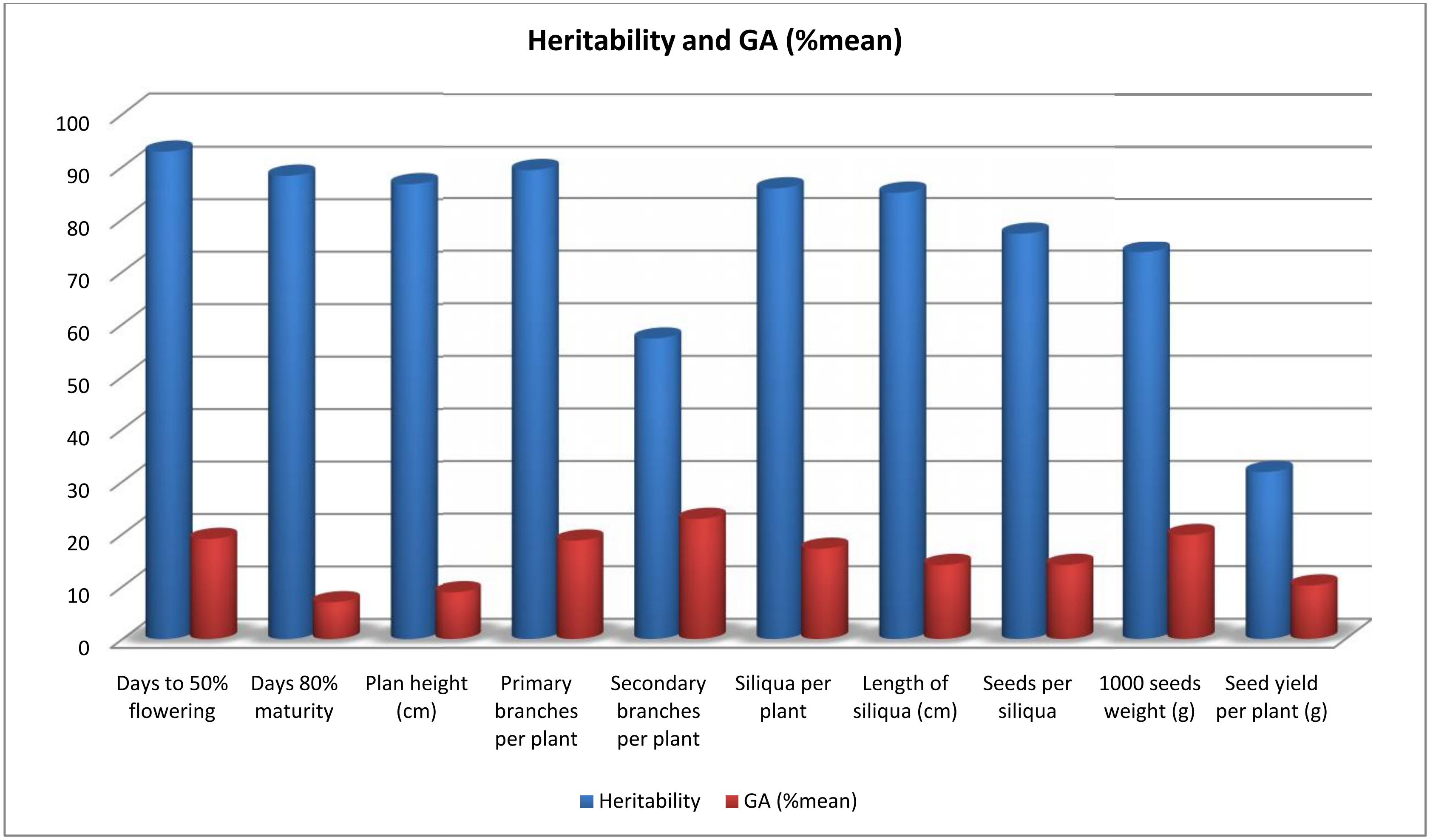

Fig. 3. Heritability & Genetic Advance (% mean) in *Brassica rapa* L.

4.1.4 Number of primary branches per plant

The mean of sum of square for number of primary branches per plant was recorded as 0.645. The maximum number of primary branches per plant were found in L7 (5.67) and the minimum number of primary branches per plant were found in L6 (4.123) with mean value 4.73 (Table 4). L7 showed the maximum no. of primary branches per plant (5.67) indicating more siliqua than the other populations which ultimately increased yield per plant.

The genotypic and phenotypic variance was recorded as 0.21 and 0.24, respectively. Low genotypic co-efficient of variation (GCV) and moderate phenotypic co-efficient of variation (PCV) of 9.61 and 10.18 per cent were observed, respectively (Table 5). Naznin *et al.* (2015) found that number of primary branches/plant showed low differences between the phenotypic variance (1.27) and genotypic variance (0.86) which indicated that there was less influence of environment on this character. Findings of Hosen *et al.* (2008) was also agreed with this result. High heritability 89.12%, low genetic advance (0.88) high genetic advance as per cent mean 18.68% shows that non-additive gene effects were present, making selection ineffective for this trait.

4.1.5 Number of secondary branches per plant

The mean sum of square for number of secondary branches per plant was significantly recorded as 0.24. The maximum number of secondary branches per plant were found in L5 (2.27) and the minimum number of secondary branches per plant were found in L2 (1.45) with mean value 1.74 (Table 4). The maximum no. of secondary branches per plant was showed by L5 (2.27) which is a good sign for increasing the yield and ultimately it showed the maximum the yield rather than the others population.

The genotypic and phenotypic variance was recorded as 0.065 and 0.114, respectively. Moderate genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 14.64 and 19.38 per cent were observed, respectively (Table 5). Dash *et al*. observed that secondary branches per plant reflected high estimates of GCV and PCV. This is an agreement with Parveen *et al*. (2015) and Naznin *et al.* (2015). Medium heritability 57.08%, low genetic advance (0.39) and high genetic advance as per cent mean 22.79% shows that non-additive gene effects were present, making selection ineffective for this trait.

