## COMPARATIVE TRIAL OF TWENTY POPULATIONS OF Brassica rapa L.

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## DEPARTMENT OF GENETICS AND PLANT BREEDING

## SHER-E-BANGLA AGRICULTURAL UNIVERSITY

## DHAKA

JUNE, 2022

#### COMPARATIVE TRIAL OF TWENTY POPULATIONS OF Brassica rapa L.

By

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#### **REGISTRATION NO. 15-06385**

A Thesis

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

#### **MASTER OF SCIENCE**

IN

## **GENETICS AND PLANT BREEDING**

#### **SEMESTER: JANUARY-JUNE, 2022**

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## CERTIFICATE

This is to certify that thesis entitled, "Comparative trial of twenty populations of Brassica rapa L." submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE in GENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried out by MUNNI DATTA, Registration No. 15-06385 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2022 Place: Dhaka, Bangladesh Dr. Md. Shahidur Rashid Bhuiyan Professor Supervisor

# DEDICATED TO MY BELOVED PARENTS

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#### ACKNOWLEDGEMENTS

All praises to the Almighty, the great, the gracious, merciful and supreme ruler of the universe who enables me to complete this present piece of work for the degree of Master of Science (MS) in the Department of Genetics and Plant Breeding.

The author would like to express her deepest sense of gratitude, respect to her research supervisor, Prof. Dr. Md. Shahidur Rashid Bhuiyan, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for his kind and scholastic guidance, untiring effort, valuable suggestions, inspiration, extending generous help and encouragement during the research work and guidance in preparation of manuscript of the thesis.

The author sincerely expresses her deepest respect and boundless gratitude to her cosupervisor Prof. Dr.Md.Harun-Ur-Rashid, Department of Genetics and Plant Breeding, for his helpful suggestion and valuable advice during the preparation of this manuscript.

It is highly appreciating words for Chairman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for the facilities provided, in carrying out this work. The author also acknowledges with deep regards the help and cooperation received from her honourable teachers, Prof. Dr. Md. Sarowar Hossain, Prof. Dr. Naheed Zeba, Prof. Dr. Firoz Mahmud, Prof. Dr. Jamilur Rahman, Prof. Dr. Mohammad Saiful Islam, Prof. Dr. Md. Ashaduzzaman Siddikee, Prof. Dr. Kazi Md. Kamrul Huda, Assoc. Prof. Dr. Shahanaz Parveen and all other staffs of Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their teaching, direct and indirect advice, encouragement and co- operation during the study period.

At last but not the least, the author feels indebtedness to her beloved parents and friends whose sacrifice, inspiration, encouragement and continuous blessing paved the way to her higher education and reach at this stage. May God bless us all.

The Author

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#### ABSTRACT

A research was conducted in the experimental farm of Sher-e-Bangla Agricultural university, by using twenty populations of Brassica rapa obtained through different inter-varietal crosses and grown in Randomized Complete Block Design with three replications at the experimental field of Sher-e-Bangla Agricultural University (SAU), Dhaka during December 2020 to February 2021. The purpose of the experiment is to study the variability, heritability, genetic advance, correlation and direct and indirect effect of different characters on seed yield. The characters visualized significant variations among the genotypes. Phenotypic variance was higher than the genotypic variance for every character. Minimum difference between phenotypic and genotypic variance was seen in number of primary branches per plant ( $\sigma^2 p=0.67$ ,  $\sigma^2 g=0.54$ ) siliqua length ( $\sigma^2 p=0.16$ ,  $\sigma^2 g=0.13$ ), days to 50% flowering ( $\sigma^2 p=3.42$ ,  $\sigma^2 g=1.57$ ), thousand seed weight ( $\sigma^2$ p=0.09,  $\sigma^2$ g=0.03) and seed yield per plant ( $\sigma^2$ p=0.45,  $\sigma^2$ g=0.18). Moderate heritability (40) with low genetic advance (1.46) and high genetic advance in percentage of mean (87.21) was found in number of secondary branches per plant while high heritability (74.63) with moderately high genetic advance in percentage of mean (7.33) was observed in number of seeds per siliqua. Significant positive association with seed yield per plant was observed in plant height (P=0.2844\*), number of siliqua per plant (G=0.8334\*\*,P=0.5110\*\*) and seeds per siliqua (P=0.3171\*). On the other hand, significant negative correlation was found in number of secondary branches per plant (-0.7773\*\*). Path coefficient analysis revealed that all the characters had positive direct effect on seed yield per plant except plant height (-0.02084), number of primary branches per plant (-1.07807) and days to 50% flowering (-0.33258). From this comparative study two populations G16 and G10 were selected based on their better performances in respect of number of siliqua per plant (G16=104.13, G10=107.67), thousand seeds weight (G16=2.83g,G10=3.00g) and seed yield per plant (G16=5.33g,G10=5.33g)) to proceed for further evaluation.

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# Some commonly used abbreviation

FULL WORD	ABBREVIATION	
Agro-ecological Zone	AEZ	
Agricultural	Agril.	
And others	et al.	
Agronomy	Agron.	
Analysis of variance	ANOVA	
At the rate	@	
Bangladesh Bureau of Statistics	BBS	
BC Backcrossed h		
Biological Biol.		
Co-efficient of Variation CV		
Degree Celsius	°C	
Degree of freedom	D.F	
Etcetera	etc.	
Environmental Variance	δ <sup>2</sup> e	
Genetic Advance	GA	
Gram	g	
Hectare ha		
Hydrogen ion potentiality p <sup>H</sup>		
Journal	J.	
Kilogram	Kg.	

Least Significant Difference	LSD
Meter	m
Mean sum of square	MSS
Millimeter	ml
Milli equivalent	meq
Muriate of Potash	MP
Number	No.
Per	/
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic Variance	$\delta^2 p$
Randomized Complete Block Design	RCBD
Science	Sci.
Sher-e-Bangla Agricultural University	SAU
Triple Super Phosphate	TSP

#### **CHAPTER I**

#### Introduction

*Brassica rapa* L. commonly known as field mustard or turnip mustard is widely cultivated as an oil crop. The primary centre of origin for *B. rapa* L. is near the Himalayan region and the secondary centre of origin is located in the European mediterranean area and Asia (Downey and Robbelen, 1989). Major producing regions of this crop are China, Canada and northern Europe and the Indian subcontinents. The genus *Brassica* has generally been divided into three groups namely rapeseed, mustard and cole. The rapeseed group includes the diploid *B. rapa*, turnip rape (AA, 2n = 20) and amphidiploid *B. napus* (AACC, 2n = 38) (Yarnell *et al.*, 1956). *B. juncea* commonly known as China mustard, Brown mustard, Indian mustard. It includes diploid *B. nigra* (BB,2n=16) and diploid *B. rapa* (AA,2n=20).

*Brassica* have great economic and commercial value and play a major role in our daily diet. It is used as a condiment, salad, green, organic manure and fodder crop and as a leaf and stem vegetable in various mustard growing countries of the world. Rapeseed is grown for the production of animal feed, vegetable oil for human consumption, and biodiesel.

Rapeseed is the second largest oilseed crop in the world providing 13% of the world's edible oil after soybean. In 2021, global oilseed production 646 million tons where rapeseed production was 82.48 million ton (BBS,2022).

In Bangladesh *B. rapa* is the main oil yielding species of *Brassica* and it occupies the 1<sup>st</sup> position in respect of area and production among the oil crops grown in Bangladesh that covers about 60% of the total acreage land (BBS, 2022). In term of area and production mustard rank first among the oilseed crop planted in Bangladesh in the fiscal year 2021-22 with 6.10 lakh hectares and 822 thousand metric tons respectively (BBS, 2022).

Though Bangladesh is an agricultural country, it is facing increasing deficiency in oil seed production and consequently import cost is increasing. In 2021, oilseeds import quantity for Bangladesh was 2.86 million tons (BBS,2022). Though in Bangladesh import quantity fluctuated in substantially in recent years, it tended to increase through 1972-2012 period. Bangladesh

import 15,981.000 BDT in December 2022. This records a decrease from the previous number of 19,893.00 BDT for November 2022 (BBS,2022).

The yield of rapeseed and mustard is generally low in Bangladesh as compared with the world average. The present seed yield per hectare of mustard in Bangladesh is far below the level attained in the developed countries of the world. The major reasons for such poor yield in Bangladesh may be attributed due to pressure of other crops, lack of improved varieties and poor management practices. Since mustard oil is more expensive than both soybean and palm oil, farmers are more motivated to increase their production.

In Bangladesh there is limited scope to increase acreage for oilseed due to pressure of other crops. The total amount of land for mustard and rapeseed was decreased due to increasing Boro rice cultivation. The area for rapeseed and mustard is reduced from 831260 acres to 667242 acres in 2016 to 2019 (BBS,2022).

There is limited scope to increase yield because farmers usually cultivate the existing low yielding varieties with low input and management. Short duration variety is still popular in Bangladesh because it can fit well into the T. Aman – Mustard–Boro rice cropping pattern. There are only few improved short duration variety of *B. rapa* which can be used to replace the existing Tori -7.

The above scenario indicated that there should be an attempt to develop short duration and high yielding varieties of mustard with more oil percentage in seed, tolerant to biotic and abiotic stress to fulfill the requirement of edible oil of the country. The improved variety also should well fit into T. Aman– Mustard–Boro cropping pattern. Due to future oil requirements we have to import huge amount of oil every year. The production of high yielding short duration varieties of *B*. *rapa* would allow to grow three crops in a year with oil seed varieties as a component of cropping pattern.

The populations generated of *B. rapa* through crossing among different existing varieties and subsequently crossed with the desired parents are used in the experiment to select populations with desired characteristics.

The present study was conducted to compare among the different populations to find out the variability, character association and the direct and indirect effect of different characters on yield per plant which will give an opportunity to select the desired plant types to meet the existing demand.

The present investigation was carried out to fulfill the below objectives-

- 1. To select high yielding population(s) along with short duration of *Brassica rapa*.
- 2. To study the genetic variability, character association and the effect of different characters on yield per plant.

#### **CHAPTER II**

#### **Review of literature**

A retrospect of pertinent literature on "Comparative trial of twenty populations of *Brassica rapa* L." has been reviewed under the following broad heads:

- 2.1 Genetic variability, heritability and genetic advance
- 2.2 Correlation coefficient
- 2.3 Path coefficient analysis

#### 2.1 Genetic variability, heritability and genetic advance

Variability can be defined as the availability of differences among the individuals of plant population. Variation usually arises as a result of differences either in genetic makeup of the individuals of a plant population or in the environment in which the plants are grown. The existence of genetic variability is essential for performance of selection in any breeding programme. Selection as a breeding method will be meaningful if there is an appreciable quantity of genetic differences within the various genotypes used in the breeding programme. Heritability is estimated by comparing individual phenotypic variation among related individuals in a population. Heritability definition is the degree of influence that genetic variations have on the production of a trait's phenotypic variations within a population. Heritability is an important concept in quantitative genetics, particularly in selective breeding and behavior genetics. Estimate of heritability help the breeder to effectively assign the necessary strategies to be adopted for a successful selection of the desired traits and to achieve the highest genetic gain within the shortest possible time and resources (Patil et al., 2015). Researchers have observed that traits with higher heritability can be more easily manipulated by selection and breeding compared to traits with lower heritability. In the same manner, genetic advance is also a useful tool in forecasting the gain to being specified selection intensity. However, when genetic advance is considered along with heritability, it becomes a more important measure in predicting responses to selection than the heritability estimates alone.

High magnitude of heritability estimates exposes good genetic relationships between parents and its offspring. The reason for a low heritability is higher contribution of an environmental variance than the contribution of genotypic variance. The scope of heritability including genotypic and phenotypic variability and correlation between different traits of crops have also been notified by many researchers and scientist for further genetic improvement.

Rameeh (2015) studied on heritability, genetic variability and correlation analysis using 21 rapeseed genotypes which were selected based on diversity of agronomic characters. He reported that Broad sense heritability estimates varied from 0.18 to 0.98. Plant height and seed yield per plant had high value of broad sense heritability. Pods on main axis and pods per plant had high value of genetic coefficient of variation.

Shaukat *et al.* (2015) conducted an experiment with eight Brassica napus genotypes to study genetic variability and heritability. They reported that analysis of variance showed highly significant differences (P $\leq$ 0.01) among *Brassica napus* genotypes for number of primary branches per plant. High broad sense heritability estimates were observed for number of primary branches per plant (0.83), plant height (0.78), pods per main raceme (0.65), seeds per pod (0.61), 1000-seed weight (0.61), while moderate heritability values were recorded for pod length (0.57), pods per plant (0.55), and seed yield per plant (0.50).

Verma *et al.* (2016) studied on genetic analysis on morphological and physiological traits in Indian mustard using eighty advanced progenies of Indian mustard and found that maturity, plant height, secondary branches per plant, siliqua per plant, seeds per siliqua, seed yield per plant, 1000 seeds weight, oil content showed high heritability.

Begum (2015) studied on variability, correlation and path analysis using 31 BC<sub>1</sub>F<sub>5</sub> genotypes of *Brassica napus* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during November 2014 to February 2015. The genotypes were found significantly variable for most of the characters. Comparatively phenotypic variances were higher than the genotypic variances for most of the character studied. Highest value of heritability was observed in Seed yield per plant (98.27) while days to 50% flowering (78.96) exhibited the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed in number of primary branches per plant, number of secondary branches per plant which indicates additive gene action is controlling these traits. High heritability with moderate genetic advance was observed in number of siliqua per plant, number of seeds per siliqua, thousand seeds weight and seed yield per plant which indicated non additive gene is controlling these traits.

