GENETIC VARIABILITY AND INTERRRELATIONSHIP OF YIELD AND COMPONENT CHARACTERS IN F_{10} GENERATION OF *Brassica napus* L.

MONIRA SARKER RISTA

DEPARTMENT OF GENETICS AND PLANT BREEDING, SHER-E-BANGLA AGRICULTURAL UNIVERSITY DHAKA-1207

JUNE, 2021

GENETIC VARIABILITY AND INTERRELATIONSHIP OF YIELD AND COMPONENT CHARACTERS IN F_{10} GENERATION OF *Brassica napus* L.

MONIRA SARKER RISTA

REGISTRATION NO. 14-06241

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, 2021

Approved by:

(Dr. Firoz Mahmud)
Professor
Supervisor

Dr. Md. Sarowar Hossain)
Professor
Co-supervisor

(Prof. Dr. Md. Abdur Rahim)
Chairman
Examination Committee
Department of Genetics and plant breeding, SAU, Dhaka

Dr. Firoz Mahmud
Professor
Department Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mobile: +8801552432589
E-mail: fmahmud08@gmail.com

CERTIFICATE

This is to certify that the thesis entitled, ***"GENETIC VARIABILITY AND INTERRELATIONSHIP OF YIELD AND COMPONENT CHARACTERS IN F_{10} GENERATION OF Brassica napus* L.** *" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***MONIRA SARKER RISTA****, Registration No.* **14-06241** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2021
Place: Dhaka, Bangladesh

Prof Dr. Firoz Mahmud
Supervisor

ACKNOWLEDGEMENTS

All praises are due to Almighty God, who created everything in the universe, empower me to complete the research work and the thesis for the degree of Master of Science in Genetics and Plant Breeding.

I pay my deepest gratitude to my research supervisor ***Professor Dr. Firoz Mahmud,*** *Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, for his Patience, motivation, enthusiasm, immense knowledge, practical co-operation, distinguishable scholastic guidance and sincere advice throughout the research work, giving valuable suggestion and timely instruction. This work would not have been possible without his guidance, support and encouragement. Under his guidance I successfully overcome many difficulties and learn a lot. I can't forget her hard work.*

It is a great pleasure for the author to express her heartfelt gratitude to his honorable ***co****-supervisor* ***Professor Dr. Md. Sarowar Hossain,*** *Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his immense help, effective guidance, and constructive criticism during the period of research work.*

I express my sincere respect to chairman, ***Professor Dr. Md. Abdur Rahim,*** *Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh for his valuable advice, encouragement, proper assistance and support during the period of research works. The author desires to extend her gratitude to the academic officers and staffs of the Department of Genetics and Plant Breeding for their sincerity during this thesis preparation. The author is thankful to the farmers of the study area for the cooperation during data collection.*

The author would like to express her respect and gratitude to Professor Dr. Alok Kumar Paul, Post Graduate Dean and Professor Dr. Md. Shahidur Rashid Bhuiyan, Vice Chancellor, Sher-e-Bangla Agricultural University, Dhaka for providing me all possible helps to conduct the research work.

The author has received cordial cooperation from her beloved husband Md. Shariful Islam during the research period. Finally, the author is highly indebted to her beloved parent Md. Abdul Malek Sarker and Umme Rabeya for their blessings, endless encouragement and affection in all stages of my life.

June, 2021 ***The Author***
Dhaka, Bangladesh

LIST OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

SOME COMMONLY USED ABREVIATIONS

FULLWORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Agricultural	Argil.
And others	*et al.*
Accessions	ACC
Agronomy Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Biological	Biol
Centimeter	cm
Co-efficient of Variation	CV
Ecology	etc.
Etcetera	Ecol.
Environmental variance	$\delta 2 e$
Figure	Fig.
Food and Agricultural Organization	FAO
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	$\delta 2 g$
Gram	g
Heritability in broad sense	$h 2 b$
Journal	J.
Kilogram	Kg
Meter	M
Mean Sum of Square	MSS
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta 2 p$
Randomized Complete Block Design	RCBD
Replication	R
Research	Res.
Science	Sci.
Sher-e-Bangla Agricultural University	SAU
Tripol super phosphate	TSP

GENETIC VARIABILITY AND INTERRELATIONSHIP OF YIELD AND COMPONENT CHARACTERS OF F_{10} GENERATION IN *Brassica napus* L.

By

MONIRA SARKER RISTA[1]

ABSTRACT

The experiment was undertaken using 33 promising advanced populations of *Brassica napas* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka during November 2019 to February 2020 considering ten yield contributing characters. To assess advanced populations, the study examined the magnitude of character variations, heritability, genetic advance, correlation, and direct and indirect effects of different characters on seed yield per plant. Analysis of variance revealed significant variations among all populations for all the traits. Minimum difference between phenotypic and genotypic variance was observed in days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and seed yield per plant. However, high genotypic and phenotypic coefficient of variation were observed in the number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, thousand seed weight and seed yield per plant. In siliqua per plant, high heritability was observed with high genetic advance, indicating that these traits were under additive gene control and that selection for genetic improvement would be efficient. Plant height (cm), secondary branches/plant, siliqua/plant, siliqua length (cm), and thousand seeds weight (g) all showed a positive significant genotypic and phenotypic correlation with seed yield per plant. The path coefficient analysis was carried out using the correlation coefficient to determine direct and indirect influence that was stated that primary branches/plant, secondary branches/plant, siliqua/plant, and thousand seed weight (g) all had a positive and direct effect on yield per plant, indicating that they were the most important contributors to seed yield per plant. Higher seed yield per plant was observed in G20 (9.59 g), G12 (9.19 g), G15 (7.45 g), G22 (7.25 g) and G5 (7.24 g) and selected as promising population for future hybridization program.

CHAPTER I

INTRODUCTION

Mustard oil is the third most important sources of edible vegetable oils in the world. It is widely known as oilseed, rapeseed. The term "rape" comes from the Latin word for *turnip, rapa* or *rapum*, cognate with the Greek word *rhapys*. It contributes a lion share to the total edible oil production in our country. It has economic and commercial value and plays an important role in fulfilling the consumers' nutritional demand in our country. Brassicas account for about 10 per cent of total oilseeds and 14 per cent of total vegetable oil production. They are mainly cultivated for edible oils but used as condiments, spices and as fodder for livestock (Pallavi, 2020).

Among the oilseed crops in Bangladesh, *Brassica napus* L. obtains the first position in respect of area cultivation and production (Naznin *et al.*, 2015). In the world, Total area covered by rapeseed was 36.50 million hectares with yield of 2.05 metric tons (MT) per hectare in 2017-2018. Whereas, In Bangladesh total area under rapeseed cultivation was 0.25 million hectares and production was 0.92 metric tons (MT) per hectare in the same year which was lower than developed countries (USDA 2019). The total esculent oil production was estimated at about 580.7 million tons from major oil producing crops in the world whereas rapeseed contributed 75.4 million tons and holding second position after soybean among major edible oil sources in 2017-1018 (FAO, 2019). The consumption of mustard oil is increasing day by day and according to US-based market researcher, Index Box (www.graincentral.com), in 2017 it had been increased 7.3 percent which indicate the importance of it.

Brassica species are actually under cultivation in Asian countries, particularly China and Indian subcontinent. According to Russian workers, eastern Afghanistan together with adjoining northwest India is one of the independent centers of origin of brown mustard. Yellow mustard grown in eastern India expresses largest diversity in Bengal. It is quite possible that its primary center of origin is northwest India. *B.napus* is European rapeseed or Swede rape and cultivated in Mediterranean region since ancient times. Brassicas are cultivated largely in India, China, Canada, Europe, Australia, USA, East Africa, Russia and South America (Pallvi, 2020).

Mustard belongs to genus Brassica of the family Cruciferae. The oilseeds brassicas contains four species: *B.compesiris* (*B. rape*), *B. juncea* (Indian mustard), *B. napus* (winter and spring rape) and *B. carinata* (Ethiopian mustard). Mustard is grown well in the tropical as well as of the temperate zone crops and requires relatively cool temperature for satisfactory growth and yield (Pallvi, 2020).