4.1.6 Number of siliquae per plant

Number of siliquae per plant ranged from 96.54 to 124.44 with mean value 115.38 in different populations. The maximum number of siliquae per plant was noticed in population L5 (124.44) followed by population L3 (122.26). The population L7 recorded the minimum number of siliquae per plant (96.54) (Table 4). Naznin *et al.* (2015) observed that the number of siliquae/plant showed the highest range of variation (78.00 -180.33) which means the presence wide range of variation for this character. The mean sum of square reported significant for this trait (339.8) (Appendix).

The phenotypic variance (125.25) was higher than genotypic variance (107.27). This indicates some influence of environment on this character. Comparatively higher phenotypic coefficient of variation (9.7%) than genotypic coefficient of variation (8.97%) (Table 5) indicated presence of less considerable variability among the populations. High genotypic variance indicates the better transmissibility of the character from parent to their offspring (Ushakumari *et al.,* 1991). The heritability (85.64%) estimates for this trait was high, moderate genetic advance (19.74) and moderate genetic advance in per cent of mean (17.11) were found (Table 5), revealed that high heritability coupled by moderate genetic advance may be due to moderate values for phenotypic standard deviation as the heritability is high for these characters and selection differential is always constant (Nadarajan and Gunasekaran, 2005). Thus, these traits could be exploited for future trial.

4.1.7 Length of siliqua (cm)

The mean of siliqua length was 5.69cm and ranged from 5.07 to 6.38cm. The L6 had long length of 6.38 cm followed by L5 (6.05). The siliqua were shorter in L7 (5.07 cm) followed by L (5.3 cm) and L (5.42 cm) (Table 4). The mean sum of square was not significant (0.56) which indicated less considerable amount of variation for this trait in the populations (Table 4). Length of siliqua was found the maximum in L6 (6.38 cm) showed 15.11 seeds per siliqua. So, selection will be effective for this trait of this population.

The genotypic and phenotypic variance for siliqua length was seen as value of 0.177 and 0.209, respectively. Siliqua length exhibited low GCV (7.4%) and PCV (8.04 %) values. As PCV is higher than GCV thus we can conclude that the trait is controlled by its genotype as well as influence of environment. A high heritability estimates of 84.82%, low genetic advance 0.80 and a moderate genetic advance as per cent of mean of 14.04% were observed. High heritability with combination of moderate genetic advance as per cent of mean allow us to speculate the presence of non-additive gene effects on this trait. Sikarwar *et al.* (2017) found high heritability with moderate genetic advance in case of length of siliqua. The experimental findings of Naznin *et al.* (2015) also found it.

4.1.8 Number of seeds per siliqua

Number of seeds per siliqua ranged from 11.98 to 16.22 in different populations. The maximum number of seeds per siliqua was recorded in population L8 (16.22) followed by population L6 (15.11). However, the minimum number of seeds per siliqua exhibited in population L7 (11.8) (Table 4). The mean observed for this trait was 14.54. Ali *et al.* (2002) observed that the hybrid of *Brassica rapa* L. produced an excellent number of seeds per siliqua (25.06) which was much higher than the parents. Number of seeds per siliqua was found maximum in L8 (16.22) indicated higher yield than the others. So, selection for this trait of this population will be effective.

The genotypic variance was (1.27) and phenotypic variance was (1.66). Low GCV and PCV were observed as 7.73 and 8.85 respectively (Table 5). This indicates very little influence of environment upon the character. Whereas, it is showed high heritability (77.02%), low genetic advance (2.04) and moderate GA %mean (14.05%) for this trait. High heritability with low genetic advance indicates that high heritability occurs due to environmental effects. Thus, selection is ineffective for the improvement of the crop. Larik and Rajput (2000) estimated the low genetic advance for seeds per siliqua irrespective of their high heritability.

4.1.9 Thousand seed weight (g)

Thousand seed weight of different populations ranged from 2.5 g to 3.63 g. The population L1 was exhibited the maximum thousand seed weight (3.63 g) followed by population L3 (3.5 g), L8 (3.2 g), L7 (3.14 g) and L3 (3.13 g). Whereas, the population L6 was recorded the minimum seed weight of (2.5 g) followed by population L2 (2.74 g) and L5 (3.1 g). The grand mean found for this trait was (3.11 g) (Table 4). The mean sum of square was not significant (0.41) in *Brassica rapa* L. which allows to show the presence of less considerable variation for this trait. Ali *et al.* (2002) found variation in thousand seed weight in *Brassica rapa* L. with some extent i.e. from 5.33 to 5.83 g in parent and from 3.60 to 6.33 g in hybrid. The maximum thousand seed weight was found in L1 (3.63) indicating that the seeds of this population are bigger than others and seeds are filled more than the others indicated ultimate higher oil than the others. So, selection for this trait of L1 population will be effective.

Thousand seed weight recorded moderate PCV (13.03%) and GCV (11.16%) (Table 5). As PCV is greater than GCV, there is considerable influence of environment on this trait (Table 5). High heritability (73.5%), low genetic advance (0.614) and moderate genetic gain as percent of mean (19.72%) were found for this trait. High heritability with low genetic advance suggests that the character is governed by the non-additive gene action. Thus, selection may be ineffective in this trait for the improvement of the crop. High heritability with low genetic advance in thousand seed weight was observed by Parveen *et al*. (2015) which indicated the possibility of non-additive gene action.

4.1.10 Yield per Plant (g)

Yield ranged from L7 (5.653 g) to L2 (7.48 g), with a mean value of 6.8 g. The maximum yield was recorded by the population L2 (7.48 g) followed by L4 (7.32 g). The lowest yield was recorded by the population L7 (5.65 g) followed by L6 (6.01 g) (Table 4). The mean sum of square was significant (1.73). L2 showed maximum yield (7.48) than the other population which indicates that selection for this trait will be rewarding for improvement.