Tahira (2016) conducted an experiment at the research area of Oilseed Research Institute during Kharif season, 2013-2014. The experimental material consisted of ten *Brassica juncea* genotypes tested in randomized complete block design (RCBD) with three replication. Days to maturity, days to flowering, plant height, number of primary branches per plant, siliqua length, seed per siliqua showed high heritability.

S. K. Roy (2015) studied on assessment of genetic variability of rapeseed-mustard by using 50 genotypes. Days to 50% flowering, days to maturity, primary branches per plant, secondary branches per plant, seeds per siliqua, seed yield per plant showed higher genetic variance.

Parvin (2015) conducted an experiment with 30 BC<sub>1</sub>F<sub>4</sub> genotypes of *Brassica napus* and find out that phenotypic variance is comparatively higher than genotypic variance for all the characteristics. High heritability with high genetic advance was observed in plant height (70.16%), number of primary branches per plant (71.79%), siliqua length (70.93%) and thousand seeds weight (72.57%).

Walle & Wakjra (2014) conducted an experiment with 36 genotypes of Ethiopian mustard and found that maximum heritability was obtained for biomass yield/plot, plant height, number of secondary branches/plant, grain filling period and days to maturity.

Afrin *et al.* (2011) studied on variability and comparison analysis using fifteen  $F_4$  population. Lowest value of heritability was observed in Primary branches per plant and the secondary branches showed the highest value. Moderate heritability was recorded in yield per plant, thousand seed weight, siliquae length, days to 50% flowering, days to 50% maturity and plant height.

Rauf *et al.* (2015) studied among genetic variability among yield and yield contributing traits in mustard with thirty-five mustard genotypes and found that , siliqua length, number of siliqua per plant, number of seeds per silique, 1000-seed weight and seed yield per plant showed high heritability with high genetic advance in percentage of mean.

Siddika (2015) conducted an experiment with 30  $F_2$  genotypes and found that genotypic coefficient of variation (GCV) was lower than phenotypic coefficient of variation (PCV) in all case. Number of primary branches per plant (57.14%), number of secondary branches per plant (66.67%), number of siliqua per plant (56.84%), number of seeds per siliqua (64.89%) and showed high heritability and high genetic advance in percentage of mean.

Aktar *et al.* (2019) conducted an experiment with eighteen *Brassica* genotypes and found that days to first flowering, days to maturity, plant height, no. of primary branches per plant, seed per pod, pod per plant, pod lrngth, thousands seed weight, yield per plant had high heritability.

Sikawar *et al.* (2017) studied on genetic variability, heritability and genetic advance in 21 diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson). Highly significant differences was observed for all the characters. High Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for number of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and number of siliqua on main raceme. Days to flowering, plant height and length of siliqua showed low PCV and GCV. Higher estimates of broad sense heritability were observed for all the characters. Number of secondary branches per plant, seed yield per plant, length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and number of primary branches per plant showed high heritability coupled with high genetic advance. High heritability with moderate genetic advance in case of length of siliqua and thousand seeds weight whereas, High heritability and low genetic advance was observed for days to flowering .

Laghari *et al.* (2020) studied on correlation and heritability analysis in rapeseed using eight genotypes and found that 75% flowering, 75% siliqua formation, number of siliqua per plant, seed yield per plant showed high heritability with high genetic advance.

Kumar *et al.* (2020) studied on genetic variability, heritability and genetic advance in fifty-five genotypes of Indian mustard. Number of siliquae per plant, plant height, main shoot length, seed yield per plant and days to maturity showed high genotypic and phenotypic coefficient of variation, heritability and genetic advance.

#### 2.2. Correlation coefficient

Correlation is a statistical technique that can show how strongly pairs of variables are related. The correlation coefficient is the specific measure that quantifies the strength of the linear relationship between two variables in a correlation analysis. The correlation coefficient, r, is a summary measure that describes the extent of the statistical relationship between two interval or ratio level

variables. Among useful breeding characteristics, genotypic and phenotypic correlations are applied to determine the extent of correlation of certain yield contributing traits with their yield . Phenotypic correlation coefficient of various grain yield and its components for its improvement of genotypic correlation coefficient has extensively studied. The phenotypic variability fraction of a character is measured and checked for attributable to genetic variation. The extent of an attribute to which it is passed on from organism to the next in the form of heritability. Genetic variation, nongenetic variation and random chance can all contribute to the expression of attributes in the body of an individual.

Sharafi *et al.* (2015) conducted an experiment with twenty winter rapeseed cultivar and the result showed positive direct effect was found in number of pods per plant, number of seeds per pod, and 1000-seed weight.

Devi (2018) conducted an experiment with twelve genotypes of Indian Mustard and found that days to 50% flowering (0.7564), silliqua on main raceme (0.6374) and biological yield per plant (0.3797) exhibited high degree of positive significant correlation with yield.

Sultana (2015) had an experiment with sixty four  $F_4$  genotypes of *Brassica Napus*. Path co-efficient analysis revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seeds per siliqua, and thousand seeds weight had the positive direct effect on yield per plant whereas days to 80% maturity, plant height, number of primary branch and siliqua length had that negative direct effect on yield per plant.

Deepti *et al.* (2016) studied on correlation and path analysis for yield contributing characters on Indian mustard and found that no. of primary branches per plant, no. of secondary branches per plant exhibited a positive correlation with seed yield per plant.

Parveen (2015) studied on genetic variability, heritability, correlation and path coefficient analysis using 30 BC<sub>1</sub>F<sub>4</sub> genotypes of *Brassica napus* L. Path co-efficient analysis revealed that plant height (0.464), number of primary branches per plant (0.436), number of secondary branches per plant (0.389), number of siliqua per plant (0.886), siliqua length (0.627), number of seeds per siliqua (0.584) and thousand seeds weight (0.608) had the positive direct effect on yield per plant and days to first flowering (-0.852) had the negative direct effect on yield per plant.

Laghari *et al.* (2020) studied on correlation and heritability analysis in rapeseed using eight genotypes and found that number of siliqua per plant, primary branches per plant, oil content showed positive and significant association with seed yield per plant.

Kashyap and Mishra (2004) studied 11 morphological characters of *Brassica campestris* Var and found that plant height, branches per plant, siliqua per plant, seeds per siliqua and 1000 seed weight had significant and positive correlation with seed yield.

Shrivastava *et al.* (2023) conducted an experiment with seventy-five Indian mustard genotype and found that number of primary branches per plant, number of secondary branches per plant, number of siliqua on main raceme and biological weight had positive and significant correlation seed yield per plant.

Uddin *et al.* (2013) conducted an experiment with seven parental and 21 F<sub>2</sub> progenies of *Brassica rapa* L. and found that number of primary branches per plant, number of secondary branches per plant and siliqua per plant had highly positive and significant relationship with yield at both phenotypically and genotypically. But yield had significant positive correlation at genotypically in days to flowering and days to maturity.

Nasim *et al.* (2013) evaluated ten *Brassica napus* L. genotypes to determine correlation between various traits and observed that pod length was positive highly significantly ( $p \le 0.01$ ) and significantly ( $p \le 0.05$ ) correlated with thousand seeds weight ( $0.59^{**}$ ) and pod width ( $0.37^{*}$ ) respectively. Pod width was revealed to have negative significant correlation with days to flowering initiation (- $0.40^{*}$ ) whereas positive significant correlations with thousand seeds weight ( $0.37^{*}$ )

Ali *et al.* (2013) experimented thirty lines of *Brassica carinata* and found that yield per plant had highly positive correlation with plant height.

Khayat *et al.* (2012) observed that plant height and siliqua per plant had high positive correlation with yield per plant.

Roy *et al.* (2018) studied forty diverse genotype of Indian mustard and found that pod length, number of seed per pod and oil content had positive significant association with seed yield per plant.

Tahira *et al.* (2011) studied ten wide genetic range of variety of *Brassica juncea*. Plant height, number of primary branches per plant, siliqua length and seeds per siliqua had highest phenotypic correlation, Seed yield was only significantly correlated with plant height and siliqua length. Plant height, number of primary branches per plant, siliqua length and thousand seeds weight were genotypically correlated with yield per plant. A highly significant and strong positive genetic relation was observed between plant height and branches per plant, siliqua length and seeds per siliqua.

Rameeh (2015) studied 36 *Brassica napus* L. cultivars to determine the associations for yield components. Yield was significantly and highly correlated with siliqua per plant.

Alam (2010) conducted an experiment with twenty six  $F_4$  population of *Brassica rapa* L. Plant height, number of primary branches per plant, number of siliqua per plant, seeds per plant had significant and positive correlation with yield.

Agarwaal *et al.* (2019) studied six genotypes of Indian mustard and observed that number of primary branches per plant, number of secondary branches per plant, main shoot length, number of siliqua on main shoot, siiqua length, seeds per siliqua, 1000 seeds weight, oil content had positive significant relationship with seed yield per plant.

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

Gangapur *et al.* (2009) experimented forty-six genotypes of Indian mustard (*Brassica junea*) under controlled and uncontrolled (disease and pest) condition and studied correlation and the result revealed that seed yield per meter was highly and significantly correlated with seed yield per plant, number of siliqua per plant, number of primary and number of secondary branches per plant, yield per plant, thousand seeds weight, number of seeds per siliqua at genotypic and phenotypic level under both protected and unprotected conditions.

Uddin (2013) conducted an experiment to study the correlation among seven parental genotypes and their twenty-one  $F_2$  progenies of *Brassica rapa* and found that seed yield had positive and significant relationship with number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant. Rashid (2007) conducted an experiment with 40 *Brassica oleiferous* 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.

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

Parveen (2007) conducted an experiment with  $F_2$  population of *Brassica rapa* and found that plant height, number of secondary branches per plant, number of seeds per siliqua and number of siliqua per plant, days to 50% flowering and length of siliqua had positive and non significant relationship with yield.

Zahan (2006) studied correlation and observed highly positive association in yield per plant with plant height, length of siliquae per plant and seeds per siliquae where insignificant negative association with days to 50% flowering and days to maturity.

Singh *et al.* (2020) studied character association and path analysis in Indian mustard using sixtyfour germplasm and observed that number of primary branches per plant, number of secondary branches per plant, plant height, length of main flower cluster, siliqua of main flower cluster had positive and significant association with yield per plant.

Mostofa *et al.* (2016) conducted an experiment with eight varities of rapeseed. He observed that thousand seeds weight, siliqua per plant, pant height, straw yield, biological yield and harvest index had positive significant correlation with seed yield.

#### 2.3 Path coefficient analysis

Path coefficients are standardized versions of linear regression weights which can be used in examining the possible causal linkage between statistical variables in the structural equation modeling approach. The standardization involves multiplying the ordinary regression coefficient by the standard 11 deviations of the corresponding explanatory variable: these can then be compared to assess the relative effects of the variables within the fitted regression model. The idea of standardization can be extended to apply to partial regression coefficients. It is well known that correlation mainly does not fulfill the purpose of the researcher because it does not detect the

characters having indirect effects on seed yield. In such situation path coefficient analysis developed by Wright (1921) put forward the real importance of such characters of partitioning the correlation coefficient in to direct as well as indirect effects.

A path coefficient indicates the direct effect of a variable assumed to be a cause on another variable assumed to be an effect. Path analysis will indicate whether the association of the yield related traits with yield is due to their direct effect on yield (true association and selection can be made for improvement), or is a consequence of their indirect effect via some other traits (s) and in such cases geneticist has to select the trait through which the indirect effect has been exerted.

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

Sultana (2015) conducted an experiment by using sixty-two  $F_4$  genotypes of *Brassica napus* L. Path co-efficient analysis revealed that yield has positive direct effect with 50% flowering, number of secondary branch, number of siliqua per plant, number of seeds per siliqua, and thousand seeds weight and negative direct effect with days to 80% maturity, plant height, number of primary branch and siliqua length.

Begum (2015) conducted an experiment with 31  $BC_1F_5$  genotypes of *Brassica napus* L. to study the variability, correlation and path analysis. Path analysis revealed that number of primary branches, number of secondary branches, number of siliqua per plant and thousand seeds weight had the positive direct effect on yield per plant.

Parveen (2015) conducted an experiment with 30 BC<sub>1</sub>F<sub>4</sub> genotypes of *Brassica napus* L. Path coefficient analysis revealed that yield has positive direct effect with plant height (0.464), number of primary branches per plant (0.436), number of secondary branches per plant(0.389), number of siliqua per plant (0.886), siliqua length (0.627), number of seeds per siliqua (0.584) and thousand seeds weight (0.608).

Siddika (2015) studied on the genetic variability, correlation and path analysis of *Brassica napus* L. with 30  $F_2$  genotypes. Path co-efficient analysis revealed that days to number of primary branches per plant (0.446), number of siliqua per plant (0.538), siliqua length (0.429), seeds per

siliqua (0.112) and thousand seeds weight (0.365) had the positive direct effect on yield per plant and days to first flowering, plant height, number of secondary branches per plant had the negative direct effect on yield per plant.

Ejaz-UI-Hasan *et al.* (2014) had conducted an experiment with *Brassica napus*. Days to maturity, days to flowering, seeds per siliqua, siliqua length and thousand seeds weight had direct and positive effect with yield. Height had direct negative effect on the yield per plant.

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

Hussain (2014) studied on heritability, genetic advance, character associations, direct and indirect effect of different characters on seed yield per plant with 24 genotypes including 4 check varieties of the species *Brassica rapa* L. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliqua per plant, siliqua length, thousand seeds weight showed positive direct effect with yield per plant. Days to 50% flowering, days to 80% maturity, number of secondary branches per plant, number of seeds per siliqua showed negative direct effect on yield per plant. Beside these days to 50% flowering, days to 80% maturity, number of secondary branches per plant, number of seeds per siliqua showed negative direct effect on yield per plant.