Mustard oil has a strong aroma and is considered a ‘strong’ oil variety. Edible oil is an essential integral part of the daily diet of the people in Bangladesh. Mustard oil plays a vital role in human nutrition. Rapeseed is one of the most important annual crops in the world and it’s also a great source of protein. It helps to absorb vitamins. It is a great source of energy, like 100g of mustard oil can give 884 Kcal of energy. It is rich with fats like, Saturated Fats, Monounsaturated Fats and Polyunsaturated Fats. Rather than that, 100g mustard oil contains around oleic acid 20%-28%, linoleic acid10%-12%, linolenic acid 9%-9.5% and erucic acid 30%-40%. Mustard oil has many health benefits in human body. It promotes a healthy heart function and reduces the risk of cardiovascular disease. Mustard oil contains rich amount of alpha-linolenic acid that has shown to exhibit anti-inflammatory properties. It also exhibits anti-microbial properties due to the presence of glucosinolate which inhibits microbial growth and is rich in allyl isothiocyanate that has been proven to decrease the growth of cancer cells in living organisms. It also promotes healthy skin and hair health (Twenty-four mantra Organic, 2021)**.**

In Bangladesh, total 3.0 million tons oils and fats was used, therein 2.5 million tons were imported in 2017-18 (FAO, 2019). A large amount of foreign exchange is expended on imports of edible oils and oilseeds to meet the increasing demand of its population. The expenses of imported edible oils and oilseeds were US$ 1,197 million and US$ 329 million respectively in 2017-2018 (www.mpoc.org.bd). Due to rice based cropping pattern the cultivation area for mustard is low and production is also low but the demand is gradually increasing day by day. So, to avoid import reliance and fulfill the demand, it is important to increase oil production. Existing low yielding varieties associated with low inputs and management are main bindings of mustard production in our country as well as farmers also need short duration variety so that, it can be successfully grown between the two rice crops. The present study was aimed at estimating the genetic variability and interrelationship of seed yield and its related traits of 33 *Brassica napus* L.

The yield is complex character and is dependent on many other morphological traits which are mostly inherited quantitatively. It is important to examine the contribution of each of the trait in order to give more attention to those having the greatest influence on seed yield (Tuncturk and Ciftci, 2007). Importance of genotypic and phenotypic variability, heritability and character association have proved by many scientists (Ali et al., 2002; Lekh et al., 1998; Saini and Sharma, 1995) for further genetic improvement. Gosh and Gulati (2001) also showed that the traits showing high heritability are under the control of additive genes and can be successfully utilized for plant selection on the basis of phenotypic performance

Objectives:

- To study the variability of important characters in F10 generations generated inter genotypic crosses to select the best promising lines.
- To access genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters and
- To select promising population considering early maturity, high yielding plants.

CHAPTER II

REVIEW OF LITERATURE

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

2.1 Genotypic and phenotypic variability

2.2 Heritability and genetic advance in *Brassica*. sp.

2.3 Correlation analysis

2.4 Path co-efficient analysis

2.1 Genotypic and phenotypic variability

Bahadur *et al.* (2021) conducted an experiment at Research Farm of Department of Genetics & Plant Breeding, ANDUAT, Narendra Nagar, Ayodhya (U.P.) during rabi, 2018 with 28 yellow mustard genotypes for assessment of genetic variability. The analysis of variance (ANOVA) was noticed significant variation for all the characters under study. The genotype NDYS-2 followed by YSCN16-3, NDYS16-6, YSCN-2 and YSCN16-5 producing higher seed yield per plant. The highest estimates of PCV and GCV was recorded in case of seed yield per plant (g) (PCV 29.193%, GCV = 25.546%) followed by primary branches per plant (PCV = 25.407%, GCV = 21.573%), and number of seed per silique (PCV = 21.645%, GCV = 20.891%) observed higher for GCV and PCV.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

2.2 Heritability and genetic advance in *Brassica*. sp.

Kadvani *et al.,* 2021 conducted a field experiment during July to October, 2018 at CastorMustard Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India to access genetic variability, heritability and genetic advance for seed yield and its attributing traits in 45 genotypes of sesame. Analysis of variance revealed significant difference among genotypes for all the eleven characters which pointed the presence of sufficient variability among the genotypes under study, hence there is an ample scope of selection for superior and desired genotypes to plant breeder for further crop improvement. High heritability was observed for 1000 seed weight, followed by leaf area plant-1, oil content, days to flowering, capsule length plant-1, number of capsules plant-1, days to maturity, seed yield plant-1 and number of effective branches plant-1 indicated that heritability may be due to higher contribution of genotypic component in these characters. High heritability with high genetic advance as percentage of mean was observed for leaf area plant-1, seed yield plant-1, number of effective branches plant-1, number of capsules plant-1, 1000 seed weight and days to flowering expressing that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for genetic improvement of seed yield in sesame.

Bahadur *et al.,* 2021 conducted an experiment at Research Farm of Department of Genetics & Plant Breeding, ANDUAT, Narendra Nagar, Ayodhya (U.P.) during rabi, 2018 with 28 yellow mustard genotypes for assessment of genetic variability. The heritability in broad sense was observed higher of character length of main raceme followed by number of seed per silique, oil content (%), silique on main raceme and seed yield per plant (g) (76.60%). The genetic advance as per cent of mean was found higher for number of seed per silique, primary branches per plant, silique on main raceme and length of main raceme, the high estimate of heritability coupled with high genetic advance for seed yield per plant (g), number of seed per silique, silique on main raceme, and length of main raceme.

Sikarwar *et al.* (2017) carried out an experiment for the assessment heritability and genetic advance in 21 diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson) for ten yield and its contributing characters. Higher estimates of broad sense heritability were observed for all the characters. High heritability along with high genetic advance was noticed for number of secondary branches per plant, seed yield per plant, length of main raceme, number of siliquae on main raceme, number of seeds per siliqua and number of primary branches per plant.

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

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

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

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

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

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

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

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

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

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

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

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

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

Ahmad *et al.* (2013) conducted a study with thirty-five advanced mutant lines along with a check variety of *B. napus* called Abasin-95 to estimate heritability and genetic advance. High heritability and genetic advance were noted for seed yield.

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

Halder (2013) experimented on eleven advanced lines of *B. rapa*. High heritability along with moderate genetic advance and genetic advance in mean percentage were observed in days to 50% flowering and days to 80% flowering whereas moderate heritability with high genetic advance and genetic advance in mean percentage were recorded in siliquae per plant and yield per hectare.

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

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

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

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

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

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

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

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

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

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

2.3 Correlation analysis

Ethiopia is the center of origin for Ethiopian mustard (*B. carinata*). The crop is one of the oldest oil crops and farmers in the highlands of the country grow as a leafy vegetable. However, no attempt lately has been made to assess the association of characters and path analysis in Ethiopian mustard leaf. Ousman *et al.*, 2021 carried out an experiment to assess association of traits among leafy vegetable yield and yield related traits and to determine the direct and indirect effects of the traits. A total of 36 Ethiopian mustard genotypes were examined at Holleta in 2017-2018. The results from correlation study expressed that the genotypic correlation coefficient among edible vegetable leaf yield as well as all of agro-morphological qualities was positive and significant apart from leaves per plant and leaf width ratio to length. Length of leaf petiole, leaf length, leaf width, petiole width and plant height had showed positive and highly significant correlation with edible vegetable leaf yield both at levels of genotypic and phenotypic. These characters also had indirect positive effect on yield either though each other or via other traits at genotypic level. The strong association of these traits with leaf yield, the high to low effects of direct and indirect through other characters at level of genotypic for these traits is an indication of the importance.

Awasthi *et al.* (2020) Studded on correlation revealed that seed yield per plant and harvest index exhibited significant positive correlation and both traits also demonstrated significant positive correlation with days to 50 per cent flowering and number of secondary branches per plant at both genotypic and phenotypic level. This expressed the strong association of seed yield per plant, harvest index, days to 50 per cent flowering and number of secondary branches per plant. Both genotypic and phenotypic correlation co-efficient for seed yield per plant was observed significant positive correlation with days to 50 per cent flowering, number of secondary branches per plant, number of silique per plant and harvest index. Number of silique per plant was recorded significant positive correlation with number of primary branches per plant, number of secondary branches per plant, number of silique per plant and seed yield per plant. Number of secondary branches per plant was recorded significant positive correlation with days to 50 per cent flowering, number of primary branches per plant, number of siliqua per plant, number of seeds per siliqua, seed yield per plant and harvest index. Further, the path co-efficient analysis presented low residual effect (0.00482, 0.00304 and 0.00167) during *Rabi* 2016-17 and 2017-18 indicating that most of the major yield components were included in the study. Harvest index percentage had showed the highest direct positive effects on seed yield per plant, number of siliqua per plant, number of seeds per siliqua, number of secondary branches per plant and days to maturity. Based on result it has been concluded that two characters namely seed yield per plant and harvest index exhibited significant positive correlation as well as direct effect on seed yield may be considered for selection and to improve the seed yield of the mustard germplasm.

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

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

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

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

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

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

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

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

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

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

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

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

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

Abideen *et al.* (2013) studied on eight genotypes of *B. napus* and the result showed that positive phenotypic correlation was observed in plant height, pod length and seed yield. Significant positive correlation was also recorded in seed yield per plant and pods per plant.

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

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

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

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

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

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

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

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

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

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

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

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

2.4 Path co-efficient analysis:

Path coefficient analysis calculates the correlations between yield and its contributing components, taking account of the cross correlation, either positive or negative. It is useful to partition the total correlation into direct and indirect effects on different components

(Tollenaar *et al.*, 2004). In agriculture, plant breeders seek assistance in identifying traits that are useful as selection criteria to improve crop yield with help of path analysis.