Yield per plant exhibited moderate estimates of PCV (15.516%) and low GCV (8.73%) in Table 5. Jahan *et al.* found high genotypic co-efficient of variation (GCV) for yield per plant by considering genetic parameters. Whereas, it also recorded moderate heritability (31.7%), low genetic advance (0.586) and lower genetic gain as per cent of mean (10.13%) for this trait. Hussain *et al.* (1998) observed the high estimates for heritability and genetic advance for yield per plant. Selection would be ineffective for this trait as there are non-additive gene effects on the gene controlling this trait.

4.2 CORRELATION ANALYSIS

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

So, the genotypic and phenotypic correlation co-efficient values for 10 characters in 8 advance populations of *Brassica rapa* L. was studied and presented in Table 6 and 7, respectively and in Figure 3.

4.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity ($r_g = 0.892$, $r_p= 0.826$). Narayan *et al.* (2006) reported that yield per plant had highly significant and positive correlation with days to 50% flowering. It exhibited also significant and positive correlation with plant height ($r_g = 0.753$, $r_p = 0.726$). It also presented significant and positive correlation with number of primary branches per plant ($r_g = 0.600$, $r_p = 0.519$), non-significant correlation number of secondary branches per plant ($r_g = 0.261$, $r_p = 0.127$), number of siliquae per plant ($r_g= -0.327$, r_p

= -0.334), siliqua length (r_g = -0.371, r_p = -0.267), number of siliquae per plant (r_g= -0.799, r_p = -0.644), yield per plant (r_g= -0.744, r_p = -0.472) and non-significant positive with thousand seed weight (r_g = 0.049, r_p = 0.081) (Table 6 and 7).

4.2.2 Days to 80% maturity

Days to 80% maturity showed significant and positive correlation with plant height (r_g = 0.595, r_p = 0.507), highly significant with number of primary branches per plant (r_g = 0.706, r_p = 0.622) at genotypic and phenotypic level. It had non-significant and positive correlation with number of secondry branches per plant (r_g = 0.238, r_p = 0.127), it had non-significant and negative correlation with number of siliquae per plant (r_g = -0.482, r_p = -0.431), length of siliqua (r_g = -0.256, r_p = -0.501), number of seeds per siliqua (r_g = -0.705, r_p = -0.611), significant negative with yield per plant (r_g = -0.975, r_p = -0.414) and positive non-significant thousand seeds weight (r_g = 0.109, r_p = 0.117. (Table 6 and 7) non-significant association of these traits indicated that the association between these traits was largely influenced by environmental factors. Lodhi *et al.* (2014) also revealed that days to maturity had non-significant and positive interaction with yield per plant. Naznin *et al.* (2015) also agreed with it.

4.2.3 Plant height (cm)

Plant height showed significant and positive correlation with number of primary branches per plant (r_g= 0.560, r_p = 0.512) and thousand seed weight (r_g = 0.457, r_p = 0.335). It was non-significant and negatively associated with number of secondary branches per plant (r_g= -0.015, r_p = -0.0001), number of siliquae per plant (r_g= -0.026, r_p= -0.026), and significant negative association with siliqua length (r_g = -0.687, r_p = -0.501), number of seed per siliqua (r_g= -0.895, r_p = -0.661) and significant negative with yield per plant (r_g = -0.410, r_p= -0.230). (Table-6 and 7).

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

Characters	DF	DM	PH	NPB/P	NSB/P	SN/P	LS	NS/S	TSW	Y/P
DF										
DM	0.892**									
PH	0.753**	0.595**								
NPB/P	0.600**	0.706**	0.560**							
NSB/P	0.261^{NS}	0.238^{NS}	-0.015^{NS}	-0.460*						
SN/P	-0.327^{NS}	-0.482*	-0.026^{NS}	0.333^{NS}	0.450*					
LS	-0.371^{NS}	-0.256^{NS}	-0.687**	-0.842**	0.614**	0.054^{NS}				
NS/S	-0.799**	-0.705**	-0.895**	-0.788**	0.449*	0.578**	0.671**			
TWS	0.049^{NS}	0.109^{NS}	0.457*	0.116^{NS}	0.255^{NS}	0.413*	-0.331^{NS}	0.031^{NS}		
Y/P	-0.744**	-0.975**	-0.410*	0.428*	0.065^{NS}	0.981**	-0.091^{NS}	0.918**	0.288^{NS}	

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

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

Table 7. Phenotypic correlation coefficient for ten characters of *Brassica rapa* L.

Characters	DF	DM	PH	NPB/P	NSB/P	SN/P	LS	NS/S	TSW	Y/P
DF										
DM	0.826**									
PH	0.726**	0.507*								
NPB/P	0.519**	0.622**	0.512*							
NSB/P	0.127^{NS}	0.127^{NS}	-0.000^{NS}	-0.230^{NS}						
SN/P	-0.334^{NS}	-0.431*	-0.026^{NS}	0.188^{NS}	0.449*					
LS	-0.267^{NS}	-0.254^{NS}	-0.501*	-0.749**	0.442*	0.041^{NS}				
NS/S	-0.644**	-0.611**	-0.661**	-0.689**	0.352^{NS}	0.462*	0.695**			
TWS	0.081^{NS}	0.117^{NS}	0.335^{NS}	0.089^{NS}	0.103^{NS}	0.333^{NS}	-0.268^{NS}	-0.071^{NS}		
Y/P	-0.472*	-0.414*	-0.230^{NS}	0.490*	0.154^{NS}	0.736**	-0.123^{NS}	0.362^{NS}	0.263^{NS}	