Uddin *et al.* (2013) evaluated seven parental and twenty one  $F_2$  progenies of *Brassica rapa*. Yield had direct and positive relation with days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliquae length, seeds per siliquae and thousand seeds weight but plant height and days to maturity showed indirect association.

Devi (2018) conducted an experiment with twelve genotypes of Indian Mustard and found that days to 50% flowering (0.7564), silliqua on main raceme (0.6374) and biological yield per plant

(0.3797) had highest direct positive effect on seed yield per plant

Khayat *et al.* (2012) studied that number of pods per plant, total dry matter, 1000- grain weight, and flowering and days to maturity had direct and positive effect on grain yield.

Afrin *et al.* (2011) studied on the path co-efficient among the characters. The plant height was found the highest positive and direct effect on seed yield per plant followed by number of siliquae per plant and siliqua length.

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

Roy *et al.* (2018) conducted an experiment with forty diverse genotype of Indian mustard. Total biomass, length of primary mother axis and days to first flowering showed negative direct effect with seed yield in late sown Indian mustard. Leaf area index had direct effect on seed yield.

Alam (2010) studied path co-efficient analysis that revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua length had the direct positive effect on yield per plant while days to 50% flowering, number of secondary branches per plant and thousand seeds weight had the negative direct effect on yield per plant.

#### **CHAPTER III**

#### Materials and methods

The present investigation was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. The detail information regarding the materials and methodology of this experiment is discussed below:

#### 3.1 Location of experimental site

The experiment was conducted at experimental farm of Sher-e -Bangla Agricultural University, Dhaka during the Rabi season of 2020-21 with planting date is 3<sup>rd</sup> November. The experimental field belongs to the Agroecological zone of "The Modhupur Tract", AEZ-28 (www.banglapedia.com). The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I)

#### **3.2 Soil and climate**

The soil of the experimental fields was clay loam. It is dark brown in colour. Loam soils generally contain more nutrients, moisture, and humus than sandy soils. The land was medium high and the fertility level was medium. The location was in the subtropical climatic zone. Climatic feature 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 experimental work was carried out by using twenty populations of *B. rapa* which were collected from Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka.

#### **3.4 Experimental layout**

The field experiment was designed in Randomized Complete Block Design (RCBD) with three (3) replications. The total land area was 220m<sup>2</sup>. The length of the plot was 11m and breadth of the

plot was 18m. Row length was maintained as 3m having 1m irrigation channels among the rows. The distance between line to line was 30cm and plant to plant was 15cm.

#### **3.5 Operational practices**

#### 3.5.1 Soil and field preparation

The field was prepared by doing several ploughing followed by laddering and harrowing using power tiller in order to make fine tilth soil and optimum level of moisture condition. Weeds were removed from the field. During final land preparation, cow dung was applied and leveled the field properly

#### 3.5.2 Fertilizer and manure application

Urea, triple super phosphate (TSP), muriate of potash (MOP), gypsum, zinc oxide (ZnO) and boric acid was applied to the field at the proper rate and proper time. Urea was applied by two installments. First half of urea and total TSP, MOP, gypsum, boric acid, ZnO and cow dung was 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.

#### 3.5.3 Seed selection and sowing time

Healthy and pure seeds were taken and selected for research work. Seeds were sown in lines in the experimental field on 3<sup>rd</sup> December, 2020. The seeds were placed at about 1.4 cm depth in the soil. Clods and pebbles were removed during sowing. Seeds were started to germinate after 4 days of sowing.

#### **3.5.4 Intercultural operations**

In the experimental field, different intercultural operations like irrigation, weeding, thinning, pest management etc. were applied in appropriate time to secure proper growth and development of the plants. A good drainage system was maintained to release and remove the rain water immediately from the experimental field during the growth plant.

SI No.	Genotype no.	Cross combination	Source
1	G1	BARI Sarisha $6 \times$ BARI Sarisha 14, F <sub>7</sub> , Yellow	
2	G2	BARI Sarisha 14 × (BARI Sarisha 9 × BARI	
		Sarisha 6),BC <sub>2</sub> , Brown	
3	G3	Yellow Special × BARI Sarisha 14, F <sub>9</sub> , Yellow	
4	G4	BARI Sarisha 14 × BARI Sarisha 15, F <sub>7</sub> , Yellow	
5	G5	BARI Sarisha $14 \times$ Yellow Special, F <sub>6</sub> , Yellow	
6	G6	BARI Sarisha 15 × BARI Sarisha 17, $F_{10}$ , Brown	
7	G7	Local Tori 7 × BARI Sarisha 14, $F_7$ , Yellow	
8	G8	BARI Sarisha 15 × Local Tori 7, F <sub>9</sub> Brown	
9	G9	Yellow Special × BARI Sarisha 15, F <sub>7</sub> , Yellow	
10	G10	BARI Sarisha 15 × (BARI Sarisha 9 × BARI	Dept. of Genetics
		Sarisha 6) ,BC <sub>2</sub> , Brown	and Plant Breeding
11	G11	Yellow Special × BARI Sarisha 17, F7, Yellow	
12	G12	BARI Sarisha 17 × BARI Sarisha 15, $F_{9}$ , Yellow	
13	G13	BARI Sarisha $14 \times BARI$ Sarisha 6, F7, Brown	
14	G14	BARI Sarisha 17 × BARI Sarisha 6, S <sub>4</sub> F <sub>10</sub> ,Brown	
15	G15	BARI Sarisha 14 ×BARI Sarisha 17, S <sub>2</sub> F <sub>7</sub> , Yellow	
16	G16	BARI Sarisha 15 $\times$ Yellow Special, F <sub>7</sub> , Yellow	
17	G17	Yellow Special $\times$ BARI Sarisha 6, F <sub>6</sub> , Yellow	
18	G18	Yellow Special × Local Tori 7, F7, Yellow	
19	G19	(BARI Sarisha 9 × BARI Sarisha 6) × Local	
		Tori 7, BC <sub>2</sub> , Brown	
20	G20	BARI Sarisha 15 × BARI Sarisha 6, $S_5F_9$ , Yellow	

Table 1. Populations used in the experiment

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

		Dose		
Sl. No.	Fertilizers/ manures	Applied in the plot	Quantity/ha	- Application procedure
1.	Urea	6.5kg	225kg	50% basal and 50% at the time of flower initiation
2.	TSP	4.75kg	235kg	as basal
3.	МОР	2.20kg	78kg	as basal
4.	Gypsum	4.2kg	135kg	as basal
5.	Boric acid	320g	11kg	as basal
6.	ZnO	82g	3kg	as basal
7.	Cow dung	100kg	5ton	as basal

## **3.5.4.1** Tagging and Tying

When the plants were visible after 8 days of germination, then tagging of each population of all replication was done. The plants were tied with rope to protect them from leaning by using bamboo.

#### 3.5.4.2 Weeding and thinning

Weeding and times thinning done according to the requirement of maintaining growth of the crop. The first weeding was done after 11 days of sowing. Second weeding was done after 15 days of sowing and the last wedding was done 20 days of sowing. Thinning was done at the same time for maintaining 30 cm from line to line and 15 cm from plant to plant.

#### 3.5.4.3 Irrigation and after care

The experimental plot was lightly irrigated after sowing in order to bring appropriate moisture condition of the soil ensuring proper germination of seeds. Second irrigation was given (20 DAS) before the flower initiation. Third irrigation was given (35 DAS) when the pod appeared. Fourth irrigation was given (55 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 could not break the shoots of the plants.

#### **3.5.4.4 Pesticide application**

Sawfly insect attacked mustard field at the time of siliqua appearance and aphid infection was found during the siliqua development stage of the crop. Pesticides were applied in the morning after vanishing dew. Malathion-57 EC @ 2mL/liter of water was sprayed to control aphids.

#### 3.5.5 Harvesting

Harvesting carried out when siliquae have turned yellow and the leaves have dried and highest oil in seed is obtained. It was started from 28<sup>th</sup> February to 7<sup>th</sup> March, 2021 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.

#### **3.5.6** Collection of data

To study genetic parameters and inter-relationships the following ten characters were taken into consideration: plant height, days to 50% flowering, days to 80% maturity, no. of primary branches/ plant, no. of secondary branches/ plant, no. of siliqua/ plant, length of siliqua, no. of seeds/ siliqua, thousand seeds wt. and yield/plant.

#### 3.6 Data collection methods

#### 3.6.1 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.

#### 3.6.2 Number of primary branches/plant

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

#### 3.6.3 Number of secondary branches/ plant

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

#### 3.6.4 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.

#### **3.6.5** 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.

#### 3.6.6 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

#### 3.6.7 Days to 50% flowering

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

#### 3.6.8 Days to 80% maturity

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



Plate 1. Initial field view of the experimental plot.



Plate 2. Seed sowing in the field.



Plate 3. Weeding operation in the field.



Plate 4. First flowering in plant.



Plate 5. Flowering stage



Plate 6. Vigorous growth and several branches during flowering stage



Plate 7. 50% flowering stage



Plate 8.80% flowering stage



Plate 9. Experimental field



Plate 10. Collecting data from experimental plot.

# **3.6.9** Thousand-seed weight (g)

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

# 3.6.10 Yield/ plant (g)

All the seeds produced by a representative plant was weighted in gram by considering it as the seed yield per plant.

# **3.7 Statistical analysis**

Data were recorded twenty inter-varietal crossed genotypes i.e. plant height(cm), number of primary branches/plant, number of secondary branches/plant, number of siliqua/plant, siliqua length(cm), number of seeds/siliqua, days to 50% flowering, days to 80% maturity, thousand seeds weight (gm). The mean values of ten randomly selected plants used for recording observations were computed for each of twenty 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 Statistix 10 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. The level of significance was tested at 5% and 1% using F test. The model of ANOVA used is presented below:

Sources of	Degrees of	Sum of squares	Mean sum of squares
variation	freedom (D.F.)		
Replication (r)	r-1	SSr	SSr/(r-1) =MSSr
Genotypes (g)	g-1	SSg	SSg/(g-1) = MSSg
Error (e)	(r-1)(g-1)	SSe	SSe/(r-1) (g-1) =MSSe

Where,

r = Number of replications,

g = Number of genotypes

SSr = Sum of squares due to replications

SSg = Sum of squares due to genotype

SSe = Sum of squares due to error

MSSr = Mean sum of squares due to replications

MSSg = Mean sum of squares due to genotypes

MSSe = Mean sum of squares due to error

The calculated F-value was compared with tabulated F-value. When F-test was found significant, critical difference was calculated to find out the superiority of one entry over the others.

The standard error and critical differences were calculated as follows:

SE(m)±	=	$\sqrt{Me/r}$
SE(d)±	=	$\sqrt{2}$ Me/r
CD0.05	=	S.E.(d)xt (0.05)(r-1)(g-1)df
SE(m)±	=	Standard error of mean

Where,

$SE(d)\pm$	=	Standard error of difference
CD0.05	=	Critical difference at 5% level of significance
		significance

# 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.

MSS due to genotypes – MSS due to error Genotypic variance  $(\sigma^2 g) =$ R Phenotypic variance = Genotypic variance  $(\sigma^2 g)$  + Error variance  $(\sigma^2 e)$ 

# 3.7.2.2 Co-efficient of variability

Both phenotypic and genotypic co-efficient of variability for all characters were estimated using 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.

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

# 3.7.2.3 Heritability in broad sense (**h**<sup>2</sup>)

The broad sense heritability ( $h^2b_s$ ) 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).

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

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).

$$\mathbf{GA} = \mathbf{h}^2 \mathbf{bs} \times \mathbf{\sigma} \mathbf{p} \times \mathbf{K}$$

Where,

 $h^2bs$  = Heritability estimate in broad sense

 $\sigma p$  = 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 percent of mean was computed by using the following formula

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

Genetic advance as percent 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.

# a. Genotypic correlation coefficient between X and Y

$$rg = \frac{Vg XY}{\sqrt{(Vg X \times Vg Y)}}$$

Where,

Vg XY = Genotypic covariance between X and Y

Vg X = Genotypic variance of X

Vg Y = Genotypic variance of Y

# b. Phenotypic correlation coefficient between X and Y

$$rp = \frac{Vp XY}{\sqrt{(Vp X \times Vp Y)}}$$

Vp XY= Phenotypic covariance between X and Y

Vp X = Phenotypic variance of X

Vp Y = Phenotypic variance of Y

Genotypic variance (Vg) = (Mg-Me) / r

Phenotypic variance (Vp) = (Vg+Ve)

### **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:

 $ryx_{1} = Pyx_{1} + Pyx_{2}rx_{1}x_{2} + Pyx_{3}rx_{1}x_{3}$  $ryx_{1} = Pyx_{1}rx_{1}x_{2} + Pyx_{2} + Pyx_{3}rx_{2}x_{3}$  $ryx_{3} = Pyx_{1}rx_{1}x_{3} + Pyx_{2}rx_{2}x_{3} + Pyx_{3}$ 

Where, r's denote simple correlation co-efficient and P's denote path coefficient (unknown). P'sin the above equations may be conveniently solved by arranging them in matrix from. Total correlation, say between x and y is thus partitioned as follows

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

 $P_{yx_2r_{x_1x_2}}$  = the indirect effect of x<sub>1</sub> via x<sub>2</sub> on y.

 $P_{yx}3r_{x1x3}$  = the indirect effect of x1 via x3 on y.