Rout *et al.*, 2018 carried out with thirty-eight germplasm accessions of Indian mustard and evaluated for seed yield and its yield components for twelve characters during rabi season of 2015-16 at Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram, Meerut, India. The results express that number of siliqua per plant and harvest index had highly significant positive association with seed yield per plant. Path coefficient analysis presented high positive and direct influence of harvest index, biological yield, number of siliqua per plant towards seed yield at genotypic level and at phenotypic level path coefficient analysis showed high positive and direct influence of harvest index and biological yield per plant towards seed yield in Indian mustard.

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

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

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

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

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

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

Afrin (2014) carried an experiment to evaluate the variability among fifteen F4 population of *B. rapa* of different cross combinations and path coefficient analysis showed that number of primary branches per plant, number of siliquae per plant, number of seeds per siliqua and thousand seed weight had the positive direct effect on seed yield per plant.

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

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

Shakera (2014) carried out an experiment using twenty F_3 and F_4 populations generated through inter-varietal crosses, along with three check variety of *B. rapa* L. to study the 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.

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

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

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

An experiment was carried out by Alam (2010) by using twenty-six (26) F4 populations of some inter-varietal crosses of *B. rapa*. Through path coefficient analysis, it was unveiled that plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliqua and siliqua length had the direct positive effect on yield per plant while days to 50% flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plant.

Singh (2010) undertook a research work to study sixty two F1 and twenty four parental lines of *B. juncea* and the path analysis revealed that the highest positive direct effect was observed in secondary branches per plant followed by plant height and seeds per siliqua on seed yield per plant while the highest negative effect was in the plant height on seed yield per plant.

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

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

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

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

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

CHAPTER III

MATERIALS AND METHODS

This chapter contains information about the materials and methods that were utilized to conduct the experiment. It includes a brief description of the experimental site, soil characteristics, climate, materials used in the experiment, experiment layout and design, land preparation, manuring and fertilizing, seedling transplanting, intercultural practices, harvesting, data recording procedure, and statistical analysis, among other things:

3.1 Experimental site

The research was carried out in the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh's experimental farm. The experiment lasted from November 2019 through February 2020. The experimental plot's soil was clay loam with a medium fertility level and a medium fertility level. The experimental site had a subtropical climatic climate with wet summers and dry winters. The experimental site was located at 230 74' north latitude and 900 35' east longitudes, with an elevation of 8.6 meters above sea level. Photograph of experimental locations is given in (Appendix I).

3.2 Soil and climate

The experimental site was in a subtropical climate. The experimental site's soil is from "The Modhupur Tract's" agro-ecological zone (AEZ-28). The soil was olive gray and clay loam in texture, with fine to medium prominent dark yellowish brown mottles. The pH ranges from 5.47 to 5.63, with 0.82 percent organic carbon content (Appendix IV). The Bangladesh Meteorological Department, Agargaon, Dhaka, kept records on air temperature, humidity, and rainfall during the trial period (Appendix II and III).

3.3 Experimental materials

Healthy seeds of 33 advanced lines of *B. napus* L. were collected from the Sher-e-Bangla Agricultural University's Department of Genetics and Plant Breeding and used as experimental materials. Intergenotypic crossings were used to create these materials. This is a list of the materials used in their experiment (Table 1).

Table 1. Materials used for the experiment

SI. No.	Genotypes	Crossing materials (F_9)
1	G1	Nap (9908 × 9901)
2	G2	Nap (9906 × 9901)
3	G3	Nap (9905 × 0130)
4	G4	Nap (108 × 2066)
5	G5	Nap (9901 × 0130)
6	G6	Nap (108 × 2066)
7	G7	Nap (9908 × 0130)
8	G8	Nap (2066 × 205)
9	G9	Nap (9908 × 2066)
10	G10	Nap (9905 × 205)
11	G11	Nap (108 × 2066)
12	G12	Nap (9906 × 205)
13	G13	Nap (9901 × 0130)
14	G14	Nap (2066 × 0130)
15	G15	Nap (108 × 9901)
16	G16	Nap (9905 × 205)
17	G17	Nap (205 × 0130)
18	G18	Nap (9905 × 108)
19	G19	Nap (2066 × 0130)
20	G20	Nap (9901 × 2066)
21	G21	Nap (108 × 9901)
22	G22	Nap (108 × 9901)

Table: 1 (Cont'd)

Sl No.	Genotypes	Crossing Materials (F_9)
23	G23	Nap (205 × 0130)
24	G24	Nap (108 × 0130)
25	G25	Nap (9906 × 205)
26	G26	Nap (2066 × 205)
27	G27	Nap (9905 × 108)
28	G28	Nap (9905 × 206)
29	G29	Nap (9906 × 0130)
30	G30	Nap (9908 × 9906)
31	G31	Nap (108 × 9901)
32	G32	Nap (9906 × 2066)
33	G33	Nap (9908 × 0130)

Plate 1. The pictorial view of showing experimental field

3.4 Methods

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

3.4.1 Land preparation

To ensure greater tilth, the experimental plot was prepared by multiple ploughing and cross ploughing, followed by laddering and harrowing with a tractor and power tiller. Weeds and other stubbles were thoroughly removed from the experimental plot before it was leveled. Plate 2 showing the land preparation.

Plate 2. The pictorial view of experimental field during land preparation

3.4.2 Application of manure and fertilizer

At proper rate and proper time, Urea, Triple Super Phosphate (TSP), Muriate of potash (MOP), Gypsum, Zinc oxide and Boric acid were applied to the field. The first half amount of urea, total amount of cowdung, TSP, MOP, Gypsum, Zinc Oxide and Boric acid were applied during final land preparation as basal dose. The rest amount of urea was applied as top dressing after 25 days of sowing. The application of fertilizers and manures list of fertilizers and manures with doses and procedures of application is shown in table 2.

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

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

Plate 3. The pictorial view of showing flowering stage

3.4.3 Experimental design and layout

After the final ground preparation, the field layout was completed. With three replications, the experiment was set up in a Randomized Complete Block Design (RCBD). The whole experimental area was 200 m^2 (18 m x 12 m). Each replication was 17 m × 3 m in size, with a 1 m spacing between them. The row to row distances were 30 centimeters and plant to plant distances were 10 cm apart. On November 16, 2019, seeds were sowed in lines in the experimental plots. The seeds were planted at a depth of around 1.5 cm in the soil. After sowing, the seeds were carefully covered with dirt to ensure that there were no clods on the seeds. Plate 3 depicts a visual picture of the experimental field at the blossoming stage.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germinatin of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. Second weeding was done after 35 days of sowing. Sap sucking insect aphid infestation was found in the crop during the siliqua development stage. Insecticide Malataf 57 EC under Malathion group @ 2 ml/liter of water was applied for controlling aphid.

3.4.5 Crop harvesting

The crop was harvested at various times depending on its maturity. Harvesting began on February 10th, 2020, and continued until February 17th, 2020, depending on maturity. The crop was considered mature when 80 percent of the plants displayed maturity symptoms such as straw-colored siliqua, leaves, stems, and ideal seed color in matured siliqua. The photograph in Plate 4 shows the harvesting was done under supervision of my research supervisor. In each replication, 10 plants were chosen at random from F_{10} progenies. The plants were gathered by uprooting them and then correctly tagging them. These plants provided data on a variety of factors were collected from these plants.

Plate 4. The pictorial view showing crop harvesting

3.4.6 Data collection

Ten characters were taken into consideration for studying different genetic parameters, association and genetic diversity. Data were recorded from ten selected plants for each genotype for each replication on following parameters. The details of data recording are given below on individual plant basis.

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

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

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

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

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

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

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

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

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

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

Plate 5. The pictorial view showing observation and data collection

3.5 Statistical analysis

The mean values of ten randomly selected plants used for recording observations were computed for each of nine traits for each genotype in each replication and subjected to statistical analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using Statistix 10 computer program. Duncan‘s Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using Statistix 10.