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

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

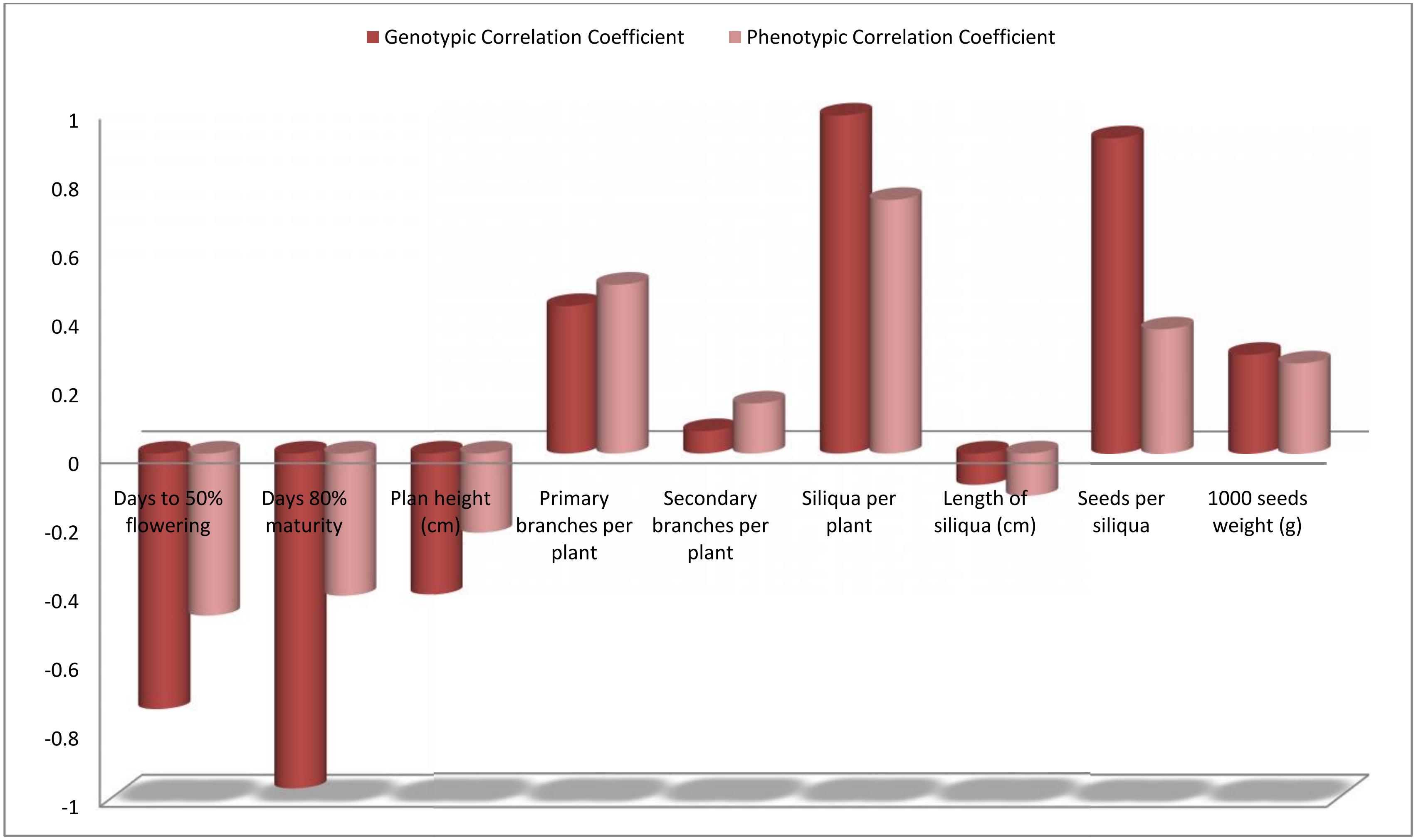

Fig. 4. Genotypic and phenotypic correlation of *Brassica rapa* L.

4.2.4 Number of primary branches per plant

Number of primary branches per plant was found to be negatively and significantly correlated with number of secondary branches per plant (r_g = -0.460, r_p = -0.230), number of seeds per siliqua (r_g = -0.788, r_p = -0.689) and length of siliqua (r_g = -0842, r_p= -0.749). Number of primary branches per plant had non-significant and positive interaction with number of siliquae per plant (r_g = 0.333, r_p = 0.188), thousand seed weight (r_g= 0.116, r_p= 0.103) and significant with yield per plant (r_g = 0.428, r_p = 0.490) Naznin*et al.* (2015) reported that yield/plant had significant positive correlation with number of primary branches/plant (Table 6 and 7). Rashid *et al.* (2007) found number of primary branches had positive and significant correlation with yield per plant.

4.2.5 Number of secondary branches per plant

The correlation of number of secondary branches per plant with number of siliquae per plant (r_g = 0.450, r_p = 0.449) was significant and positive association and yield per plant (r_g= 0.065, r_p = 0.154) was non-significant and positive which indicated that the traits were more influenced by environment. These findings showing similar to the reports of Rashid *et al*. (2007). It also had positive and highly significant correlation with siliqua length (r_g = 0.614, r_p = 0.442), and significant with number of seeds per siliqua (r_g = 0.449, r_p = 0.352), non significant thousand seed weight (r_g = 0.255, r_p = 0.101) (Table 6 and 7). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.2.6 Number of siliquae per plant

Siliqua per plant exhibited highly significant and positive correlation with number of seeds per siliqua (r_g = 0.578, r_p = 0.462) and yield per plant (r_g = 0.981, r_p = 0.736). Ara *et al.* (2010) reported that number of siliquae per plant had positive and significant effect on yield per plant. Islam *et al.* (2016) revealed that number of siliquae per plant had significant positive association with yield per plant. Naznin *et al.* (2015) also found it. The non-significant and positive interaction was found with siliqua length (r_g = 0.054, r_p = 0.041) and thousand seed weight (r_g = 0.413, r_p = 0.333) (Table 6 and 7). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.2.7 Siliqua length (cm)

Siliqua length was found significant and positive association with number of seed per siliqua (r_g = 0.671, r_p = 0.695), non-significant and negative association with thousand seed weight (r_g = -0.331, r_p = -0.268) and yield per plant (r_g = -0.091, r_p = -0.123) indicating very little contribution of this trait towards the increase in number of seeds per siliqua and ultimately to yield per plant (Table 6 and 7).

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant and positive interaction with yield per plant (r_g= 0.918, r_p = 0.362). Ara *et al.* (2010) observed that seed yield had positive and highly significant association with number of seeds per siliqua both at genotypic and phenotypic levels. It showed positively non-significant association with thousand seed weight (r_g = 0.031, negative phenotypic correlation (r_p = -0.071) (Table 6 and 7). Lodhi *et al*. (2014) also revealed that number of seeds per siliqua had non-significant and positive correlation with yield per plant.