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

 $PRY^2 = 1 - \sum P_{iy}$ . R<sub>iy</sub> Where,  $PRY^2 = (R^2)$ ; and hence residual effect,  $R = (P^2RY)^{1/2}P_{iy} = Direct$  effect of the character onyield

Riy = Correlation of the character with yield

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

# **CHAPTER IV**

### **Results and discussion**

Results obtained from the present study have been presented and discussed in this chapter with a view to study the genetic variability in mustard population. The results have been discussed and positive interpretations are given under the following headings:

- 4.1 Mean performance
- 4.2 Genetic variability
- 4.3 Correlation analysis
- 4.4 Path coefficient analysis

# 4.1 Mean performance

The means of different traits of the different populations were compared to measure specific differences between pairs of means.

### 4.1.1 Plant height (cm)

Maximum number of plant height of 113.73 was observed in G17 and G14 populations. G17 required 90 days to mature and gave 5.27g yield/plant. G14 required 88.33 days to mature and gave 2.67g yield/plant. Minimum number of plant height of 90.06 was observed in G15. G15 required 90.33 days to mature and gave 5.33g yield/plant. It indicated that population having minimum number of plant height showed maximum yield/plant

### 4.1.2 Number of primary branches per plant

The maximum number of primary branches per plant was found in G7 (6.33). G7 required 89.33days to mature and gave 4.67g yield/plant. G18 required 86.67 days to mature and gave 4.8g yield/plant. The minimum number of primary branches per plant of 3.80 was found in G18.G1 required 86.67 days to mature and gave 2.89g yield/plant. It indicated that population having minimum number of primary branches per plant other populations.

### 4.1.3 Number of secondary branches per plant

Maximum number of secondary branches per plant of 4.63 was observed in both G7 and G8 populations. G7 required 89.33 days to mature and gave 5.67g yield/plant. G8 required 87 days to mature and gave 3.87g yield/plant. Minimum number of secondary branches per plant of 0.17 was found in G1. G1 required 86.67 days to mature and gave 4.63g yield/plant. It indicated that population having minimum number of secondary branches per plant took minimum days to mature and showed higher yield than the other populations.

### 4.1.4 Number of siliqua per plant

Number of siliqua per plant ranged from 88.57 to 112.47 with mean value 101.88 in different genotypes. The maximum number of siliqua per plant of 112.46 was observed in G20.G20 required 89.33 days to mature and gave 5.67g yield/plant. The value of days to 80% maturity was 89.33 and yield per plant was 5.27. The minimum number of siliqua per plant was observed in G19 and the value was 88.57. G19 showed minimum value of yield per plant (3.53). It indicated that population having lowest number of siliqua per plant showed lowest amount of yield per plant.

#### 4.1.5 Length of siliqua (cm)

The mean of siliqua length was 5.29 cm and ranged from 4.7 to 6.03 cm. Maximum number of siliqua length of 6.03 was observed in G19.G19 required 89 days to mature and gave 3.53g yield/plant. Minimum value of siliqua length was observed in G15 (4.76). G15 required 90.33 days to mature and gave 5.33g yield/plant. It indicated that population having minimum value of siliqua length showed higher yield than other populations.

#### 4.1.6 Number of seeds per siliqua

Number of seeds per siliqua ranged from 10.80 to 27.21 in different populations. The maximum number of seeds per siliqua of 27.21 was recorded in G16. G16 required 85 days to mature and gave 5.33g yield/plant. Minimum value of seeds per siliqua was 10.80 and was observed in G7.G7 required 89.33 days to mature and gave 5.33g yield/plant. It indicated that population having minimum number of seeds per siliqua showed higher yield than other population.

	PH	PBP	SBP	SPP	SL	SPS	DF	DM	TSW	Y/P
G1	91.27c	4.13efg	0.17d	99.40cd	4.87efg	22.73bc	35.33с-е	86.67eg	2.28d	4.63a-d
G2	103.13abc	4.03fg	3.07abc	102.70bcd	5.37cd	14.89f-j	35.00с-е	86.67eg	2.45b-d	5.06abc
G3	99.70bc	4.33efg	1.00b-d	101.10bcd	5.20de	21.84bc	36.33а-е	89.67abc	2.36cd	4.20с-е
G4	98.09bc	5.40bc	2.03b-d	103.40bcd	4.70g	19.26b-f	35.00с-е	90.33a	2.81abc	4.87a-d
G5	96.91bc	6.00ab	2.46a-d	107.63abc	5.36cd	20.49b-d	35.33с-е	87.67а-е	2.96ab	5.06abc
G6	99.13bc	4.73de	1.47b-d	97.83d	5.33cd	18.21c-g	36.67a-d	90.00ab	2.93ab	4.87a-d
G7	106.70ab	6.33a	4.63a	103.47bcd	5.00d-g	10.80j	34.33de	89.33bc	2.65a-d	4.67a-d
G8	96.27bc	5.43bc	4.63a	98.47d	5.16de	11.27ij	38.00ab	87.00fg	2.94ab	3.87de
G9	94.93bc	4.13efg	0.67b-d	98.57d	4.80fg	16.21d-h	37.33abc	85.67h	2.62a-d	4.67a-d
G10	96.00bc	5.73abc	2.63a-d	107.67abc	5.33cd	13.18hij	33.66e	87.33fg	3.00a	5.33a
G11	96.50bc	4.07efg	1.03b-d	105.00a-d	5.13def	19.84b-e	38.33a	87.67ef	2.78a-d	4.73a-d
G12	103.23а-с	4.03fg	0.33d	98.17d	5.36b-d	23.60ab	36.67a-d	88.33de	2.45b-d	5.27ab
G13	106.23ab	4.00fg	0.50cd	97.60d	5.90ab	15.39e-i	35.67b-е	85.67h	2.84abc	4.27b-e
G14	113.73a	5.43bc	1.06b-d	109.00ab	5.63bc	18.14e-g	38.67a	88.33de	2.67a-d	5.27ab
G15	90.06c	5.23cd	0.70b-d	99.47cd	4.76g	19.07b-f	35.33с-е	90.33a	2.91ab	5.33a
G16	100.80bc	5.16cd	0.50cd	104.13bcd	5.80ab	27.21a	38.33a	85.00h	2.83abc	5.33a
G17	114.04a	5.50bc	0.67b-d	102.80bcd	5.63bc	23.2ab	37.33abc	90.00ab	2.51a-d	5.27ab
G18	100.11bc	3.80g	2.00b-d	100.20cd	5.30cd	14.16g-j	35.66b-e	86.67eg	2.89ab	4.8a-d
G19	94.25bc	4.70def	3.23ab	88.57e	6.03a	14.81f-j	35.00с-е	89.00cd	2.66a-d	3.53e
G20	105.9ab	4.50efg	0.63b-d	112.47a	5.13def	19.31b-f	38.00ab	89.33bc	2.36cd	5.27ab
CV	6.73	7.54	82.28	4.26	3.69	13.21	3.77	1.89	9.55	10.99
LSD(0.05%)	11.17	0.60	2.27	7.17	0.32	3.96	2.26	2.25	0.42	2.15
SE	3.90	0.21	0.79	2.50	0.11	1.38	0.15	0.96	0.15	0.30

Table 3: Mean performance of ten characters of twenty genotypes of Brassica rapa L.

PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliqua per plant, SL = Length of siliqua (cm), SPS = Number of seeds per siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity TSW = Thousand seeds weight (g), Y/P = Yield per plant

\* In a column, figures having same letters do not differ significantly.

Table 4. Estimation of genetic parameters in ten characters of twenty genotypes in *Brassica rapa* L.

	Range			CV(%)					GCV	ECV
Parameters	Min	Max	Mean		δ <sup>2</sup> P	δ <sup>2</sup> G	δ²E	PCV (%)	(%)	(%)
Plant height (cm)	90.06	114.04	100.35	6.73	73.22	27.56	45.66	8.52	5.23	6.73
Number of primary branches per plant	3.80	6.33	4.83	7.54	0.67	0.54	0.13	16.91	15.18	2.69
Number of secondary branches per plant	0.17	4.63	1.67	82.28	3.15	1.26	1.89	106.27	67.22	7.54
No. of siliqua per plant	88.57	112.47	101.88	4.26	39.64	20.78	18.86	6.18	4.47	4.27
Siliqua length (cm)	4.70	6.03	5.29	3.70	0.16	0.13	0.03	7.75	6.82	3.16
No. of seeds per siliqua	10.80	27.21	18.18	13.21	22.74	16.97	5.77	26.26	22.68	13.23
Days to 50% flowering	33.66	38.33	36.30	3.77	3.42	1.57	1.85	5.10	3.45	3.75
Days to 80% maturity	85.67	90.33	88.03	1.89	4.64	1.88	2.76	2.45	1.56	1.87
Thousand seeds weight (g)	2.28	3.00	2.69	9.55	0.09	0.03	0.06	11.11	6.415	9.55
Seed yield per plant (g)	3.53	5.33	4.80	10.99	0.45	0.18	0.27	13.97	8.84	10.83

 $\delta^2 P$  = Phenotypic variance,  $\delta^2 G$  = Genotypic variance,  $\delta^2 E$  = Environmental variance, PCV = Phenotypic coefficient of variation,

GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

 Table 5. Heritability, genetic advance and genetic advance in percent of mean for yield and yield contributing characters of 20 genotypes of *Brassica rapa* L.

Parameters	Heritability	Genetic advance (GA) (5%)	Genetic advance (% mean)		
Plant height (cm)	37.64	6.52	6.5		
Number of primary branches per plant	80.60	1.36	28		
Number of secondary branches per	40.00	1.46	87.21		
Plant					
No. of siliqua per plant	52.42	6.80	6.70		
Siliqua length	76.47	0.65	12.30		
No. of seeds per siliqua	74.63	7.33	40.40		
Days to 50% flowering	45.91	0.55	11.46		
Days to 80% maturity	40.5	0.21	7.78		
1000 seed weight (g)	33.33	1.75	4.82		
Seed yield per plant (g)	40.00	1.80	2.04		

### 4.1.6 Days to 50% flowering

Significant variance was observed in days to flowering (Table 3). The maximum value of days to flowering of 38.67 was found in G11 and G16. Days to maturity recorded by the G11 population was 87.67 and the value of yield was 4.73. G16 required 85 days to mature and the value of yield/plant was 5.33. Minimum number of days to 50% flowering of 33.66 was observed in G10 and the value of yield per plant was 5.33. Both G16 and G11 showed maximum value of yield per plant, but G16 required less days to mature So, selection of G16 population would be rewarding.

### 4.1.7 Days to 80% maturity

The days to maturity was observed with a range of 85.00 to 90.33 days. Maximum number of days to 80% maturity of 90.33 were observed in G4 and G15 populations. The value of yield/plant of G4, G15 populations were 4.87 and 5.33 respectively. Minimum number of days to 80% maturity of 85 was observed in G16 population. G16 showed maximum value of yield per plant (5.33). It indicated that population having minimum number of days to 80% maturity showed higher yield than the other population.

#### 4.1.8 Thousand seeds weight

Thousand seeds weight observed with a range of 2.28 to 3.80. Maximum thousand seeds weight of 3kg was observed in G10. Minimum value of thousand seeds weight of 2.28 was recorded in G1.G10 required 87.33 days to mature which was higher than G1 population (86.67 days).

### **4.1.10** Yield per plant

Yield per plant observed with a range of 5.33 to 3.53. Maximum yield per plant was observed in G10 and G16.Minimum yield per plant was observed in G19.

#### **4.2 Genetic variability**

The results of the analysis of variance showed that there was significant genetic variation among the mustard population. Table 4 and 5 displayed the mean, variance components, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance expressed as a percentage of the mean.

# 4.2.1 Plant height (cm)

Maximum number of plant height of 114.04 was observed in G17 and the minimum number of plant height of 100.7 was recorded in G15. The mean value was recorded as 100.35cm.

Genotypic and phenotypic variance was observed 27.56 and 73.22, respectively for plant height with large environmental influence. The plant height exhibited higher phenotypic coefficient of variation (8.52) than the genotypic coefficient of variation (5.23) (Table 4). Low GCV and moderate PCV indicated that the trait was more influenced by environment. Low heritability of 37.64 percent, high genetic advance 6.5 along with low genetic advance as percent mean (6.5%)was recorded. Low heritability with low 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 percent of mean for plant height.

# 4.2.2 Number of primary branches per plant

The maximum number of primary branches per plant were found in G7 (6.33) and the minimum number of primary branches per plant were found in G18 (3.8) (Table 4).

The genotypic and phenotypic variance was recorded as 0.54 and 0.67 respectively. Genotypic coefficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 15.18 and 16.91 percent were observed, respectively (Table 5). Slightly higher GCV than PCV indicated that this character was less influenced by environment. Heritability (80.60) and genetic advance percent of mean (28) was found to be high. The character was influenced but additive gene effect. Selection based on this character would be effective.

### 4.2.3 Number of secondary branches per plant

The Maximum number of secondary branches per plant of 4.33 were found in G7 and G8 populations and the value was (4.33) and the minimum number of secondary branches per plant were found in G1 (0.17) followed by with mean value 1.67 (Table 5).

The genotypic and phenotypic variance was recorded as 1.26 and 3.15 respectively. High genotypic co-efficient of variation (GCV) and high phenotypic co-efficient of variation (PCV) of 67.22 and 106.27 percent were observed, respectively (Table 5). Highest value of GCV and PCV indicated the presence of high variability in the trait. Heritability (40.00), genetic advance (1.46), genetic advance

in percent of mean (87.21) indicated that this character was influenced by additive gene effect. Selection of this trait might not be rewarding.