3.5.1 Analysis of variance:

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

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

Where, p = number of treatments (population)
r = number of replications
σ_r^2 = variance due to replications
σ_p^2 = variance due to treatments (population)
σ_e^2= variance due to error

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

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

Where, S. E = Standard error of mean

Me = Mean sum of square for error (Intra block)
r = Number of replications
q = Number of population in each sub-block
u = Weightage factor computed

3.5.2 Estimation of Least Significant Differences (LSD):

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

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

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

3.5.3 Study of variability parameters:

Estimation of the variability among the populations for traits related to yield per plant in *Vigna radiata* were narrated below:

3.5.4 Estimation of Genotypic variance and phenotypic variance:

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

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

Where,

MSG = Mean sum of square for genotypes
MSE = Mean sum of square for error, and
r = Number of replication
b. Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where,

σ_p^2= Phenotypic variance

σ_g^2= Genotypic variance

σ_e^2 = Environmental variance = Mean square of error

3.5.5 Estimation of genotypic and phenotypic coefficient of variation:

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

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

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

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

σ_g= Genotypic standard deviation

σ_p= Phenotypic standard deviation

$\bar{x}$ = Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficients of variation (PCV) and genotypic coeffcients of variation (GCV) as

Low (0-10%),

Moderate (10-20%) and

High (>20%)

3.5.6 Estimation of heritability in broad sense:

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

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

Where, $\mathrm{h}_{\mathrm{b}}^{2}$=Heritability in broad sense

σ_{g}^{2}= Genotypic variance

σ_{p}^{2}= Phenotypic variance

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

Categories: Low: 0-30%

Moderate: 30-60%

High: >60%

3.5.7 Estimation of genetic advance:

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

$$\mathrm{GA} = \frac{\sigma_{\mathrm{g}}^{2}}{\sigma_{\mathrm{p}}^{2}} \, . \, \mathrm{K} \, . \, \sigma_{\mathrm{p}}$$

Where,

GA = Genetic advance

σ_{g}^{2} = Genotypic variance

σ_{p}^{2} = Phenotypic variance

σ_p = Phenotypic standard deviation

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

Categories: Low (<10%)

Moderate (10-20%)

High (>20%)

3.5.8 Estimation of genetic advance in percentage of mean:

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

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

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

Categories:

Less than 10% - Low

10-20% -Moderate

More than 20% -High

3.5.9 Correlation coefficient analysis:

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

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

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

Where,

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

Cov_{gxy}, Cov_{pxy} are the genotypic and phenotypic covariance of x and y, respectively. σ^2_{gx}= Genotypic variance of the trait x and σ^2_{gy} = Genotypic variance of the trait y.

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

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

3.5.10 Path coefficient analysis:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

r_{iy}=Correlation of the character with yield

Categories:

Negligible (0.00 to 0.09);

Low (0.10 to 0.19);

Moderate (0.20 to 0.29);

High (0.30 to 1.0);

Very High (>1.00)

CHAPTER IV

RESULT AND DISCUSSION

The results of the present exploration of genetic variability, character association and path analysis studies in 33 genotypes of *B. napus* carried out during Rabi season from November 2019 through February 2020 are presented in the following sections.

4.1 Analysis of variance

The success of crop improvement program depends on the amount of genetic variability presented in the population. The extent of genetic variability can determine the speed genetic improvement through selection or hybridization followed by selection. The analysis of variance of 33 genotypes of *Brassica napus* for yield and yield contributing traits are shown in Table 3. The analysis of variance indicated highly significant amount of variability among the genotypes for all the characters studied viz., days to 50% flowering, days to maturity, plant height (cm), primary branches/plant, secondary branches/plant, siliqua/plant, siliqua length (cm), seeds per siliqua, thousand seed weight (g) and seed yield per plant (g). The outcome clearly indicated the presence of high variability for yield and yield contribution traits among the genotypes studied. Therefore, there is a lot of opportunities for selection for majority of the traits in the genotypes. The mean sum of squares of all the ten characters is presented in Table 3. Significant differences among the genotypes was observed by many researchers like Shalini *et al.* (2000), Thakral *et al.* (2004), Uddin *et al.* (2005), Khan *et al.* (2006) etc.

The presence of narrow gap and large gap between PCV and GCV for the characters suggested that these traits studied had low and large environmental influence, respectively for the traits. These are shown for ten characters in table 5 and figure 5.

Table 3. Analysis of variance of 33 genotypes of *B. napus*

Source of variance	DF	Mean sum of square									
		DFF	DM	PH	PB	SB	SP	SL	SS	TSW	SYP
Replication	2	1.18	6.98	2.65	5.12	0.14	278.53	4.91	31.08	2.26	1.48
Genotype	32	42.67**	51.68**	331.16**	3.73**	6.21**	2743.66**	4.04**	20.90**	2.59**	8.02**
Error	64	4.19	6.15	38.89	0.31	0.26	47.11	0.47	5.55	0.16	0.21
CV (%)		5.81	2.84	5.79	13.94	15.55	5.88	9.10	12.10	9.14	8.57

**, indicates 1% level of significant

DFF= Days to 50% flowering. DM= Days to Maturity, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SP = Siliqua per plant, SL = Siliqua length (cm), SS = Seeds per siliqua, TSW = thousand seed weight (g) and SYP = seed yield per plant (g).

4.1.1 Days to 50% flowering

Analysis of variance (Table 3) revealed significant differences among the 33 genotypes for days to 50% flowering (42.67**). The highest days to 50% flowering was recorded in G15 (43.00 days) followed by G23 (42.33), G8 (42.00) and G7 (41.00); whereas the minimum days to 50% flowering was recorded in G33 (30.33 days) followed by G32 (30.67) and G21 (31.33); and the mean value is 35.24 (Table 4) (Figure 1).

Phenotypic variance (17.02) was higher than genotypic variance (12.83) that indicated environmental effect over the trait. Least difference between PCV (11.71%) and GCV (10.16%) values indicated that less variability was found on this character (Table 5). According to Engida (2007) traits that showed the different genotypic, phenotypic and environmental values indicates the presence of variation among the traits used.

4.1.2 Days to maturity

Highly significant variation among 33 genotypes for days to maturity (51.68**) (Table 3) was found. The G1 showed the highest (93.00) days to maturity among 33 genotypes followed by G2 (91.00 days), G20 (91.00 days), G5 (90.67 days) and G15 (90.67 days); whereas the G10 showed the minimum (76.67) days to maturity followed by G11 (77.67 days), G4 (78.00 days) and G23 (78.67 days); and the mean value was 87.26 (Table 4) (Figure 1).

The value of phenotypic (21.33) and genotypic (15.18) variance for days to maturity with a difference between them suggested the role of environment on the character. The difference between phenotypic (5.29%) and genotypic (4.46%) coefficient of variances was low for days to maturity which indicated the existence of less variation among the genotype (Table 5). The less GCV values of this character suggested that there was less possibility of improvement of this trait through selection.

Table 4. Mean performance of 33 genotypes of *B. napus*

Genotypes	DFFF	DM	PH	PB	SB	SP	SL	SS	TSW	SYP
G1	32.67 i-m	93.00 a	103.33 hj	4.68 c-h	3.55 fg	128.11 f-h	6.47 k-p	23.43 ac	3.35 f	3.23 n
G2	32.00 k-m	91.0 ab	91.33 kl	5.00 a-e	3.77 ef	83.57 m	6.79 i-n	24.26 a	3.42 ef	3.40 mn
G3	32.67 i-m	90.33 a-c	90.33 l	3.97 g-j	1.53 mn	103.83 ij	8.35 b-f	22.19 ae	5.31 ab	5.56 d-g
G4	31.667 lm	78.00 g	109.67 e-i	2.03 mn	2.80 g-j	106.73 i	7.21 g-l	17.99 f-l	3.21 f	3.60 l-n
G5	31.67 lm	90.67 a-c	126.10 ab	1.33 n	7.53 a	143.00 c-e	8.68 a-e	16.93 i-m	5.17 ab	7.24 b
G6	40.33 a-d	89.67 a-d	101.13 i-k	4.17 e-i	1.23 n	88.47 k-m	6.55 j-o	20.83 a-h	3.28 f	3.27 n
G7	41.00 a-c	89.33 a-e	127.93 a	4.80 b-g	2.13 j-m	106.87 i	8.55 a-e	19.07 d-k	5.38 ab	5.70 d-g
G8	42.000 ab	87.67 b-f	115.67 c-f	2.67 lm	4.47 c-e	144.93 cd	8.96 a-d	16.53 jm	5.31 ab	5.97 d-f
G9	39.00 b-f	85.67 d-f	108.67 e-i	3.03 k-l	1.8 l-n	136.00 d-f	7.07 h-n	18.48 e-l	3.27 f	3.53 l-n
G10	35.00 g-l	76.67 g	102.67 h-j	4.00 g-j	2.63 hl	96.67 il	8.14 c-h	18.83 dk	3.26 f	5.42 e-h
G11	35.67 f-j	77.67 g	105.67 f-i	5.20 a-d	2.70 h-k	105.40 ij	8.36 b-f	21.75 a-f	4.34 d	4.18 j-l
G12	32.33 j-m	83.67 f	90.75 l	2.07 m-n	5.13 bc	66.67 n	9.19 a-c	14.08 m	5.80 a	9.19 a
G13	35.67 f-j	86.67 c-f	121.78 a-d	3.20 j-l	2.17 j-m	136.20 d-f	7.01 i-n	17.46 g-m	5.03 bc	7.01 b
G14	40.00 a-e	85.67 d-f	111.33 e-h	5.63 a-b	2.27 i-m	94.47 j-m	5.46 op	20.13 b-j	2.80 f	3.64 l-n
G15	43.00 a	90.67 a-c	102.82 h-j	5.73 a	5.00 bc	152.53 c	8.19 c-g	14.67 lm	5.19 ab	7.45 b
G16	36.6 e-h	88.33 b-e	102.13 h-j	2.73 l-m	1.97 k-n	86.11 lm	7.90 d-i	17.11 h-m	4.28 d	5.26 f-i
G17	38.33 c-g	85.33 ef	104.33 g-j	3.77 h-k	2.20 j-m	106.67 i	9.16 a-c	20.33 b-j	5.12 b	6.11 de
G18	37.67 c-g	89.3 a-e	104.24 g-j	4.98 a-f	3.17 f-h	118.89 h	7.66 e-j	19.60 c-k	3.22 f	5.10 g-i
G19	33.67 h-m	89.67 a-d	123.78 a-d	4.16 e-i	2.23 j-m	67.67 n	5.36 p	22.11 a-e	3.27 f	3.57 l-n
G20	32.67 i-m	91.00 ab	107.56 e-i	3.54 i-l	5.08 bc	182.93 a	9.59 a	19.47 d-k	5.80 a	9.59 a
G21	31.33 m	87.33 b-f	109.89 e-i	4.47 d-h	1.77 mn	140.80 de	7.58 e-k	15.87 k-m	3.29 f	5.05 g-i