4.2.9 Thousand seed weight (g)

Thousand seed weight showed non-significant and positive interaction with yield per plant (r_g = 0.288, r_p = 0.263) (Table 6 and 7). Naznin *et al.* (2015) reported that thousand seed weight had non-significant and positive interaction with yield per plant. Positive associations between thousand seed weight and yield per plant indicate that yield per plant would increase if thousand seed weight increases. Interestingly, thousand seed weight exhibited significant positive correlation with siliqua length and seeds per siliqua observed by Kumari *et al*. (2017). However, Parveen *et al.* (2015)

revealed that thousand seed weight had highly significant positive association with yield per plant both genotypic and phenotypic level.

4.3 PATH COEFFICIENT ANALYSIS

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

Thus, it is possible to calculate both direct and indirect effects of yield components on yield per plant through the other components. Genotypic and phenotypic paths were worked out in the present study (Table 8) considering yield per plant as dependent character and its attributes as independent characters *viz*. days to 50% flowering, days to 80% maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua and thousand seed weight. Each component has two path actions *viz.* direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.3.1. Days to 50% flowering

Days to 50% flowering showed highly positive direct effect (2.312) towards yield per plant. Islam *et al.* (2016) found that days to 50% flowering had the negative direct effect on yield per plant. It showed highly negative indirect effect towards yield per plant via days to 80% maturity (-1.353). Further, it showed negligible negative indirect effect towards yield per plant via number of primary branches per plant (-0.0098), number of secondary branches per plant (0.1993) (Table 8). However, it was recorded highly negative indirect effect yield per plant via plant height (-1.353), number of siliquae per plant (-0.3207), siliqua length (0.169), number of seeds per siliqua (0.0801), thousand seed weight (0.0447). It showed negative and non-significant genotypic correlation (-0.744) with yield per plant.

4.3.2. Days to 80% maturity

Days to maturity found highly negative direct effect (-1.516) towards yield per plant. Rashid *et al*. (2013) demonstrated that days to maturity had positive direct effect towards yield per plant. Naznin *et al.* (2015) also found it. Further, it recorded negligible negative indirect effect towards yield per hectare via number of primary branches per plant (-0.0115) (Table 8). However, it was recorded highly positive indirect effect towards yield per plant via days to 50% flowering (2.063), plant height (-1.039), number of secondary branches per plant (-0.1813), number of siliquae per plant (-0.426), siliqua length (0.0116), number of seeds per siliqua (0.070) and thousand seed weight (-0.101). It showed negative and significant genotypic correlation (-0.975) with yield per plant.

4.3.3 Plant height (cm)

Plant height recorded highly negative direct effect (-1.745) towards yield per plant. Uddin *et al.* (2013) found that plant height had the negative direct effect on yield per plant. In the present study the correlation was negative and significant (-0.410) with yield per plant (Table 8). Further, it was recorded highly negative indirect effect towards yield per plant via days to 80% maturity (-0.903).However, it was found negligible negative indirect effect towards yield per plant via number of primary branches per plant (-0.0092), number of secondary branches per plant (-0.0112), number of seeds per siliqua (0.0897) and thousand seed weight (0.421). Naznin *et al.*

(2015) observed positive indirect effect on seed yield/plant through length of siliqua. It showed highly and positive indirect effect towards yield per plant via days to 50% flowering (1.742), number of siliquae per plant (-0.025) and siliqua length (0.0312).

4.3.4 Number of primary branches per plant

Number of primary branches per plant recorded negligible negative direct effect (-0.0163) towards yield per plant. Islam *et al.* (2013) was recorded that number of primary branches per plant had negative direct effect on yield per plant. Further, it was recorded highly positive indirect effect towards yield per plant via days to 50% flowering (1.3871), number of secondary branches per plant (0.351),length of siliqua (0.0384), number of seeds per siliqua (0.079), thousand seed weight (0.1068) and highly negative indirect effect yield per plant via days to 80% maturity (-1.0711),plant height (-0.976), (Table 6). However, it was found highly significant and very high positive indirect effect towards yield per plant via number of siliquae per plant (-0.326). The genotypic correlation of significant and negative (-0.428) with yield per plant was found.

Table 8. Partitioning of genotypic correlations into direct (bold) and indirect effects of important characters by path analysis of *Brassica rapa L.*

	D50%F	D80%M	PH	PBP	SBP	SN/P	LS	NS/S	TSW	**Genotypic correlation with yield**
D50%F	**2.3125**	-1.3534	-1.31438	-0.00983	-0.19936	-0.32079	0.01691	0.08012	0.04467	-0.744**
D80%M	2.0637	**-1.5166**	-1.03908	-0.01157	-0.18139	-0.47268	0.01167	0.07071	0.10055	-0.975**
PH	1.7418	-0.9030	**-1.74506**	-0.00917	-0.01132	-0.02504	0.03129	0.08971	0.42055	-0.410*
PBP	1.3871	-1.0711	-0.97638	**-0.01638**	0.35088	-0.32654	0.03831	0.07902	0.10684	-0.428*
SBP	0.6041	-0.3604	-0.02587	0.00753	**-0.76317**	0.44085	-0.02797	-0.04498	0.23460	0.065^{NS}
SN/P	-0.7569	0.7314	0.04459	0.00546	-0.34329	**0.98007**	-0.00245	-0.05800	0.37981	0.981**
LS	-0.8591	0.3887	1.19961	0.01379	-0.46896	0.05272	**-0.04551**	-0.06730	-0.30473	-0.091^{NS}
NS/S	-1.8471	1.0694	1.56119	0.01291	-0.34233	0.56691	-0.03055	**-0.10027**	0.02834	0.918**
TSW	0.1124	-0.1658	-0.79820	-0.00190	-0.19473	0.40487	0.01509	-0.00309	**0.91942**	0.288^{NS}

Residual effect: **0.57** ** = Significant at 1%.