# 4.2.4 Number of siliqua per plant

Number of siliqua per plant ranged from 88.57 to 112.47. The maximum number of siliqua per plant was noticed in population G20 (112.47). The population G19 recorded the minimum number of siliqua per plant (88.57) (Table 4). Naznin *et al.* (2015) observed that the number of siliqua/plant showed the highest range of variation which meant the presence wide range of variation for this character.

The phenotypic variance (39.64) was higher than genotypic variance (20.78). This indicates more influence of environment on this character. The lower phenotypic coefficient of variation (6.18%) and lower genotypic coefficient of variation (4.47%) (Table 4) indicated presence of less considerable variability among the populations. Low genotypic variance indicates the less transmissibility of the character from parent to their offspring (Ushakumari *et al.*, 1991). Slightly higher PCV than GCV indicated that the character was less influenced by environment. The heritability (52.42%) estimates for this trait was moderate, high genetic advance (6.8%) and low genetic advance in percent of mean (6.70) were found (Table 5). It indicated that this character was influenced by additive gene effect.

# 4.2.5 Length of siliqua (cm)

The mean was ranged from 4.7 to 6.03 cm. The maximum value of length of siliqua of 6.03 was recorded in G19. The minimum value of length of siliqua of 4.70 was recorded in G4 (Table 4). The genotypic and phenotypic variance for siliqua length were seen as value of 0.13 and 0.16, respectively. Siliqua length exhibited low GCV (6.82%) and PCV (7.75%) values. As GCV is lower than PCV thus we can conclude that the trait is controlled by its environment. A high heritability estimates of 76.47%, low genetic advance 0.65% and a moderate genetic advance as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent of mean of 12.30 were observed. High heritability with combination of moderate genetic advance as percent of mean was found.

### 4.2.6 Number of seeds per siliqua

Number of seeds per siliqua ranged from 10.80 to 27.21 in different populations. The maximum number of seeds per siliqua was recorded in population G16 (27.21). However, the minimum number of seeds per siliqua exhibited in population G7 (Table 4).

The genotypic variance was (16.97) and phenotypic variance was (22.74). GCV and PCV were observed as 22.68 and 26.26 respectively (Table 4). This indicated that the character was more influenced by environment. Whereas, it showed high heritability (74.63%), high genetic advance (7.33%) in mean and high genetic advance with 5% of mean (40.40%) for this trait. High heritability with high genetic advance in 5% mean indicated that heritability occurs due to genetic effects. Thus, selection is effective for the improvement of the crop.

### 4.2.7 Days to 50% flowering

The maximum duration to days to 50% flowering was found in G14 with 38.67 DAS and the minimum in G7 with 34.33 DAS (Table 4). The mean value was 38.67. 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 matured early. The minimum days to 50% flowering was found in C7 (25) indicated that flower came early DAS and it was short durable population.

The phenotypic variance (3.42) was higher than genotypic variance (1.57). 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 coefficient of variation) and PCV (Phenotypic coefficient of variation) were low with value of 3.45 and 5.10 percent. It indicated less variability existed in the environment. Moderate heritability of 45.91% with moderate genetic advance as percent mean of 11.46%` and low genetic advance (0.55) (Table 4) was observed. 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). The flowering trait of the plant was quite sensitive and influenced by the temperature fluctuation which was reflected in the present study. Low heritability and low genetic advance indicating that the traits were being exhibited due to influence of environment rather than genotype. Thus, it is indicative that non- additive gene action might be



Plate 10 (a). Yellow special ×BARI Sarisha 6,  $F_{6}$ , Yellow



Plate 10(b). BARI Sarisha14×BARI Sarisha6, F7, Brown



Plate 10(c). BARI Sarisha14×(BARI Sarisha9×BARI Sarisha6), BC2, Brown



Plate 10(d). BARI Sarisha17×BARI Sarisha15, F9,Yellow



Plate 10(e). BARI Sarisha15×Local Tori7,F9, Brown



Plate 10 (f). BARI Sarisha15×BARI Sarisha6, S<sub>5</sub>F<sub>9</sub>, Yellow



Plate 10(g). Yellow special ×Local Tori 7, F7, Yellow



Plate 10(h). BARI Sarisha15×BARI Sarisha17, F<sub>10</sub>, Brown



Plate 10(i). Yellow special ×BARI Sarisha14, F9, Yellow



Plate 10(j). Yellow special ×BARI Sarisha17, F7, Yellow



Plate10(k). BARI Sarisha14×BARI Sarisha15, F7, Yellow



Plate 10(1).( BARI Sarisha9×B BARI Sarisha6)×Local Tori7, BC2



Plate10(m). BARI Sarisha17×BARI Sarisha6, S4F10, Brown



Plate 10(n). BARI Sarisha15×Yellow special, F7, Yellow



Plate 10(0). Local Tori7×BARI Sarisha14,F7, Yellow



Plate 10(p). Yellow special× BARI Sarisha15, F7, Yellow



Plate10(q). BARI Sarisha14×BARI Sarisha17, S<sub>2</sub>F<sub>7</sub>, Yellow



Plate10(r). BARI Sarisha14×BARI Sarisha15, F7, Yellow



Plate10(s). BARI Sarisha14×Yellow special, Yellow



Plate10(t). BARI Sarisha15×(BARI Sarisha9×BARI Sarisha6),BC2

controlling the trait of expression and selection for this trait may not be recommended. In the contrast to the present results, low heritability was being exhibited due to influence of environment rather than genotype.

# 4.2.8 Days to 80% maturity

Maximum value of days to 80% maturity of 90.33 was observed in G4 and G15. The G14 required the least number of days to mature (85 days) whereas the maximum number of days to 80% maturity was observed in the population of G4 and G13 and the value was (90.33 days) (Table 4). The shortest time required for 80% maturity in Tori-7 (81 days) were reported by Ali *et al.* (2002). G14 showed the lowest days to maturity (62 days) which indicating that it maturedearly rather than the other populations.

Days to 80% maturity exhibited low GCV and PCV of 1.56 and 2.45 percent, respectively along with low heritability of 40.5 percent, low genetic advance 0.21 and low genetic advance as percent mean of 7.78 percent (Table 4). This low heritability with low genetic advance was indicative of non-additive gene action. Low heritability is 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 were recorded as 1.88 and 4.64, respectively. Phenotypic variance was higher than genotypic variance which indicated that there was influence of environment in the expression of genes for this trait.

### 4.2.9 Thousand seeds weight (g)

Thousand seeds weight of different populations ranged from 2.28 to 3.00g. Maximum thousand seeds weight of 3.00g was observed in G10 followed by population G18. Whereas, the populationG1 recorded the minimum seed weight of (2.28g). The maximum thousand seeds weight was found in G10 (3.00g) indicating that seeds of this population was bigger than others. So, selection for this trait of G10 populationwould be effective.

Thousand seeds weight recorded moderate PCV (11.11%) and low GCV (6.415%) (Table 4). As PCV is greater than GCV, there was considerable influence of environment on this trait (Table4). Low heritability (33.33%), low genetic advance (1.75%) and was found for this trait. Low heritability with low genetic advance suggested that the character was 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 seeds weight was observed by Parveen *et al.* (2015) which indicated the possibility of non-additive gene action.

# 4.2.10 Yield per plant (g)

Yield ranged from 3.53 to 5.33g. The maximum yield was recorded by G12, G15, G16 and the value was 5.33. The lowest yield was recorded by the population G19 (3.53g) followed by G2 (4.20 g) (Table 3).

The genotypic variance was (0.18) and phenotypic variance was (0.27). Yield per plant exhibited moderate PCV (13.97%), low GCV (8.84%) in Table 4. As PCV is greater than GCV, there was considerable influence of environment on this trait. Jahan *et al.* found high genotypic co-efficient of variation (GCV) for yield per plant by considering genetic parameters. Whereas, it also recorded low heritability (40.00), low genetic advance in 5% mean (2.04) which indicated the influence of non-additive gene action and selection of this trait might not be rewarding.

# 4.3 Correlation analysis

The phenotypic and genotypic correlation express the extent of association between different characters, thus, it assists to base selection procedure to a required balance, when two alternative desirable characters affecting the main characters are being selected. The analysis of correlation reveals the association between morphological and physiological including quantitative and quantitative yield traits and yield of a plant. A positive correlation happens due to coupling phase of linkage and negative correlation arises due brepulsion 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 separated chromosomes. Yield being a mixed character, is governed by a large number of genes. The influence of each character on yield could be identified through correlation studies with in order t o determine the extent and nature of relationships between yield and yield attributing characters. So, the genotypic and phenotypic correlation co-efficient values for ten characters in twenty *Brassica rapa* L. populations studied are presented in following respectively.

### 4.3.1 Plant height

Plant height showed positive and significant correlation with siliqua per plant (G=0.4795\*,P=0.3067\*), siliqua length (G=0.6407\*\*), days to 50% flowering (G=0.5185\*), seed yield per plant (P=0.2844\*) (Table 6). It indicated that if plant height increased then siliqua per plant, siliqua length, days to 50% flowering and yield per plant also increased. It also indicated that plant height and characters were highly correlated and they were governed by the same gene. The genotypic correlation coefficient is higher than the phenotypic correlation coefficient. It indicated that the characters are genotypically associated, but due to environment interaction the phenotypic value was lessened. Plant height had positive and insignificant relationship with number of primary branches per plant (G=0.1511), siliqua length (P=0.2296), seeds per siliqua (G=0.0731, P=0.0567), days to 50% flowering (P=0.1795), days to 80% maturity (G=0.2357, P=0.0338), 1000 seed weight (G=0.3406) seed yield per plant(G=0.3425). It indicated that these character was largely influenced by both environment and gene factor. It had negative and nonsignificant relationship with number of primary branches per plant (P=-0.1565), secondary branches per pant (G=-0.1738, P=-0.0047), 1000 seeds weight (P=-0.2050). It indicated that they were largely influenced by the environment and mostly independent in nature.

### 4.3.2 Number of primary branches per plant

Number of secondary branches per plant (G= $0.5469^*$ ), seeds per siliqua (P= $0.2699^*$ ), days to 80% maturity (P= $0.3021^*$ ) had positive and significant correlation with number of primary branches per plant. It indicated that if number of primary branches per plant increased then number of secondary branches per plant, seeds per siliqua, days to 80% maturity increased and vice versa. It showed positive nonsignificant relationship with siliqua per plant (G=0.4051), days to 80% maturity (G=0.4007), thousand seeds weight (G=0.5727, P=0.2541), seed yield per plant (G=0.1828, P=0.2307). These nonsignificant association indicated that these character were highly influenced by environmental factor and they were independent in nature. It expressed negative insignificant association with siliqua per plant (P=-0.0047), siliqua length (G=-0.2120, P=-0.1463). It indicated that if number of primary branches per plant increased then seeds per siliqua, siliqua per plant, siliqua length were decreased and vice versa.

		РН	PBP	SBP	SPP	SL (cm)	SPS	DF	DM	TSW (g)	Y/P (g)
PH	G	1									
(cm)	Р	1									
PBP	G	0.1511	1								
	Р	-0.1565	1								
SBP	G	-0.1738	0.5469*	1							
	Р	-0.0047	-0.0047	1							
SPP	G	0.4795*	0.4051	-0.2983	1						
	Р	0.3067*	0.2699*	0.0603	1						
SL	G	0.6407**	-0.0415	-0.0636	-0.2416	1					
(cm)	Р	0.2296	-0.0331	-0.0528	-0.1509	1					
SPS	G	0.0731	-0.1770	-0.9328**	0.2371	0.0816	1				
	Р	0.0567	-0.1197	-0.5897**	0.0746	0.0697	1				
DF	G	0.5185*	-0.2120	-0.4739*	0.3466	0.1491	0.4747*	1			
	Р	0.1795	-0.1463	-0.3177*	0.1147	0.1496	0.3204*	1			
DM	G	0.2357	0.4007	0.0648	0.2089	0.3611	0.0716	-0.1980	1		
	Р	0.0338	0.3021*	0.0784	-0.1178	-0.1260	0.0370	-0.0926	1		
TSW	G	0.3406	0.5727	0.5808*	0.0101	0.1413	-0.4798*	-0.2568	-0.2710	1	
(g)	Р	-0.2050	0.2541	0.1714	-0.0503	0.0444	-0.2406	0.0427	0.0028	1	
SYP	G	0.3425	0.1828	-0.7773**	0.8334**	-0.2415	-0.5457*	0.1622	0.0560	0.0218*	1
(g)	Р	0.2844*	0.2307	-0.1197	0.5110**	-0.0713	0.3171*	0.0551	0.1190	0.0326*	1

Table 6. Phenotypic and Genotypic correlation coefficient among different pairs of yield and yield contributing characters for twenty genotypes of *Brassica rapa* L.

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

PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliqua per plant, LS = Length of siliqua (cm), SPP = Number of seeds per siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity TSW = Thousand seeds weight (g), Y/P = Yield per plant (g)

#### 4.3.1. Number of secondary branches per plant

Number of secondary branches per plant had positive and significant relationship with thousand seeds weight (G=0.5808\*). It expressed that if number of secondary branches per plant increased then thousand seeds weight also increased. It expressed negative significant relationship with seeds per siliqua (G=-0.9328\*\*, P=-0.5897\*\*), days to 50% flowering (G=-0.4739\*, P=-0.3177\*), seed yield per plant (G=-0.7773\*\*). It indicated when number of secondary branches per plant increased then seeds per siliqua, days to 50% flowering, seed yield per plant decreased. It had positive nonsignificant association with seeds per siliqua (G=0.0603), days to 80% maturity (G=0.0648, P=0.0784), thousand seeds weight (P=0.1714). It indicated that these characters were largely influenced by environment.