Table: 4 (Cont'd)

G22	36.33 f-h	89.00 a-e	103.67 h-j	4.20 e-i	3.08 f-i	168.56 b	7.25 f-l	13.87 m	5.29 ab	7.25 b
G23	42.33 ab	78.67 g	114.27 d-g	4.30 d-i	1.63 mn	98.40 i-k	9.01 a-d	18.92 d-k	5.28 ab	6.01 d-f
G24	36.00 f-i	88.33 b-e	94.67 j-l	4.10 e-j	3.77 ef	134.3 d-g	5.97 n-p	20.17 b-j	3.35 f	3.98 k-n
G25	35.33 g-k	87.33 b-f	84.56l	5.60 ab	1.90 k-n	124.07 gh	7.16 g-m	20.39 b-i	4.43 cd	4.77 h-j
G26	32.67 i-m	90.00 a-c	106.22 f-i	2.67 lm	3.22 f-h	136.44 d-f	8.46 b-e	19.66 c-k	5.35 ab	5.64 d-g
G27	37.00d-h	88.67 b-e	114.67 d-f	2.94 k-m	2.63 h-l	105.22 ij	7.15 g-m	23.53 ab	4.207 d	4.763 h-j
G28	31.67 lm	90.33 a-c	108.92 e-i	5.57 a-c	3.90 d-f	86.78 lm	6.20 l-p	21.24 a-g	4.24 d	4.13 j-m
G29	31.67 lm	89.67 a-d	106.33 f-i	4.39 d-i	2.66 h-k	101.11 ij	6.05 m-p	19.33 d-k	4.01 de	4.03 j-m
G30	32.0 kl-m	89.33 a-e	117.10 b-e	3.77 h-k	4.42 c-e	96.78 i-l	9.34 ab	19.71 b-j	4.31 d	6.22 cd
G31	32.00 k-m	89.00 a-e	109.47 e-i	4.08 f-j	4.63 cd	86.89 lm	6.83 i-n	22.56 a-d	4.28 d	4.55 i-k
G32	30.67 m	83.67 f	124.98 a-c	4.37 d-i	5.53 b	133.33 e-g	6.90 i-n	21.82 a-f	5.58 ab	6.90 bc
G33	30.33 m	88.33 b-e	110.17 e-i	5.00 a-e	4.82 bc	186.00 a	6.81 i-n	19.98 b-j	4.153 d	4.54 i-k
Min	30.33	76.67	84.56	1.33	1.23	66.67	5.36	13.87	2.8	3.23
Max	43.00	93.00	127.93	5.73	7.53	186	9.59	24.26	5.8	9.59
Mean	35.24	87.26	107.76	4.00	3.25	116.80	7.55	19.46	4.35	5.31
SE	1.67	2.02	5.09	0.46	0.41	5.60	0.56	1.92	0.32	0.37
LSD (%)	3.34	4.04	10.17	0.91	0.83	11.20	1.12	3.84	0.65	0.74

DFF= Days to 50% flowering. DM= Days to Maturity, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SP = Siliqua per plant, SL = Siliqua length (cm), SS = Seeds per siliqua, TSW = thousand seed weight (g) and SYP = seed yield per plant (g).

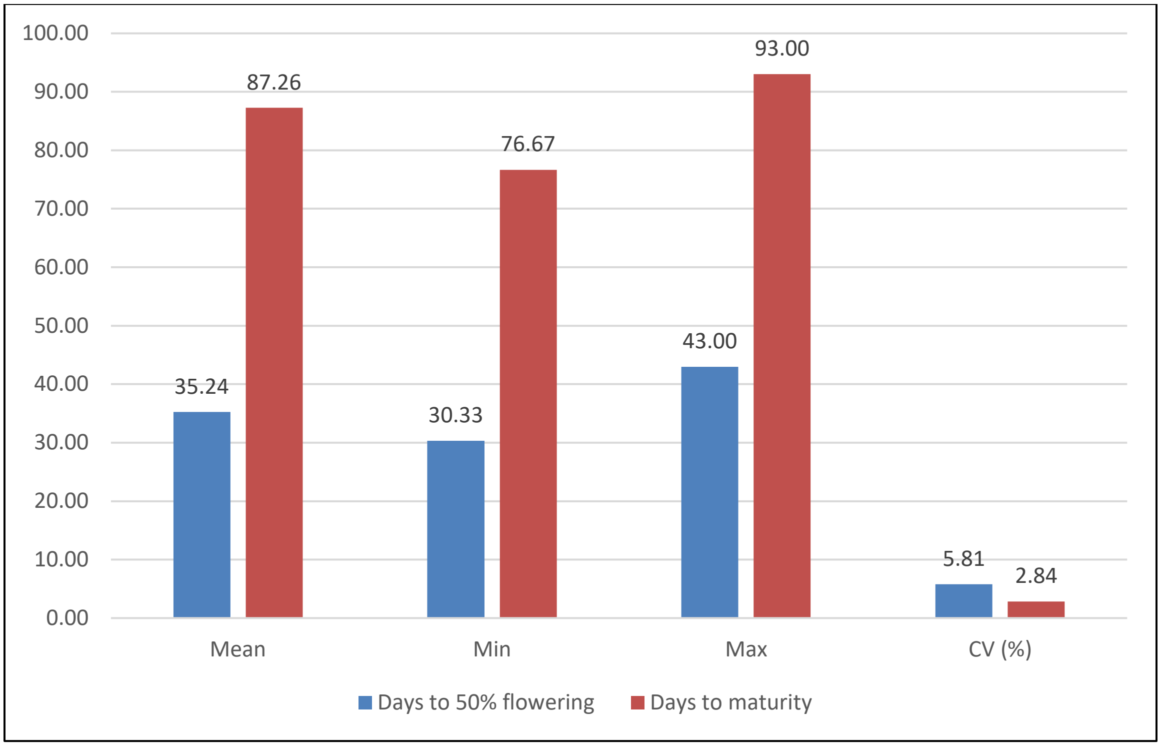


Figure 1. Mean, minimum, maximum and CV (%) of Days to 50% flowering and Days to maturity in 33 advanced populations of *Brassica napus* L.

4.1.3 Plant Height

The mean square due to genotype was found highly significant (331.16**) at for plant height (cm) indicating the presence of genotypic differences present among 33 genotypes (Table 3). The highest plant height (cm) was recorded in G7 (127.93 cm) followed by G5 (126.10 cm), G32 (124.98 cm) and G19 (123.78 cm); whereas the lowest was found in G25 (84.56 cm) followed by G3 (90.33 cm), G12 (90.75 cm) and G2 (91.33); and the mean value was 107.76 (Table 4) (Figure 2).

The phenotypic variance (136.31) highly greater than the genotypic variance (97.42) for plant height (cm) suggested that high influence of environment on the expression of the genes controlling this trait. The difference between phenotypic (10.83%) and genotypic (9.16%) coefficient of variances was low for maturity level which indicates the existence of less variation among the genotype (Table 5). The less GCV values of this character suggested that there was less possibility of improvement of this trait through selection. Same result was also found by Seyoum *et at.* (2012). The values of PCV and GCV were 8.74% and 7.30%, respectively which indicated that the genotype had less variation for this trait (Table 3).