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

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant observed highly negative direct effect (-0.763) towards yield per plant. It was also recorded negligible positive indirect effects to yield per plant via days to 50% flowering (0.6041), negligible negative indirect effects with days to 80% maturity (-0.0258), plant height (-0.0258), length of siliqua (-0.0279), negative with number of seeds per siliqua (-0.0449) and negligible positive thousand seed weight (0.234) (Table 8). On the other hand, it was found negligible positive indirect effect towards yield per plant through number of primary branches per plant (-0.0075) and moderately positive significant indirect effect via number of siliquae per plant (0.4408). Naznin *et al.* (2015) observed number of secondary branches/plant had high positive indirect effect on yield. The genotypic correlation of number of secondary branches per plant (0.065) with yield per plant was positive and non-significant.

4.3.6 Number of siliquae per plant

Number of siliquae per plant exhibited highly significant and very high positive direct effect (0.9801) towards yield per plant. Uddin *et al.* (2013) observed that number of siliquae per plant had the positive direct effect on seed yield per plant. However, it showed highly negative indirect effect towards yield per plant via days to 50% flowering (-0.7569), positive with plant height (0.0445), negative with length of siliqua (-0.00245), number of seeds per siliqua (-0.058) and moderately positive and indirect effect with thousand seed weight (0.3789) , indirect effect of days to 80% maturity (0.731), negligible positive with number of primary branches per plant (0.0054) and number of secondary branches per plant (-0.343) (Table 8). Islam *et al.* (2015) found negative indirect effect on number of siliquae per plant. The genotypic correlation of number of siliquae per plant (0.981) with yield per plant was positive and highly significant.

4.3.7. Siliqua length (cm)

Siliqua length showed negligible negative direct effect (-0.0455) towards yield per plant. Ara*et al.* (2010) revealed that siliqua length had direct effect and high positive correlation with yield per plant. Islam *et al.* (2016) also got these findings. It was found highly negative indirect effect towards yield per plant via days to 50% flowering (-0.859), highly positive plant height (1.199), negligible negative effect with number of seeds per siliqua (-0.0673), thousand seed weight (-0.3047) and low positive indirect effect of number of siliquae per plant (0.0527). Islam *et al.* (2016) also found positive indirect effect of plant height towards yield. On the other hand, it was also recorded positive indirect effects to yield per plant via days 80% to maturity (0.388), number of primary branches per plant (0.0137), number of secondary branches per plant (-0.4689) (Table 8). The genotypic correlation of leaf area (-0.091) with yield per plant was negative and non-significant. Islam *et al.* observed negative indirect effects to yield per plant.

4.3.8 Number of seeds per siliqua

Number of seeds per siliqua showed low negative direct effect (-0.1003) towards yield per plant. Islam *et al.* (2016) observed that this trait showed positive indirect effect on length of siliqua. Further, it was recorded highly positive indirect effect towards yield per plant via days to 80% maturity (1.069), plant height (1.5611), negligible negative effect with length of siliqua (-0.0305), negligible positive effect with thousand seed weight (0.0283) and high positive significant indirect effect of number of siliquae per plant (0.566) (Table 8). It also found very high positive indirect effect towards yield per plant via days to 80%maturity (1.069) and negligible positive effect to number of primary branches per plant (0.0129). It also recorded moderate negative effect towards yield per plant via number of secondary branches per plant (-0.3423). It had highly significant and positive genotypic correlation (0.918) with yield per plant.

4.3.9 Thousand seed weight (g)

Thousand seed weight showed highly significant and positive direct effect (0.9194) towards yield per plant. Parveen *et al.* (2015) revealed that thousand seed weight had the maximum direct effect towards yield per plant. Further, it was recorded negligible positive indirect effect towards yield per plant via days to 50% flowering (0.112), length of siliqua (0.0159), negative with number of seeds per siliqua (-0.0031) (Table 8). It also reported negligible negative indirect effect towards yield per plant via days to 80% maturity (-0.1658), plant height (-0.7982), number of primary branches per plant (-0.0019) and number of secondary branches per plant (-0.1947). Naznin *et al.* (2015) found negative indirect effect for thousand seed weight towards yield per plant. The trait was genotypically moderate, positive and non- significant (0.288) correlated with yield per plant.

4.3.10 Residual effect

The magnitude of residual effect (0.5705) indicated that traits included in the path analysis explained about 43.00% of the variation in yield. However, the remaining variation in yield (57%) can be attained by incorporating other yield related traits in the path analysis as far as studies involving association of traits is concerned. Naznin*et al.* (2015) found residual effect 0.45 in case of yield per plant.Islam *et al.* (2016)found 0.430 in case of yield per plant.

4.4 SELECTION

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

The objectives of our study were to select short duration and high yielding population of *Brassica sp.* which fit in the Aman-Mustard-Boro cropping system. Variability was found for most of the characters of different cross combinations. Selection was carried out among the 8 populations as per objectives. The most promising advanced plant populations with high yielding and short duration were selected from the materials of the different cross combinations.

4.4.1. L2 (BARI Sarisha-6 X Tori-7 F_{16}, S3)

Average number of siliqua of L2 was recorded 120.85 (Table 4). The average thousand seed weight was recorded as 2.75 g (Table 4) which was higher than Tori-7 (2.13 g) that meant seeds of this population were larger than tori-7 and had comparatively higher oil content. Yield per plant was recorded 7.48 g (Table 4) which was higher than Tori-7 (6.82 g).

4.4.2. L1 (BARI Sarisha- 9 X BARI Sarisha-6 F_{16}, S5)

Average number of siliquae per plant of L1 was recorded 117.72 (Table 4) which was higher than BARI sarisha-15 (120.40). This population was recorded with average thousand seed weight 3.63 g by the duration 79.00 days (Table 4) which was higher than Tori-7 (2.13 g) that meant seeds of selected plant were larger than tori-7 and had comparatively higher oil content and the selected population were short durable than Tori-7 (82 days) and BARI sarisha-15 (84 days).