### 4.3.2. Siliqua per plant

It had positive insignificant association with seeds per siliqua (G=0.2371, P=0.0746), days to 50% flowering (G=0.3466, P=0.1147), days to 80% maturity (G=0.2089), thousand seeds weight (G=0.0101). It indicated that these character were highly influenced by environment. It had positive and significant relationship with seed yield per plant (G=0.8334\*\*, P=0.5110\*\*)

### 4.3.5 Siliqua length

Siliqua length had positive and nonsignificant relationship with seeds per siliqua (G=0.0816, P=0.0697), days to 50% flowering (G=0.1491, P=0.1496), days to 80% maturity (G=0.3611), thousand seeds weight (G=0.1413, P=0.0444). It indicated that these character were highly influenced by environment. It had negative nonsignificant association with days to 80% maturity(P=-0.1260) and seed yield per plant (G=-0.2415, P=-0.0713).

# 4.3.6 Seeds per siliqua

It had positive significant association with days to 50% flowering (G= $0.4747^*$ , P= $0.3204^*$ ), seed yield per plant (P= $0.3171^*$ ). It indicated that if seeds per siliqua increased, 50% flowering and seed yield per plant also increased. It had negative direct association with thousand seeds weight (G= $-0.4798^*$ ), seed yield per plant (G= $-0.5457^*$ ). It had positive nonsignificant association with days to 80% maturity (G=0.0716, P=0.0370).

### 4.3.7 Days to 50% flowering

It had positive nonsignificant association with thousand seeds weight (P=0.0427), seed yield per plant (G=0.1622, P=0.0551). It indicated that these characters were highly influenced by environment. It had negative nonsignificant association with days to 80% maturity (G=-0.1980, P=-0.0926), thousand seeds weight (G=-0.2568).

### 4.3.8 Days to 80% maturity

It had positive nonsignificant association with thousand seeds weight (P=0.0028), seed yield per plant (G=0.0560, P=0.1190). It expressed that these characters were highly influenced by environment. It had negative nonsignificant association with thousand seeds weight (G=-0.2710).

### 4.3.9 Thousand seeds weight

It had positive significant association with seed yield per plant (G=0.0218\*, P=0.0326\*). It indicated that when thousand seeds weight increased, seed yield per plant also increased.

### **4.4 Path coefficient analysis**

Path coefficient analysis was an effort to access the magnitude of contribution of various traits to the yield in the form of cause and effect. It was simply called standardized partial regression coefficient. It estimated the direct impacts of various variables on one another. It split the coefficient of correlation into direct and indirect effect. In this method there was occurrence of cause and effects between different variables. The direction of the experiment required casual system related to evidence of experiment. So, in this way, selection of the best performing traits could be possible in breeding program. A clear picture of the inter relationship between seed yield and others yield contributing characters, direct and indirect effects of them can be worked out by using path analysis at genotypic level which also measure the relative importance of each component on yield. Estimation of direct and indirect effects of them can be influenced on yield to a medium extent, have been denoted as 'R'.

# 4.4.1 Plant height

Plant height showed positive indirect effect towards yield per plant via total siliqua (0.93394), siliqua length (0.56810), seeds per siliqua (0.06235) and days to 80% maturity (0.10562). It showed negligible negative indirect effect towards yield per plant via primary branch (-0.16287), secondary branches per pant (-0.14641), days to 50% flowering (-0.17243), thousand seeds weight (-0.04335) (Table7). The relationship between plant height and seed yield per plant was nonsignificant and positive as was pointed out by genotypic coefficient of correlation (0.34250). However, its direct effect was low and negative (-0.02084).

## 4.4.2. Number of primary branches per plant

The relationship between number of primary branches per plant and seed yield per plant was nonsignificant and positive as was pointed out by genotypic coefficient of correlation (0.1828). However its direct effect was negative (-1.07807). Number of primary branches per plant showed positive indirect effect towards yield per plant via number of secondary branches per plant (0.46076), siliqua per plant (0.78904), days to 80% maturity (0.17951). It showed negligible negative effect towards plant height (-0.12401), siliqua length (-0.03679), seeds per siliqua (-0.15106), days to 50% flowering (-0.07052) (Table7).

### 4.4.3 Number of secondary branches per plant

Number of secondary branches per plant showed negative direct effect (-0.7773\*) on seed yieldper plant. Its direct effect was positive (0.84248). Number of secondary branches per plant showed positive indirect effect towards yield per plant via plant height (0.14265), days to 50% flowering (0.15760), days to 80% maturity (0.02905), thousand seeds weight (0.07395). It showednegligible negative indirect effect towards primary branch (-0.58961), number of siliqua per plant(-0.58102), total siliqua (-0.05630), seeds per siliqua (-0.79605) (Table7).

# 4.4.4 Number of siliqua per plant

Siliqua per plant showed positive indirect effect towards yield per plant via number of seeds per siliqua (0.20234), days to 80% maturity (0.09358), thousand seeds weight (0.00129). It showed negligible indirect effect towards plant height (-0.39963), number of primary branches per plant(-

	Direct effect	РН	РВР	SBP	SPP	SL	SPS	DF	DM	TSW	Genotypic correlation with yield
РН	-0.02084	-0.02084	-0.16287	-0.14641	0.93394	0.56810	0.06235	-0.17243	0.10562	-0.04335	0.34250
PBP	-1.07807	-0.12401	-1.07807	0.46076	0.78904	-0.03679	-0.15106	-0.07052	0.17951	0.07290	0.18280
SBP	0.84248	0.14265	-0.58961	0.84248	-0.58102	-0.05630	-0.79605	0.15760	0.02905	0.07395	-0.77730*
SPP	1.94758	-0.39963	-0.43677	-0.25134	1.94758	-0.21441	0.20234	-0.11527	0.09358	0.00129	0.83340**
SL	0.88739	-0.52587	0.04470	-0.05346	-0.47057	0.88739	0.06967	-0.04958	-0.16178	0.01798	-0.24150
SPS	0.85341	-0.05997	0.19083	-0.78586	0.46175	0.07245	0.85341	-0.15788	0.03208	-0.06109	-0.54570*
DF	-0.33258	-0.42556	0.22589	-0.39921	0.67499	0.13227	0.40513	-0.33258	-0.08870	-0.03269	0.16220
DM	0.44803	-0.19351	-0.43195	0.05464	0.40679	-0.32043	0.06111	0.06584	0.44803	-0.03450	0.05600
TSW	0.12730	-0.27954	-0.61739	0.48936	0.01967	0.12530	-0.40950	0.08540	-0.12143	0.12730	0.02180*

Table 7. Path coefficient analysis showing direct and indirect effects of different characters on yield of Brassica rapa L.

PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliqua per plant, LS = Length of siliqua (cm), SPP = Number of seeds per siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity TSW = Thousand seeds weight (g), Y/P = Yield per plant (g) Residual are 0.2755. \*\* = Significant at 1%. ,\* = Significant at 5%. 0.43677), number of secondary branches per plant (-0.25134), siliqua length (-0.21441), days to 50% flowering (-0.11527) (Table7). The relationship between siliqua per plant and seed yield per plant was significant and positive as was pointed out by genotypic coefficient of correlation (0.83340\*\*). Its direct effect was positive (1.94758).

### 4.4.5 Siliqua length

The relationship between siliqua per plant and seed yield per plant was nonsignificant and negative as was pointed out by genotypic coefficient of correlation (-0.24150). Its direct effectwas positive (1.94758). Siliqua length showed positive and indirect effect towards yield per plantvia number of primary branches per plant (0.04470), seeds per siliqua (0.06967), thousand seeds weight (0.01798). It showed negligible indirect effect towards plant height (-0.52587), secondarybranches (-0.05346), siliqua per plant (-0.47057), days to 50% flowering (-0.04958), days to 80% maturity (-0.16178) (Table7).

#### 4.4.6 Seeds per siliqua

Seeds per siliquae showed positive and indirect effect towards yield per plant via number of primary branches per plant (0.19083), siliqua per plant (0.46175), siliqua length (0.07245), daysto 80% maturity (0.03208) (Table7). It showed negative indirect effect towards plant height (-0.05997), number of secondary branches per plant (-0.78586), days to 50% flowering (-0.15788), thousand seeds weight (-0.06109). Genotypic correlation of seeds per siliqua (-0.5457) is significant. The relationship between seeds per siliqua and seed yield per plant was significant and negative as was pointed out by genotypic coefficient of correlation (-0.54570\*). Its directeffect was positive (0.85341).

# 4.4.7 Days to 50% flowering

Days to 50% flowering showed positive and indirect effect towards yield per plant via number of number of primary branches per plant (0.22589), siliqua per plant (0.67499), siliqua length (0.13227) and seeds per siliqua (0.40513). It showed negative indirect effect towards plant height (-0.42556), number of secondary branches per plant (-0.39921), days to 80% maturity (-0.08870) and thousand seeds weight (-0.03269). Genotypic correlation of days to 50% flowering (0.16220)

was nonsignificant and positive. Its direct effect was negative (-0.33258).

# 4.4.8 Days to 80% maturity

Days to 80% maturity showed positive and indirect effect towards yield per plant via number of secondary branches per plant (0.05464), siliqua per plant (0.40679), seeds per siliqua (0.06111) and days to 50% flowering (0.06584) (Table7). It showed negative indirect effect towards plant height (-0.19351), number of primary branches per plant (-0.43195), siliqua length (-0.32043), thousand seeds weight (-0.03450). The relationship between days to 80% maturity and seed yield per plant was nonsignificant and positive as was pointed out by genotypic coefficient of correlation (0.0560). Its direct effect was positive (0.44803).

### 4.4.9 Thousand seeds weight

Thousand seeds weight showed positive and indirect effect towards yield per plant via number of secondary branches per plant (0.48936), siliqua per plant (0.01967), siliqua length (0.12530) and days to 50% flowering (0.08540). It showed negative indirect effect towards yield per plant via plant height (-0.27954), number of primary branches per plant (-0.61739), seeds per siliqua (-0.40950) and days to 80% maturity (-0.12143). The relationship between thousand seeds weight and seed yield per plant was significant and positive as was pointed out by genotypic coefficient of correlation (0.02180). Its direct effect was positive (0.12730).

#### **CHAPTER V**

#### **Summary and conclusion**

This research work was carried out to compare the populations of *Brassica rapa* obtained through different intervarietal crosses and to estimate the variability among the characters, heritability, genetic advance, character association and direct and indirect effect of different traits on yield.

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University during December 2020 to February 2021 using 20 populations of *Brassica rapa*.

From variability analysis of populations, it was observed that significant variation existed among all the genotypes used for most of the characters studied. The highest plant height found in G17 (114.04) and the lowest in G15 (90.06). The highest number of primary branches per plant was observed in G7 (6.33) and the lowest number of primary branches per plant was found in G18 (3.08). The highest number of secondary branches per plant was found in G7, G8 and the value was 4.63. The lowest number of secondary branches per plant was observed in G1 (0.17).

Number of siliqua per plant was found maximum in G20 (112.47) followed by G14 (109.00), G10 (107.67) and the lowest was found in G19 (88.57). The highest siliqua length was recorded in G19 (6.03) followed by G13 (5.90) and G16 (5.80), and the lowest was found in G15 (4.76). The number of seeds per siliquae was found maximum in the G16 (27.21). and the lowest was found in G7 (10.80).

Minimum days to 50% flowering was found in G10 (33.66) followed by G15 (35.33) and G17 (37.33). The maximum days to 50% flowering was observed in G11 (38.33). The maximum value of days to 80% maturity of 90.33 was observed in G15 and G4 populations. The minimum days to 80% maturity was observed in G16 (85.00). Thousand seeds weight was found maximum in G10 (3.00) and minimum in G1 (2.28). The seed yield per plant was found maximum in G15, G16 and the value was 5.33. The minimum value was found in in G19 (3.53).

However, the phenotypic variance and phenotypic co-efficient of variation was found higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. Higher phenotypic variance than the genotypic variance for all the characters indicated the greater influence of environment to express the characters. Higher phenotypic and genotypic differences were found in case of secondary branches of plant, number of seeds per siliqua, seed yield per plant that stated the more environmental effect to control the characters. On the other hand, siliqua length, days to 50% flowering, days to 80% maturity, number of primary branches per plant, siliqua length, number of seeds per siliqua, showed least difference between phenotypic and genotypic variance indicated least environmental influence and additive gene action for the expression of the characters.

Moderate heritability (40.00) with low genetic advance (1.46) and high genetic advance in percentage of mean (87.21) was found in case of number of secondary branches per plant indicated moderate effect of environment and presence of non-additive genes in the expression of the character, which resulted the lower possibility of the selection of genotypes but high genetic advance in percentage of mean which indicated the possibility of predominance of additive gene, so much scope to improve. High heritability with moderately genetic advance in percentage of mean was observed in number of primary branches per plant (80.60), number of seeds per siliqua (74.63) indicated medium possibility of selecting genotypes for further improvement.

High heritability (76.47) with low genetic advance (0.65) and genetic advance in percentage of mean (12.30) was found in siliqua length indicated that non-additive gene effects were involved for the expression of these characters and selection for genetic improvement for these traits would be ineffective.