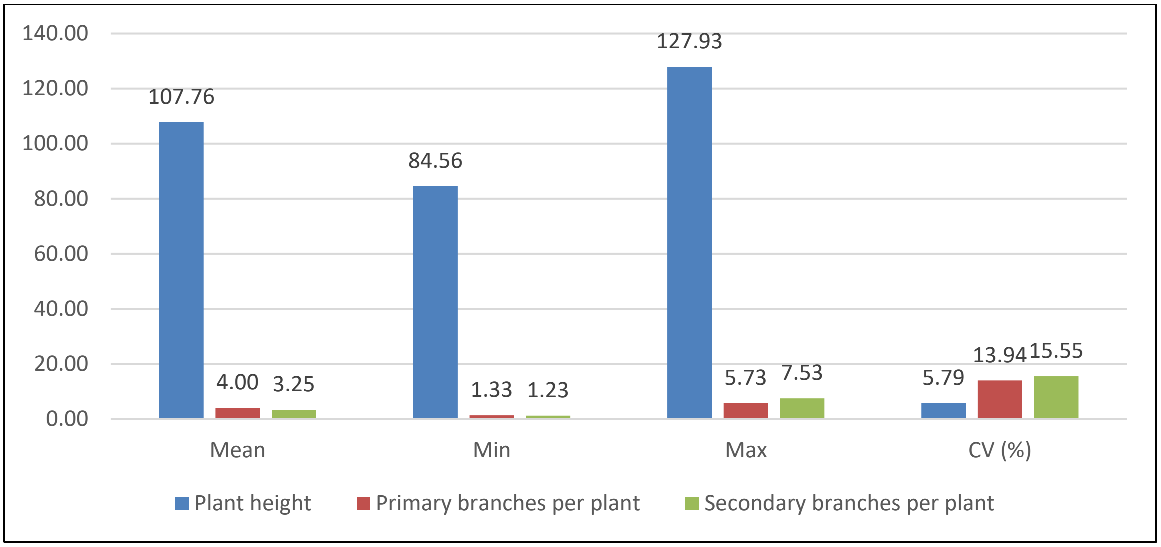


Figure 2. Mean, minimum, maximum and CV (%) of Plant height, Primary branches per plant and Secondary braches per plant in 33 advanced populations of *Brassica napus* L.

4.1.4 Primary Branches/plant

Highly significant variations were observed among the 33 genotypes (3.73**) in primary branches/pant (Table 3). The highest primary branches/pant was taken in G15 (5.73a) followed by G14 (5.63), G25 (5.60) and G28 (5.57); on the other hand, the minimum no. of primary branches/pant was recorded in G5 (1.33) followed G4 (2.03), G12 (2.07), G8 (2.67), and G26 (2.67) among 33 genotypes (Table 4) and the mean value is 4.00 (Figure 2).

The phenotypic and genotypic variance for primary branches/pant was observed (1.45) and (1.14), respectively with slightly differences between them, suggested that the environment had small role in the expression of trait. The phenotypic coefficient of variation (30.07%) was higher than genotypic coefficient of variation (26.65%) (Table 5) suggested that environment had influence on the expression of the genes controlling this trait.

4.1.5 Secondary Branches/plant

Analysis of variance (Table 3) revealed highly significant differences among the genotypes for secondary branches/pant. (6.21**). The highest value for secondary branches/pant was observed in G5 (7.53) followed by G32 (5.53), G12 (5.13) and G20 (5.08); whereas the minimum value for secondary branches/pant was recorded in G6 (1.23) followed by G3 (1.53), G23 (1.63) and G21 (1.77); and the mean value was 3.25 (Table 4) (Figure 2).

Phenotypic variance (2.24) was slightly different from the genotypic variance (1.99) that indicated small environmental effect over the trait. Difference between PCV (46.03%) and GCV (43.32%) values indicated the influence of environment on this character (Table 5). Singh *et al.* (2011) and Kumar *et al.* (2013) reported high values for PCV and GCV for the number of secondary branches per plant and for seed yield per plant.

4.1.6 Siliqua/plant

From the ANOVA (Table 3), it was found that siliqua/plant showed highly significant variations among the genotypes (2743.66*). Siliqua/plant was maximum in G33 (186.00) followed by G20 (182.93), G22 (168.56) and G15 (152.53); on the other hand, the minimum value was observed in G12 (66.67) and G19 (67.67) followed by G16 (86.11) and G2 (83.57); and the mean value was 116.80 (Table 4) among 33 genotypes (Figure3).

The phenotypic and genotypic variances for siliqua/plant were 945.96 and 898.85, respectively. The phenotypic variance was higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 26.33% and 25.67% respectively for siliqua/plant which indicating that variation exists among different genotypes (Table 5).

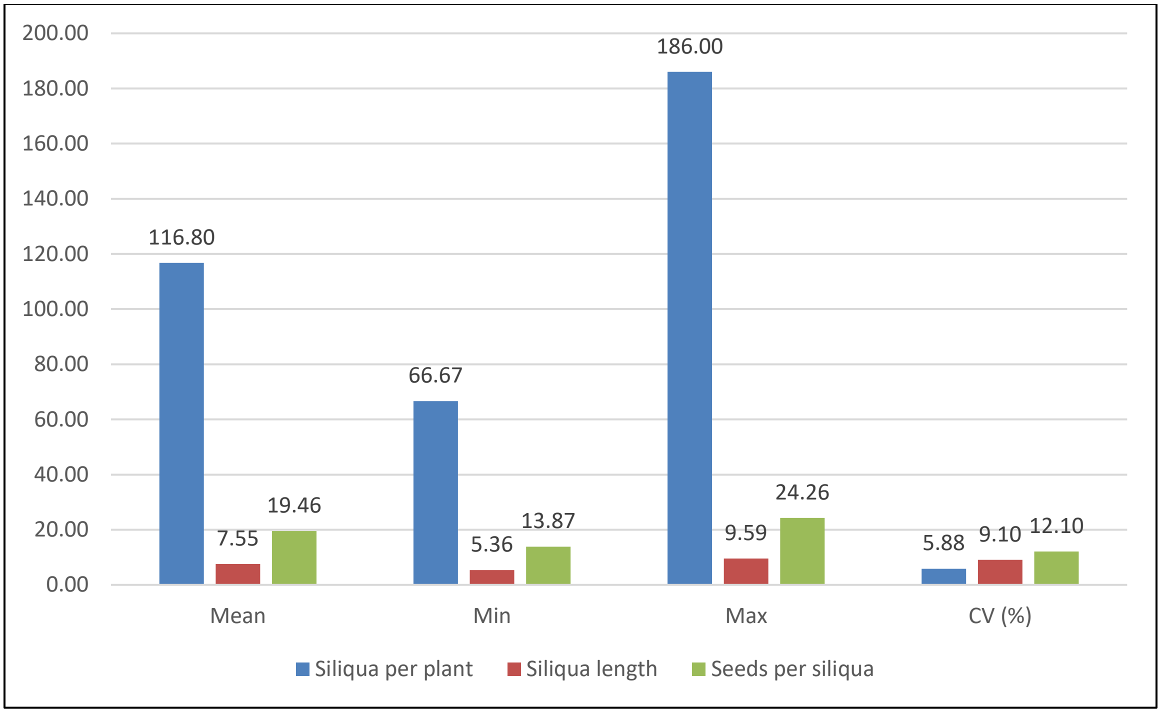


Figure 3. Mean, minimum, maximum and CV (%) of Siliqua per plant and Siliqua length and Seeds per siliqua in 33 advanced populations of *Brassica napus* L.

4.1.7 Siliqua Length

Highly significant variation (4.04**) among 33 genotypes for siliqua length (Table 3) was found. The G20 showed the highest (9.59) siliqua length among 32 genotypes followed by G30 (9.34), G12 (9.19) and G17 (9.16); whereas the G19 showed the minimum (5.36) followed by G14 (5.46), G24 (5.97) and G29 (6.05m) siliqua length; and the mean value was 7.55 (Table 4) (Figure 3).

The value of phenotypic (1.66) was slightly higher than the value of genotypic (1.19) variance for siliqua length suggested small role of environment on the character. The difference between phenotypic (17.07%) and genotypic (14.44%) coefficient of variances were high for siliqua length which indicated the existence of adequate variation among the genotype (Table 5).

4.1.8 Seeds per siliqua

From the ANOVA (Table 3), it was found that seeds per siliqua showed highly significant variations among the genotypes (20.90*). Seeds per siliqua was maximum in G2 (24.26) followed by G27 (23.53), G1 (23.43) and G31 (22.56); whereas, minimum was observed in G22 (13.87) followed bt G12 (14.08), G15 (14.67) and G21 (15.87); and the mean value was 19.46 (Table 4) among 33 genotypes (Figure 3).

The phenotypic and genotypic variances for seeds per siliqua were 10.66 and 5.12, respectively. The phenotypic variance was higher than the genotypic variance suggested influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 16.78% and 11.62%, respectively for seed per siliqua which indicating that high variation exists among different genotypes (Table 5).

4.1.9 Thousand seeds weight (g)

The mean square due to genotype was found highly significant (2.59**) at for thousand seeds weight (g) indicating the presence of genotypic differences present among 33 genotypes (Table 3). The highest value for thousand seeds weight (g) was recorded in G12 (5.80 g) followed by G32 (5.58 g), G7 (5.38 g) and G26 (5.35 g); whereas the lowest value was found in G14 (2.80 g) followed by G18 (3.22 g) and G10 (3.26 g); and the mean value is 4.35 (Table 4) (Figure 4).

The phenotypic (0.97) and genotypic (0.81) variance for thousand seeds weight (g) suggests that small influence of environment on the expression of the genes controlling this trait. The values of PCV and GCV were 22.62% and 20.69%, respectively which indicated that the genotype had less variation for this trait (Table 5).