4.4.3. L4 (BARI Sarisha- 6 X Tori-7 F_{16}, S2)

Average number of siliquae per plant of L4 was recorded 121.78 (Table 4). This population was recorded with average thousand seed weight 3.13 g (Table 4) which was higher than Tori-7 (2.13 g) that meant seeds of selected plant were larger than tori-7 and had comparatively higher oil content.

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

Populations	D80%M	SPP	TSW	SYP
L1	79.00	117.72	3.63	7.03
L2	78.33	120.85	2.74	7.48
L4	79.33	121.78	3.13	7.32

CHAPTER V
SUMMARY AND CONCLUSION

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

The study was conducted to study the nature and magnitude of genetic variability, the pattern of character association among the characters, the direct and indirect effects of component characters on yield per plant with yield contributing characters among the populations of *Brassica rapa* L. The material for the present study comprised of 8 advanced lines collected from Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, were evaluated using RCBD design for 10 quantitative characters at Sher-e-Bangla Agricultural University, Dhaka. The time duration was from November, 2017 to February, 2018.

The study exhibited wide range of variability for most of the characters studied. The lowest days to 50% flowering (27.33 days) was found in L2 followed by L1 and L6 (28.33 days). The lowest days to maturity (78.33 days) were observed in L2 followed by L1 (79.00 days). Plant height exhibited highest in L7 (107.73 cm) and lowest in L8 (94.56 cm). The highest number of primary branches per plant (5.66) was recorded in L7. The highest number of secondary branches per plant (2.27) was observed in L5. The highest number of siliquae per plant (124.44) was in L5. The L6 had long length of (6.38 cm) followed by L5 (6.05). The siliqua were shorter in L7 (5.07 cm). The number of seeds per siliqua (16.22) was found the highest in L8. The population L1 was exhibited the maximum thousand seed weight (3.63 g) followed by population L3 (3.5 g) whereas, the population L6 was recorded the minimum seed weight of (2.5 g). The maximum yield was recorded by the population L2 (7.48 g) followed by L4 (7.32 g). The lowest yield was recorded by the population L7 (5.65 g) followed by L6 (6.01 g) so, these populations for these traits can be used for future trial.

The genotypic variance of the materials was considerably lower than the phenotypic variance for all the characters studied. Number of primary branches per plant, number of secondary branches per plant, length of siliqua and thousand seed weight and yield per plant showed least difference between genotypic and phenotypic variance which indicated low environmental influence on these characters. Hence, selection will be beneficial for these traits.

The low magnitude of genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for the characters e.g. days to 50% flowering (GCV- 9.60%, PCV- 9.96%), days to 80% maturity (GCV- 3.61%, PCV- 3.84%), plant height (GCV- 4.61%, PCV- 4.95%), number of primary branches per plant (GCV- 9.61%, PCV- 10.17%), length of siliqua (GCV- 7.4%, PCV- 8.03%), number of siliquae per plant (GCV- 8.97% and PCV- 9.7%) and number of seeds per siiqua (GCV- 7.77% and PCV- 8.85%) except number of secondary branches per plant (GCV- 14.64% and PCV- 19.38%), thousand seed weight (GCV- 11.16%, PCV- 13.02%), yield per plant (GCV- 8.73%, PCV- 15.51%) . The differences between PCV and GCV for the characters were narrow indicating lesser influence of environment on these characters and could be improved by following phenotypic selection.

High values for heritability and genetic advance for various traits designates good genetic potential for selection and for use in future trial. High heritability estimates were observed for days to 50% flowering (92.88%), days to 80% maturity (88.28%), plant height (86.67%), number of primary branches per plant (89.13%), number of secondary branches per plant (57.08%), number of siliquae per plant (85.64%), length of siliqua (84.82%), number of seeds per siliqua (77.01%), thousand seed weight (73.50%). Yield per plant (31.70%) recorded moderate genetic gain and selection based on these characters may result in development of high yielding populations. High heritability coupled with moderate genetic advance was found in plant height and number of siliquae per plant.

In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Association of the character yield per plant was highly significant and positive with number of primary branches per plant (r_g= 0.428, r_p= 0.490), number of siliquae per plant (r_g= 0.981, r_p= 0.736), number of seeds per siliqua (r_g= 0.918, r_p= 0.362) at both genotypic and phenotypic level. It shows that yield per plant in *Brassica rapa* L. can be improved by making direct selection based on these traits.

Path co-efficient analysis for yield per plant revealed that days to 50% maturity exerted highest direct effect on the yield (2.312) followed by number of siliquae per plant(0.9800). The indirect contribution of component characters *viz.* number of primary branches per plant (1.741), number of secondary branches per plant (0.6041), and number of seeds per siliqua (1.5611) was high through seed yield per plant.

Selection was carried out among the populations of *Brassica rapa* L. for most promising populations with having high yield short duration. Based on the variability and as per our objectives three most promising populations L1 (BARI 9 X BARI 6 S5 F_{16}), L2 (BARI 6 X TORI7 S3 F_{16}) and L4 (BARI 6 X TORI 7 S2 F_{16}) with short duration and higher yield were selected from the 8 populations. Among the populations the highest yield per plant (7.48 g) was found in L2 (BARI 6 X TORI 7 S3 F_{16}). It was also matured early (78.33 days). So, these populations possessed excellent potential for use in future trial.