Correlation coefficient among the characters were studied to determine the association between yield and yield components. It is evident that in some of the cases genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficient in case of plant height (G=0.3425, P=0.2844), siliqua per plant (G=0.8334, P=0.5110), days to 50% flowering (G=0.1622, P=0.0551) indicated a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. On the other hand, in some cases, phenotypic correlation coefficient was higher than their corresponding genotypic correlation coefficient in case of number of primary branches per plant (G=0.1828, P=0.2307), number of secondary branches per plant (G=-0.7773, P=-0.1197), siliqua length (G=-0.2415, P=-0.0713), seeds per siliqua (G=0.5457, P=0.3171), days to 80% maturity (G=0.0560, P=0.1190), thousand seeds weight (G=0.0218, P=0.0326) suggested that both environmental and genotypic correlation in these cases

act in the same direction and finally maximize their expression at phenotypic level. Significant positive association with seed yield per plant was found in case of number of plant height (P=0.2844\*), number of siliqua per plant (G=0.8334\*), seeds per siliqua (P=0.3171\*) and thousands seed weight (G=0.0218\*, P=0.0326\*). On the other hand, significant negative correlation was found in number of secondary branches per plant (G=-0.7773\*), number of seeds per siliqua (G=-0.5457\*).

Path coefficient analysis revealed that plant height (0.3425), number of primary branches per plant (0.1828), number of siliqua per plant  $(0.8334^*)$ , days to 50% flowering (0.1622), days to 80% maturity (0.0560) and thousand seeds weight (0.0560) had the positive direct effect on yield per plant whereas, number of secondary branches per plant  $(-0.7773^*)$ , siliqua length (-0.2415) and seeds per siliqua (-0.5457) had the negative direct effect on yield per plant.

The path coefficient studies indicated that that number of siliqua per plant (0.8334\*\*) was the most important contributor to seed yield per plant.

- Moderate heritability (40.00) with low genetic advance (1.36) and high genetic advance in percentage of mean (28) was found in case of number of secondary branches per plant. High genetic advance in percentage of mean indicated the possibility of predominance of additive genes and selection for genetic improvement for this trait would be effective.
- 2. High heritability with moderately high genetic advance in percentage of mean was observed in number of primary branches per plant (heritability=80.60, genetic advance in percentage of mean=28) number of seeds per siliquae (heritability=74.63, genetic advance in percentage of mean=40), siliqua length (heritability=76.47, genetic advance in percentage of mean=12.30) indicated medium possibility of selecting genotypes for further improvement.
- 3. Significant positive correlation with seed yield per plant was found in case of plant height (P=0.2844\*), siliqua per plant (G=0.8334\*, P=0.5110\*), seeds per siliqua (P=0.3171\*) and thousands seed weight (G=0.0218\*, P=0.0326\*). This result suggested that yield per plant can be increased by improving these characters.
- 4. Path co-efficient analysis revealed that plant height (0.3425), number of number of

primary branches per plant (0.1828), number of siliqua per plant (0.8334\*\*), days to 50% flowering (0.1622), days to 80% maturity (0.0560) and thousand seeds weight (0.0218\*) had the positive direct effect on yield per plant. So, yield improvement was associated with these characters.

## **Recommendation:**

Based on the results of the study and above discussion it can be said that two populations G16 and G10 were selected based on their better performances and other populations in respect of days to maturity, number of primary branches per plant, number of siliqua per plant, thousand seeds weight and seed yield per plant for release as a new variety.

### **CHAPTER VI**

### References

- Agaarwal, M., & Punia, M. S. (2019). Correlation and Heterosis Studies in various Populations of Indian Mustard (Brassica juncea L. Czern & Coss). *International Journal of Current Microbiology and Applied Sciences*, 8(3),ISSN: 2319-7706.
- Afrin, K.S., Mahmud, F., Bhuiyan, M.S.R. and Rahim, M.A (2011). Assessment of genetic variation among advanced lines of *Brassica napus* L. Agronomski Glasnik. 73(4-5): 201-226.
- Agaarwal, M., & Punia, M. S. (2019). Correlation and Heterosis Studies in various Populations of Indian Mustard (Brassica juncea L. Czern & Coss). *International Journal of Current Microbiology and Applied Sciences*, 8(3),ISSN: 2319-7706.
- Akbar, M., M. Tariq, M. Yaqub, M. Anwar, M. Ali and N. Iqbal. (2003). Variability, correlation and path coefficient studies in summer mustard (*Brassica juncea L.*). Asian J. Pl. Sci. 2(9): 696-698.
- Aktar, T., Nuruzzaman, M., Rana, M. S., Huda, M. M., Hossain, M. A., & Hassan, L. (2019). Genetic parameters and diversity studies of yield and yield contributing characters in Brassica genotypes. *Journal of Bangladesh Agricultural University*, **17**(3): 295.
- Alam, M.F. (2010). Variability studies in F4 progenies of *Brassica rapa*, obtained through intervarietal crosses. M.S. Thesis. Dept. of Genetics and plant Breeding, SAU, Dhaka
- Ali, N., Javidfar, F., Elmira, J.Y. and Mirza, M.Y. (2003). Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus* L.). *Pakistan J. Bot.* 35(2):167-174.
- Ali, N., F. Javaidfar and A.A. Attary. (2002). Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus L.*). *Pakistan. J. Bot.* 34(2): 145-150.

- Ara, S. (2010). Variability, correlation and path coefficient in segregating population of *Brassica rapa* obtained through inter-varietal crosses. M.S. thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.
- BBS (Bangladesh Bureau of Statistics). (2022). Bangladesh Bureau of Statistics. Monthly Statistical
   Bulletin of Bangladesh. January, Statistics Div., Ministry of Planning, Govt. People's Repub.
   Bangladesh; p.46.
- Begum, M. (2015). Genetic variability, correlation and path analysis in BC1 F5 segregating generation of *Brassica napus*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.
- Belet, Y.S. (2011). Genetic variability, correlation and path analysis studies in Ethiopian Mustard (*Brassica carinata* A. Brun). Genotypes. *Int. J. Plant Breed. Genet.* 5(4): 328-338
- Bibi, T., Rauf, S., & Mahmud, T. (2016). Genetic Variability and Heritability Studies in Relation to Seed Yield and its Component Traits in Mustard (Brassica Juncea L.). Academia Journal of Agricultural Research, 4(8): 478-482.
- Bind, D., Singh, D. and Dwivedi, V.K. (2014). Genetic variability and character association in Indian mustard [*Brassica juncea (L.)* cezerns and cross] *Agric. sci. Digest.* 34(3):183-188.
  Burton, G.W. (1952). Quantitative inheritance in grass pea. Proc. 6<sup>th</sup> Grassl. Cong. 1: 277-283.
- Chakraborty, P. K., A. Majumdar and B. N.Chatterjee. (1991). Physiological process in Indian mustard *Brassica juncea*) and yellow sarson (*Brassica napus var Glauca*) and their agronomic appraisal in mild and short winter prevailing in Gangetic plains of eastern India.
- Dar Z., S. Wani, G. Zaffar, M. Habib and M. Wani. "Variability studies in brown sarson (*Brassica rapa* L.)". *Res J Agric Sci*, **1**: 273-274.

*Indian J. Agric. Sci.* **61**(11): 851-858.

Deepti, Chawla, V., & Priyanka. (2016). Correlation and path coefficient analysis for yields contributing parameters in indian mustard [. *American Journal of Pharmatech Research*, 6(2),ISSN: 2249-3387.

Devi, B. (2018). Correlation and path analysis in Indian mustard (Brassica juncea L.) in agro - climatic

conditions of Jhansi (U.P.). Journal of Pharmacognosy and Phytochemistry, 7(1): 1678-1681.

- Dewey, O.R. and Lu, KH. (1959. Correlation and path coefficient analysis of component of creasted wheat grass seed production. *J Agron* **57**: 515-518.
- Downey, R. K. and Robbelen, G.(1989). *Brassica species*: Oil crops of the world, their breeding and utilization. Mc Graw Hill Publishing Co., New York. pp. 339-374.

Dixet, P. and D.K. Dubey. (1984). Path analysis in Lentil (*Lens culinaris Med.*). *Lens Newsletter*, **11**(2): 15-17.

- Ejaz-UI-Hasan, Mustafa, H.S.B., Bibi, T. and Mahmood, T. (2014). Genetic variability, correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. *Cercetari Agronomice in Moldova*. XLVII. 1(157).
- Emrani, S.N., Arzani, A.H., Saeidi, G.O., Abtahi, M., Banifatemeh, M.O., Parsa, M.B. and Fotokian, M.H. (2012). Evaluation of induced genetic variability in agronomic traits by gamma irradiation in canola (*Brassica napus* L.). *Pakistan J. Bot.* 44(4):1281-8.
- Esmaeeli-Azadgoleh, M.A., Zamani, M. and Esmaeil, Y. (2009). Aagronomical important traits correlation in Rapeseed (*Brassica napusL.*) genotypes. *Res. J. Agric. Biol. Sci.* **5**(5) 798-802
- Falconer, D.S., and T.F.C. Mackay. (1996): Introduction to Quantitative Genetics (4th Ed.) Longman, Essex, UK.
- Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron. J.* **48**(6), 268-275.

Hussain, M.A. (2014). Genetic variability and character association of advanced lines in *Brassica rapa*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.

Hossain, M.D. (2013). Food for the poor: achievement and challenges. The Daily Star. March 24.

http://bbs.portal.gov.bd/sites/default/files/files/bbs.portal.gov.bd/page/1b1eb817\_9325\_4 354\_a756\_3d18412203e2/Yearbook-2016-Final-19-06-2017.pdf http://nmoop.gov.in/Publication/StatusPaper\_RandM\_2017.pdf http://www.banglapedia.com http://www.fao.org/3/a-I7695e.pdf http://www.thebangladeshpost.com/national/5046/pdf

https://drive.google.com/file/d/1x07AMUkjglHIaeqyQlZAUvsnoXluR\_AU/view?ts=5a684f26 https://drive.google.com/file/d/1x07AMUkjglHIaeqyQlZAUvsnoXluR\_AU/view?ts=5a684 f26 https://www.pfaf.org/user/Search\_Use.aspx?glossary=Oil

- Iqbal, S., Farahtullah, Shah, S., Kanwal, M., Fayyaz, L. and Afzal, M. (2014). Genetic variability and heritability studies in indigenous *Brassica rapa* accession. *Pakistan J. Bot.* 46(2): 609-612.
- Iqbal, A.M., Shikari, A.B., Ashaq, H. and Dar, Z.A. (2015). Genetic variability in *Brassica rapa*L. Var. Brown sarson for maturity, yield and yield attributing traits. *Environ. Ecol.* 33(1): 267-270.
- Jahan, N., Khan, M.H., Ghosh, S., Bhuiyan, S.R. and Hossain, S. (2014). Variability and heritability analysis in F4 genotypes of *Brassica rapa* L. *Bangladesh J. Agril. Res.* 39(2): 227-241.
- Jeromela, M. A., Marinkovic, R., Mijic, A., Jankulovska, Zdunic, M. (2007). Interrelation between oil yield and other quantitative traits in rapeseed (*Brassica napus* L.). Sci. J. Agri. 8(2): 165-170.
- Johnson HW, Robinson HF, Comstoc R. Estimates of genetic and environmental variability in soybeans. *Agron. J.* 1955; **47:** 314-318.
- Kashyap, S.C. and Mishra, M.N. (2004). Correlation and path co-efficient analysis studies in toria (*Brassica campestris* Var. toria). *An. Agri. Bio. Res.* **9**(2): 123-126.
- Khan, F.A., Ali, S., Saeed, A. and Abbas, G. (2006). Genetic variability and genetic advance analysis for some morphological traits in *B. napus L. J. Agri. Res.* **44**(2):83-88.
- Khayat, M., Lack, S. and Karami, H. (2012). Correlation and path analysis of traits affecting grain yield of Canola (*Brassica napus* L.) varieties. *J. Basic. Appl. Sci. Res.* **2**(6): 5555-5562.
- Kumar, A., Chauhan, R., & Singh, K. P. (2020). Genetic variability, heritability and genetic advance

among Indian mustard (Brassica juncea) genotypes. *Annals of Plant and Soil Research*, **22**(1): 92-95.

- Laghari, K., Baloch, M., Sootacher, J. K., Menghwar, K., Kachi, M., Kumbhar, Z. M., . . . Daudpotto,
  I. (2020). Correlation and heritability analysis in rapeseed (Brassica napus L.) genotypes. *Pure* and Applied Biology, 9(1): 507-516.
- Li, J.N., Qiu, J. and Tang, Z.L. (1990). Analysis of variability of some genetic parameters in segregating hybrid generations of *B. napus. Oil .crops.china* .11(6): 4-7.
- Li, J. N., and Chen, L. (1990). Correlation analysis of the major yield and quality charactersin oilseed rape (*B. napus*). *Oil .crops.china*.**1** : 11-16.
- Lodhi, B., Thakral, N.K., Ram, A. and Amit, S. (2014). Genetic variability, association and Path analysis in Indian mustard (*Brassica juncea L.*) 26J. *Oilseed Brassica*. **5**(1):55.
- Marwede, V., Schierholt, A. and Becker, H.C. (2004). Genotype environment interactions and heritability of tocopherol contents in canola. *Crop Sci.* **44**:728731.
- Mather, K. (1949). Biometrical Genetics: The study of continuous variation. J.K. Jinks, (1<sup>st</sup>ed.). Methuen and Co., Ltd., London. p.162.
- Maurya, N., Singh, A.K. and Singh, S.K. (2012). Inter-relationship analysis of yield and yield components in Indian mustard, *Brassica juncea* L. *Indian J. Plant Sci.* **1**(23): 90-92.
- Mostofa, H. U., Islam, N., Monjurul, K., & Miah, H. N. (2016). Performance of Rapeseed and Mustard (Brassica sp.) Varieties/Lines in North-East Region (Sylhet) of Bangladesh. Agricultural Research & Technology, 2(1),ISSN: 2471-6774.
- Nadarajan, N. and Gunasekaran, M. (2005). Quantitative genetics and biometrical techniques in plant breeding. KP, Ludhiana, New Delhi, India. pp. 50-54.
- Nasim, A., Farhatullah, Iqbal, S., Shah, S. and Azam, S.M. (2013). Genetic variability and correlation studies for morpho-physiological traits in *Brassica napus* L. *Pakistan J. Bot.* 45(4): 1229-1234.