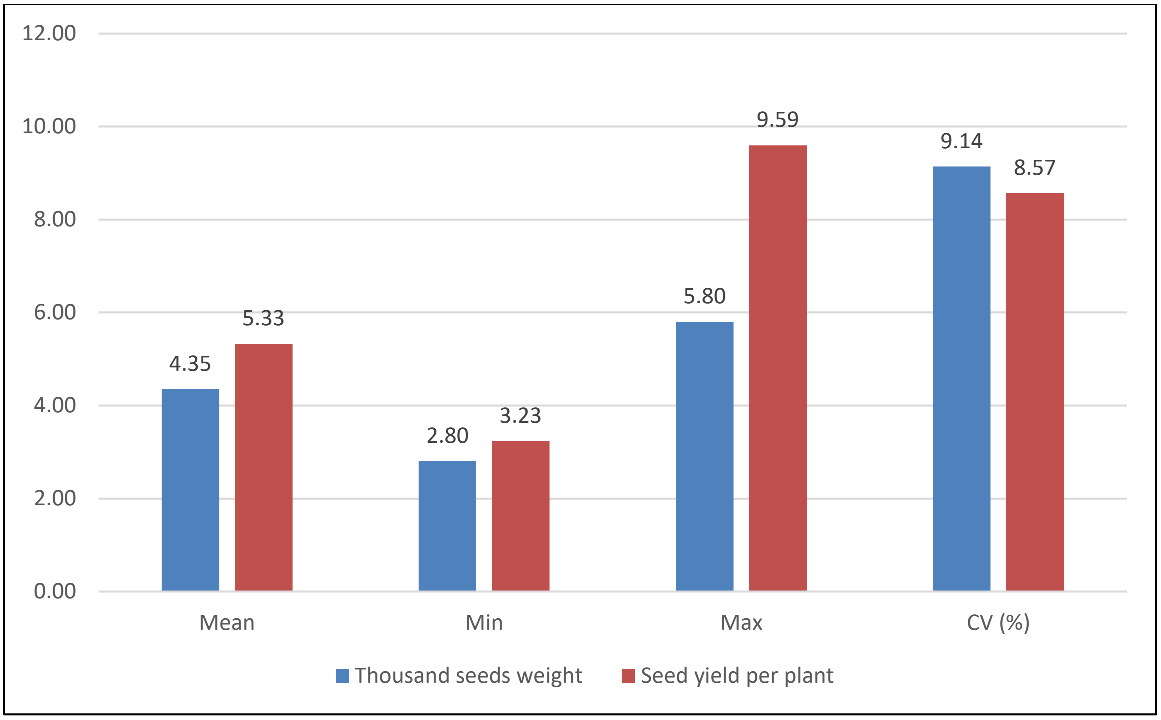


Figure 4. Mean, minimum, maximum and CV (%) of Thousand seeds weight and Seed yield per plant in 33 advanced populations of *Brassica napus* L.

4.1.10 Seed yield per plant (g)

The mean square due to genotype was found highly significant (8.02**) at for seed yield per plant (g) indicating the presence of genotypic differences present among 33 genotypes (Table 3). The highest value for seed yield per plant (g) was recorded in G20 (9.59 g) followed by G12 (9.19 g), G15 (7.45 g) and G22 (7.25 g); whereas the lowest value was found in G1 (3.23 g) followed by G6 (3.27 g), G2 (3.40 g) and G9 (3.53 g); and the mean value is 5.31 (Table 4) Figure 4).

The phenotypic (2.81) and genotypic (2.60) variance for seed yield per plant (g) suggests that small influence of environment on the expression of the genes controlling this trait. The values of PCV and GCV were 31.46% and 30.28%, respectively which indicates that the genotype had less variation for this trait (Table 5). Singh *et al.* (2011) and Kumar *et al.* (2009) reported high values for PCV and GCV for the number of secondary branches per plant and for seed yield per plant.

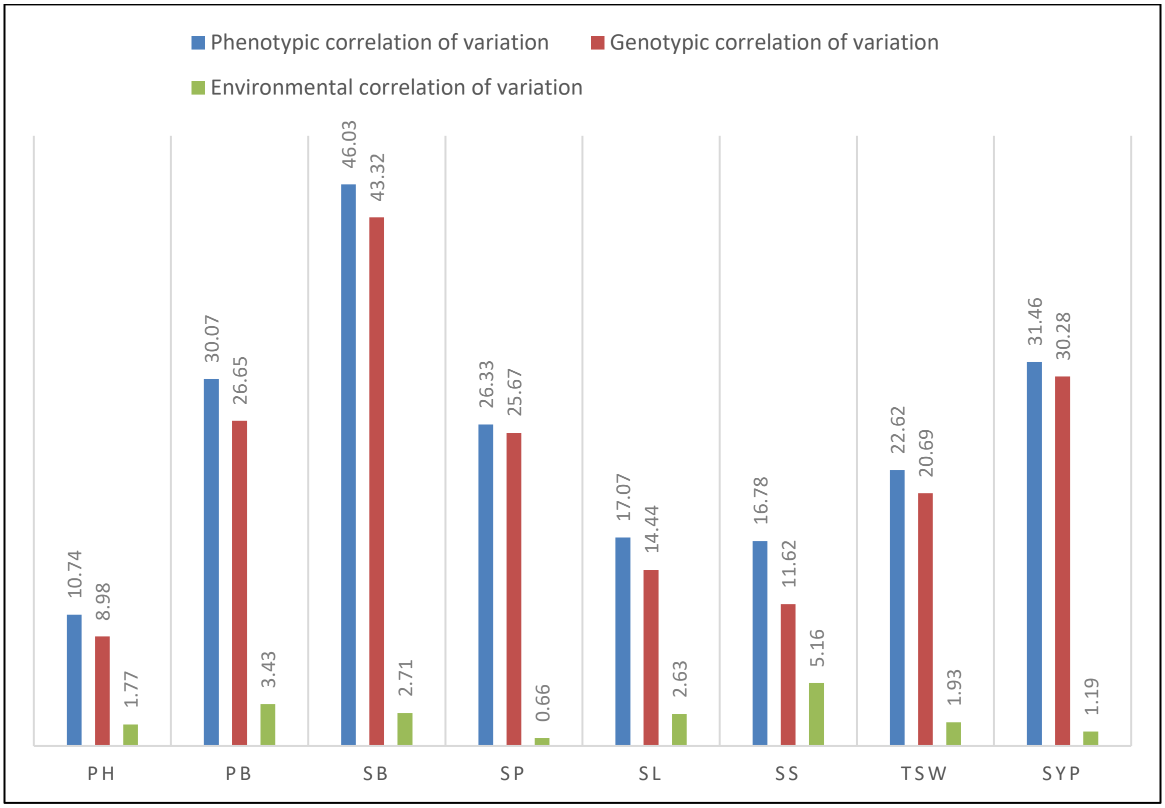


Figure 5. Phenotypic correlation of variation, Genotypic correlation of variation and Environmental correlation of variation of 10 characters in 33 advanced populations of *Brassica napus* L.

Table 5. Genotypic parameter of 10 characters of *B. napus*

Parameters	**σ^2p**	**σ^2g**	**σ^2 e**	**PCV**	**GCV**	**ECV**	**Heritability**	**Genetic Advance (5%)**	**Genetic Advance (% of mean)**
DFFF	17.02	12.83	4.19	11.71	10.16	1.54	75.37 **h**	6.40 **L**	18.17 **m**
DM	21.33	15.18	6.15	5.29	4.46	0.83	71.18 **h**	6.77 **L**	7.76 **L**
PH	136.31	97.42	38.89	10.83	9.16	1.67	71.47 **h**	17.19 **m**	15.95 **m**
PB	1.45	1.14	0.31	30.07	26.65	3.43	78.51 **h**	1.95 **L**	48.63 **h**
SB	2.24	1.99	0.26	46.03	43.32	2.71	88.59 **h**	2.73 **L**	83.99 **h**
SP	945.96	898.85	47.11	26.33	25.67	0.66	95.02 **h**	60.20 **h**	51.54 **h**
SL	1.66	1.19	0.47	17.07	14.44	2.63	71.56 **h**	1.90 **L**	25.17 **h**
SS	10.66	5.12	5.55	16.78	11.62	5.16	47.97 **m**	3.23 **L**	16.58 **m**
TSW	0.97	0.81	0.16	22.62	20.69	1.93	83.67 **h**	1.70 **L**	38.98 **h**
SYP	2.81	2.60	0.21	31.46	30.28	1.19	92.58 **h**	3.20 **L**	60.01 **h**

DFF= Days to 50% flowering. DM= Days to Maturity, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SP = Siliqua per plant, SL = Siliqua length (cm), SS = Seeds per siliqua, TSW = thousand seed weight (g) and SYP = seed yield per plant (g).

4.2 Heritability, Genetic Advance and Genetic Advance (%mean)

The heritability estimates separate the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. It aims in determining the relative amount of heritable portion of variation. As such the heritability in broad sense is the proportion of genotypic variability to the total variability, its importance had been emphadized by Lush (1949) in animals and by Johnson *et al.* (1995b) in plants. Heritability, genetic advance and genetic advance in % mean of ten characters of this study is shown in Table 5 and Figure 6.