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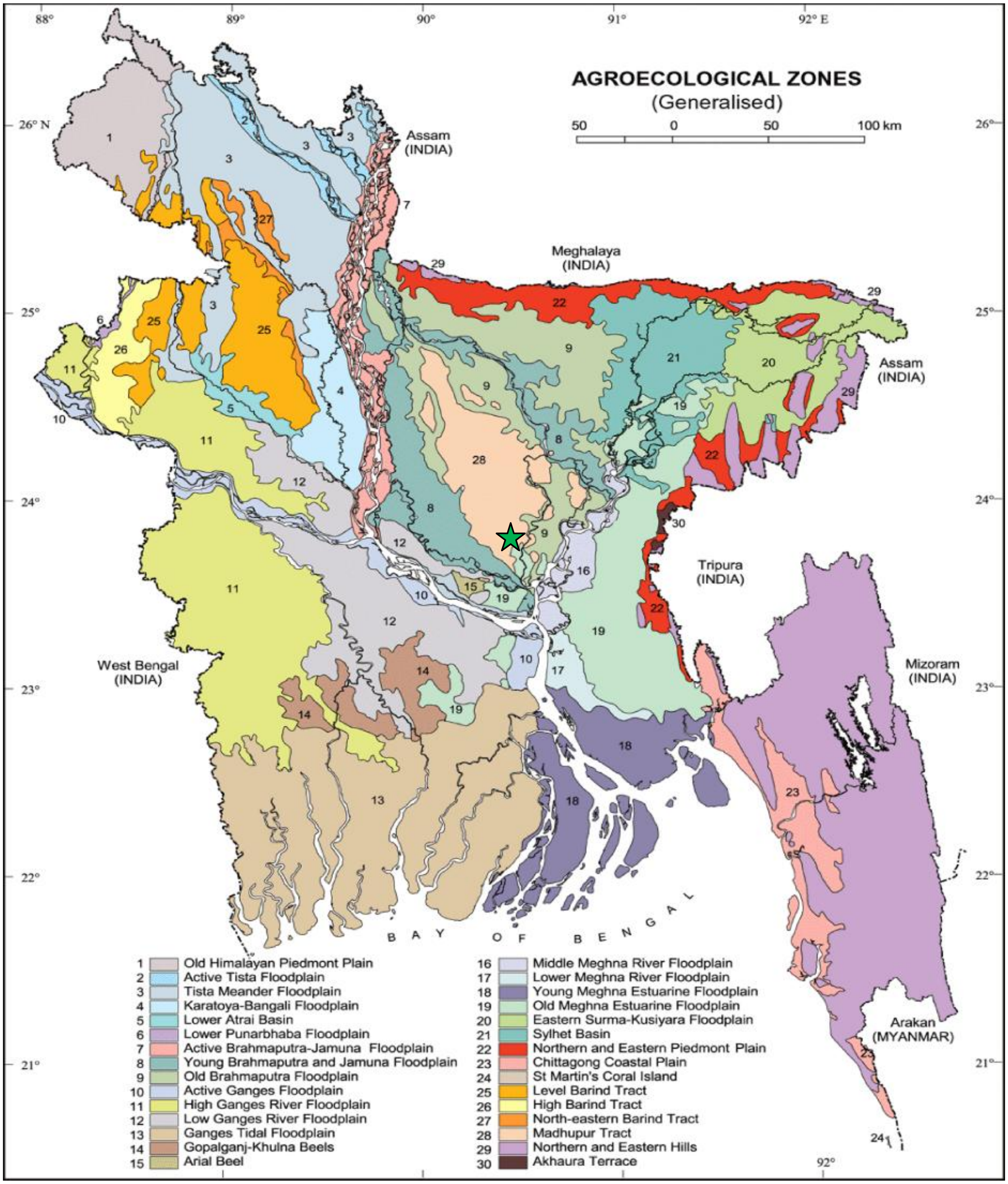
APPENDICES

Appendix I. Map showing the experimental site under the study



★ This sign sowing the experimental site under study, at SAU Dhaka.

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

A. Morphological characteristics of the experimental field

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

B. Physical composition of the soil

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

C. Chemical composition of the soil

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

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

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

Month	Air temperature (ºc)		Relative humidity (RH%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2017	28.2	18.0	77	2.27	**5.7**
December, 2017	32.4	16.3	69	0	**7.8**
January, 2018	29.1	13.0	79	0	**3.9**
February, 2018	**28.1**	**11.1**	**72**	**1**	**5.6**

Source: Bangladesh Meteorological Department (BMD)(Climate & Weather Division), Agargoan, Dhaka – 1207.

Appendix IV. Analysis of variance for different characters in *Brassica rapa L.* genotypes

Parameters	Mean Sum of Square		
	Replication (df = 2)	Treatment (df = 7)	Error (df = 14)
Days to flowering	0.792	26.42**	0.649
Days to maturity	2.375	26.85**	1.370
Plant height (cm)	1.874	68.46**	3.335
No. of primary branches per plant	0.047	0.64*	0.025
No. of secondary branches per plant	0.011	0.24	0.049
No. of siliqua per plant	7.580	339.80**	17.984
Length of siliqua (cm)	0.016	0.56	0.032
No. of seeds per siliqua	0.560	4.26**	0.381
1000 seed weight (g)	0.234	0.47*	0.044
Yield per plant (g)	1.100	1.37**	0.550

* Denote Significant at 5% level of probability **Denote Significant at 1% level of probability.

Appendix V. Mean performance by DMRT test of 8 advance lines of *Brassica rapa L.*

A. L.	DF	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Y/P
L1	28.33d	79.00cde	103.57bc	4.37cde	1.75bc	117.72ab	5.59abc	14.66bc	3.63a	7.03ab
L2	27.33e	78.33e	99.27bcd	5.02ab	1.45cd	120.85ab	5.30de	14.52c	2.74d	7.48a
L3	28.67cd	80.67cd	100.77bcd	4.80bc	1.60bcd	122.25ab	5.69abc	14.87bc	3.50a	6.94abc
L4	31.67bc	79.33cde	102.57bc	4.65bcd	1.67bcd	121.78ab	5.42cd	14.54c	3.13bc	7.32ab
L5	33.33b	83.33bc	105.47ab	4.56bcd	2.27a	124.44a	6.05ab	14.43cd	3.05cd	6.53bcd
L6	28.33cd	79.33cde	94.60de	4.12e	1.60bcd	100.54de	6.38a	15.11ab	2.50e	6.01cde
L7	35.67a	87.33a	107.73a	5.66a	1.51e	96.54e	5.07e	11.98e	3.13bc	5.65de
L8	29.00cd	81.67cd	94.57e	4.65bcd	2.06ab	118.90ab	6.00ab	16.22a	3.21bc	7.30ab

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