- Naznin, S., Kawochar, M.A., Sultana, S. and Bhuiyan, M.S.R. (2015). Genetic variability, character association and path analysis in *Brassica rapa* L. *Bangladesh J. Agric. Res.* **40**(2): 305-323.
- Pankaj, S., Gyanendra, T., Gontia, A.S., Patil, V.D. and Shah, P. (2002). Correlation studies in Indian mustard. *Agric. Sci. Digest.* 22(2): 79-82.
- Parveen, S., Rashid, M.H. and Bhuiyan, M.S.R. (2015). Assessment of breeding potential of rapeseed germplasm using D<sup>2</sup> analysis. J. Expt. Bio. Sci. 6(1): 59-64.
- Parveen, S., Rashid, M.H. and Bhuiyan, M.S.R. (2015). Genetic variation and selection criteria for seed yield related traits in rape seed (*Brassica napus* L.). *Bangladesh J. Plant Breed.Genet.* 26(2): 15-22.
- Parveen, S. (2007). Variability study in F2 progenies of Inter-varietal crosses of *Brassica rapa*.MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.
- Parvin, F. (2015). Genetic variability and character association in BC1F4 generation of *Brassica napus*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.
- Patil, S., Shivanna, S., Irappa, B., & Sheweta, K. (2015). Genetic variability and character Association studies for yield and yield contributing components in: Groundnut (Arachishypogaea L.). *International Journal of Recent Scientific Research*, 6(6):4568-4570.
- Prasad, L. Singh, M and Dixit R.K. (2001)- Analysis of heritability and genetic advance in Indian Mustered (Brarsica Junea (L.) (Czern & Coss. *Advances in Plant Sci.* 14(2): 577-581.
- Podder, P.M. Kader., B.K. Biswas., M.S. Alam and M.R.Amin 1996. Stability analysis for
   Yield and Yield Components in Mustard Under different dates of sowing.
   Bangladesh J.Agril.Sci. 23(2):1-6
- Rao, G. U., A. Jain and K.T. Shivana. (1992). Effect of high temperature stress on Brassica
  Pollen: Viability, germination and ability to set fruits and seeds. Ann. Bot. (London) 69 : 193-198

- Rameeh, V. (2014). Correlation and factor analyses of quantitative traits in rapeseed (*Brassica napus* L.). Int. J. Agri. Innov. Res. 1(1): 2319-1473.
- Rameeh, V. (2015). Heritability, genetic variability and correlation analysis of some important agronomic traits in rapeseed advanced lines. *Cercetari Agronomice* in Moldova. 48(4): 71-80.
- Rashid, M. H. (2007). Characterization and diversity analysis of the Oleiferous SAU, Dhaka.
- Rauf, M. A., & Rahim, M. A. (2018). Genetic Variability Studies among Yield and Its Contributing Traits in Mustard (Brassica napus L.). *Advances in Zoology and Botany*, 6(4): 101-108.
- Raymer, P.L. (2002). Canola: An emerging oilseed crop. In: J. Janick and A. Whipkey (eds.), Trends in new crops and new uses. ASHS Press, Alexandria, VA. p. 122–126.
- Robinson, H.F., Comstock, R.E. and Harvey, P. (1966). Quantitative genetics in relation to breeding on the centennial of mendelism. *Indian J. Genet.* **26**: 171-177.
- Roy, R. K., Kumar, A., Kumar, S., Kumar, A., & Kumar, R. R. (2018). Correlation and Path Analysis in Indian Mustard (*Brassica juncea* L. Czern and Coss) under Late Sown Condition. *Environment and Ecology*, 36(1A) : 247—254.
- Roy, S. K., Kale, V. A., & Nagnathwar, V. A. (2015). Assessment of genetic variability of rapeseedmustard germplasm under Teriaregion of West Bengal. *Electronic Journal of Plant Breeding*, 6(4):1132-1136.
- Sabaghnia, N., H. Dehghani, B. Alizadeh and M. Mohghaddam. (2010). Heterosis and combining ability analysis for oil yield and its components in rapeseed. Australian. J. Crop Sci. 4(6):390
- Sarma, R.N. and A. Roy. (1993). Phenotypic stability for seed yield and maturity in toria (*Brassica napus Var.napus*) and Indian mustard (*Brassica juncea*) Indian J.Agril 63(12):814-817.
- Shakera, A. (2014). Variability and inter relation of traits in segregating generations of rapeseed (*Brassica rapa* L.). MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.

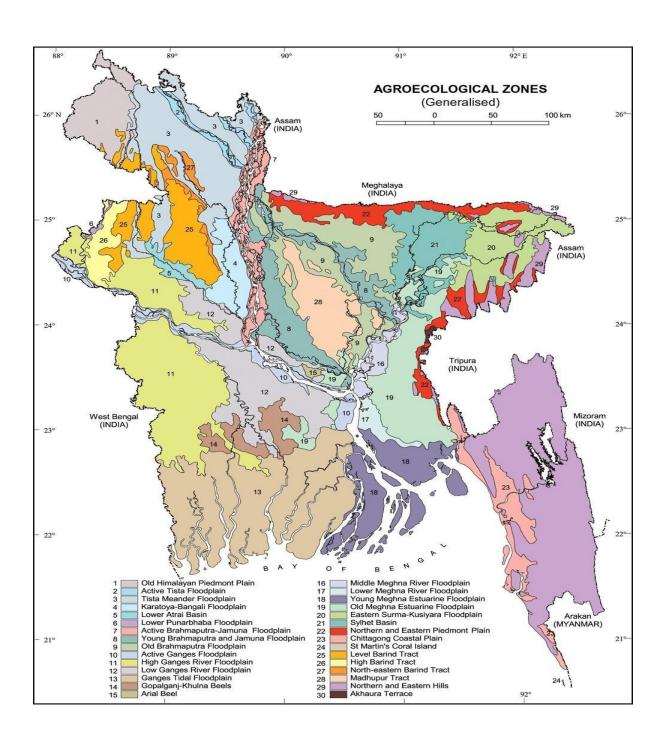
- Sharafi, Y., Majidi, M. M., Jafarzadeh, M., and Mirlohi, A. (2015). Multivariate analysis of genetic variation in winter rapeseed (*Brassica napus* L.) cultivars. J. Agric. Sci. Tech. 17(5): 1319-1331.
- Shaukat, S., Khan, F. U. and Khalil, I. A. (2015). Genetic potential and heritability estimates of yield and yield associated traits in rapeseed *Brassica napus* L. *Int. J. Environ.* **4**(2): 330-340.
- Shekhawat, G. Jadeja C., Singh, J. and Shekhawat, R.S. (2014). Character association among Yield and its Component characters in Indian mustard (*Brassica juncea* L Crezen and Cross). *The Biosean.*9 (2): 685-688.
- Shrivastava, A., Tripathi, K. M., Solanki, R. S., Tiwari, S., Tripathi, N., Singh, J., & Yadav, R. (2023). Genetic Correlation and Path Coefficient Analysis of Yield Attributing Parameters in Indian Mustard . *Current Journal of Applied Science and Technology*, 42(7):42-53.
- Sikawar, S. R., Satankar, N., Kushwah, M. K., & Singh, A. K. (2017). Genetic Variability, Heritability and Genetic Advance Studies in Yellow Sarson (*Brassica rapa* var. Yellow Sarson). *International Journal of Agriculture Innovations and Research*, 5(5),ISSN 2319-1473.
- Singh, S., Ashutosh, Dwivedi, A. K., Kumar, O., Kumar, K., & Verma, O. P. (2020). Study of Character Association and Path Analysis in Indian mustard (*Brassica juncea* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences*, 9(2),ISSN: 2319-7706.
- Siddika, K.S. (2015). Genetic variability, correlation and path analysis in F<sub>2</sub> segregating generation of in *Brassica napus*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.
- Singh, M., Swarnker, G.B., Prasad, I. and Rai, G. (2002). Genetic variability, heritability and Genetic advance for quality traits in Indian mustard. *Plant Arch.* **2**(1): 27-31.
- Singh, M. and Singh, G. (1997). Correlation and path analysis in Indian mustard (*Brassica juncea L*.) under mid hills of Sikkim. *J. Hill Res. India*, **10**(1): 10-12.
- Subrahamanyam, D. and Rathore, V.S. (1994). Effect of high temperature on CO<sub>2</sub> assimilation and Partitioning in Indian Mustard. Journ. *Agron. Crop. Sci.***172:** 188-193.

Sultana, S. (2015). Genetic variability, correlation and path analysis in F4 generation of Brassica

napus. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.

- Tahira, Mahmood, T., Tahir, M.S., Saleem, U., Hussain, M. and Saqib, M. (2011). The estimation of heritability, associated and selection criteria for yield components in mustard (*Brassica juncea*). *Pakistan J. Agri. Sci.* **48**(4): 251-254.
- Uddin, M.S., Bhuiyan, M.S.R., Mahmud, F. and Kabir, K. (2013). Study on Correlation and PathCoefficient in F Progenies of Rapeseed (*Brassica rapa*). Acad. J. Plant Sci. **6**(1): 13-18.
- Ullah, N., Khan, J., Khan, M.W., Raza, H., Alam, M., Ullah, H. and Ali, F. (2017). Genetic variability for biochemical traits among advanced lines of *Brassica*. *Pure Applied*. *Biol.* 6(1):
  1.
- Ushakumari, R.M., Subramanian, M. and Subramaniam. (1991). Studies on coefficient of variation and heritable components of some quantitative characters of Brinjal. *Indian J. Hort.* **48**(1): 75-78.
- Verma, S., Singh, V. V., Meena, M. L., Rathore, S. S., Ram, B., Singh, S., . . . Singh, B. R. (2016).
  Genetic analysis of morphological and physiological traits in Indian mustard (Brassica juncea L.). SABRAO Journal of Bredeing and Genetics, 48 (4): 391-401.
- Walle, T., & Wakjra, A. (2014). Analysis of genetic parameter on Ethiopian mustard (Brassica carinata a.Braun) genotype in Northwestern Ethiopia.*Plant Breeding and Seed Science*Yarnell, S.H., Rai, B. and Singh, B. (1956). Component analysis of harvest index in *Brasica* oilseeds. *Indian. J. Agric. Res.* 20(3): 129-134.
- Zahan, M.I. (2006). Morphological characterization and genetic diversity in oleiferous *Brassica species*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

## **APPENDICES**



Appendix I. Map showing the experimental site under the study

Appendix II: Morphological, physical and chemical characteristics of initial soil (0-15cm) depthof 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

Chemical composition of the soil

Sl.	Soil characteristics	Analytical data	Methods employed
No.			
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 sunshineof the experimental site during the period from December, 2020 to February, 21.

Month	Air temperature (°c)		Relative	Rainfall	Sunshine	
			humidity(%)	(mm)	(hr)	
	Maximum Minimum					
December, 2020	33.4	16.9	64	0	7.9	
January, 2021	29.8	15.0	75	0	3.4	
February, 2021	28.7	12.3	70	1	5.8	

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

	PH	PBP	SBP	SPP	SL	SPS	DF	DM	TSW	Y/P
G1	91.27	4.13	0.17	99.40	4.87	22.73	35.33	86.67	2.28	4.63
G2	103.13	4.03	3.07	102.70	5.37	14.89	35.00	86.67	2.45	5.06
G3	99.70	4.33	1.00	101.10	5.20	21.84	36.33	89.67	2.36	4.20
G4	98.09	5.40	2.03	103.40	4.70	19.26	35.00	90.33	2.81	4.87
G5	96.91	6.00	2.46	107.63	5.36	20.49	35.33	87.67	2.96	5.06
G6	99.13	4.73	1.47	97.83	5.33	18.21	36.67	90.00	2.93	4.87
G7	106.70	6.33	4.63	103.47	5.00	10.80	34.33	89.33	2.65	4.67
G8	96.27	5.43	4.63	98.47	5.16	11.27	38.00	87.00	2.94	3.87
G9	94.93	4.13	0.67	98.57	4.80	16.21	37.33	85.67	2.62	4.67
G10	96.00	5.73	2.63	107.67	5.33	13.18	33.66	87.33	3.00	5.33
G11	96.50	4.07	1.03	105.00	5.13	19.84	38.33	87.67	2.78	4.73
G12	103.23	4.03	0.33	98.17	5.36	23.60	36.67	88.33	2.45	5.27
G13	106.23	4.00	0.50	97.60	5.90	15.39	35.67	85.67	2.84	4.27
G14	113.73	5.43	1.06	109.00	5.63	18.14	38.67	88.33	2.67	5.27
G15	90.06	5.23	0.70	99.47	4.76	19.07	35.33	90.33	2.91	5.33
G16	100.80	5.16	0.50	104.13	5.80	27.21	38.33	85.00	2.83	5.33
G17	114.04	5.50	0.67	102.80	5.63	23.2	37.33	90.00	2.51	5.27
G18	100.11	3.80	2.00	100.20	5.30	14.16	35.66	86.67	2.89	4.8
G19	94.25	4.70	3.23	88.57	6.03	14.81	35.00	89.00	2.66	3.53
G20	105.9	4.50	0.63	112.47	5.13	19.31	38.00	89.33	2.36	5.27

Appendix IV: Mean performance of various growth parameter and yield components of Brassica rapa L.

PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliqua per plant, LS = Length of siliqua (cm), SPP = Number of seeds per siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, TSW = Thousand seeds weight (g), Y/P = Yield per plant