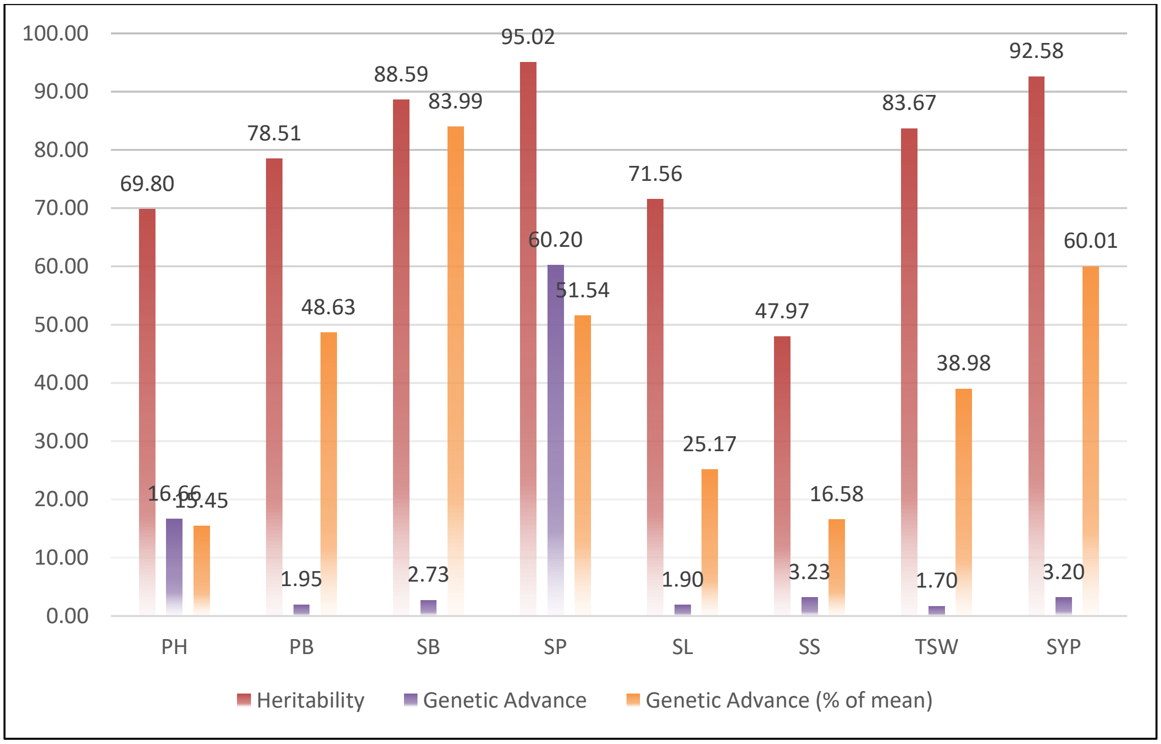


Figure 6. Heritability, Genetic advance and Genetic advance in (%mean) of 10 characters in 33 advanced populations of *Brassica napus* L.

4.2.1. Days to 50% Flowering

Days to 50% flowering showed high heritability (75.37%) coupled with low genetic advance (10.41) and moderate genetic advance in percentage of mean (18.17 %) (Table 5). The result revealed that character was controlled by additive genes the selection based on this character would be effective.

4.2.2 Days to Maturity

High heritability (71.18%) accompanied with low genetic advance (6.77) and low genetic advance in percentage of mean (7.76 %) was calculated in respect of days to maturity (Table 5). These findings discovered the action of additive genetic effects on the expression of this trait. The high heritability was being exhibited due to high environmental effects. Selection may be effective in such character. According to Johnson *et al.* (1955) high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The estimates of heritability accompanied by estimates of genetic advance as percent of means are more meaningful from the point of expected genetic gain. Genetic advance is the measure of improvement that can be achieved by practicing selection in a population.

4.2.3 Plant Height

High heritability (71.47%) accompanied with moderate genetic advance (17.19) and moderate genetic advance in percentage of mean (15.95%) was calculated in respect of days to maturity (Table 5). These findings discovered the action of additive gene effects on the expression of this trait. The high heritability was being exhibited due to high environmental effects. Selection may be effective in such character. Mahamood *et al.* (2003) also reported high heritability and corresponding genetic advance values for plant height.

4.2.4 Primary Branches/Plant

Primary branches/plant showed high heritability (78.51%) coupled with low genetic advance (1.95) and high genetic advance in percentage of mean (48.63%) (Table 5). Genetic advances in percent of mean were higher which was in accordance with the findings of Singh *et al.* (1977).

4.2.5 Secondary Branches/Plant

Secondary branches/plant showed high heritability (88.59%) coupled with low genetic advance (2.73) and high genetic advance in percentage of mean (83.99%) (Table 5). Aytac and Kinaci (2009) recorded highest heritability and genetic advance over mean was supported this results.

4.2.6 Siliqua/Plant

Siliqua/plant showed high heritability (95.02%) coupled with high genetic advance (60.20) and high genetic advance in percentage of mean (51.54%) (Table 5). High heritability for siliqua/plant suggested considerable influence of environment on the expression of genes controlling this trait. Mahamood *et al.* (2003) reported high heritability and corresponding genetic advance values for number of siliqua per plant was founded.

4.2.7 Siliqua Length

Siliqua length showed high heritability (71.56%) coupled with low genetic advance (1.90) and high genetic advance in percentage of mean (25.17%) (Table 5). High heritability for siliqua length suggested considerable influence of environment on the expression of genes controlling this trait. Lodhi *et al.* (2014) reported high heritability in conjunction with high genetic advance were observed for siliqua length suggesting predominant role of additive gene action for expression of these traits.

4.2.8 Seeds per Siliqua

Moderate heritability (47.97) coupled with low genetic advance (3.23) and moderate genetic advance in percentage of mean (16.58 %) was found for seeds per siliqua among 33 genotypes (Table 5).

4.2.9 Thousand Seeds Weight

High heritability (83.67) coupled with low genetic advance (1.70) and high genetic advance in percentage of mean (38.98%) was observed for thousand seeds weight among 33 genotypes (Table 5). High heritability suggested considerable influence of environment on the expression of genes controlling this trait. Lodhi *et al.* (2014) reported high heritability in conjunction with high genetic advance were observed for 1000 seed weight suggesting predominant role of additive gene action for expression of these traits.

4.2.10 Yield/Plant

Yield/plant showed high heritability (92.58) coupled with low genetic advance (3.20) and high genetic advance in percentage of mean for 33 genotypes of *B. napus* (60.01%) (Table 5). Momena (2015) revealed that seed yield per plant exhibits the highest value of heritability. Lodhi *et al.* (2014) reported high heritability in conjunction with high genetic advance were observed for seed yield/ plant suggesting predominant role of additive gene action for expression of these traits.

4.3 Correlation Coefficient Analysis

Relationship between seed yield and yield contributing characters was studied through analysis of correlation between them. The correlation coefficients between all the ten characters were presented in genotypic and phenotypic level in (Table 6).

4.3.1 Days to 50% Flowering

Days to 50% flowering showed highly significant and positive correlation with primary branches/plant (G=0.333, P=0.294). It also observed that highly significant but negative correlation with seed per siliqua (G=-0.277) and secondary branches/plant (G=-0.277). It was found non-significant and positive correlation with Plant height (cm) (G=0.053, P=0.060), siliqua/plant (G=0.177, P=0.142), siliqua length (cm) (P=0.006), thousand seeds weight (g) (G=0.053, P=0.052) and seed yield/plant (g) (G=0.110, P=0.112). It was also found non-significant but negative correlation with days to maturity (G=-0.152, P=0.083), secondary branches/plant (P=-0.181), siliqua length (G=-0.051) and seed per siliqua (P=-0.141) (Table 6).

4.3.2 Days to Maturity

Days to maturity showed highly significant and positive correlation with siliqua/plant (G=0.323, P=0.273). It was found non-significant and positive correlation with primary branches/plant (G=0.051, P=0.051), secondary branches/plant (G=0.019), seed per siliqua (G=0.010, P=0.009) and thousand seeds weight (g) (P=0.001). It was also found non-significant but negative correlation with plant height (cm) (G=-0.040, P=-0.017), secondary branches/plant (P=-0.015), siliqua length (cm) (G=-0.081, P=-0.113), thousand seeds weight (g) (G=-0.026) and seed yield/plant (g) (G=-0.106, P=-0.112) (Table 6). Kumar *et al.* (1984) found positive and significant correlation between plant height and days to maturity.

4.3.3 Plant Height

Plant height (cm) showed highly significant and positive correlation with siliqua/plant (G=0.471, P=0.433), siliqua length (cm) (G=0.242), thousand seeds weight (g) (G=0.444, P=0.327) and seed yield/plant (g) (G=0.401, P=0.311). It also expressed highly significant but negative correlation with primary branches/plant (G=-0.303) and seed per siliqua (G=-0.506, P=-0.337). It was found non-significant and positive correlation with secondary branches/plant (G=0.005, P=0.003) and siliqua length (cm) (P=0.131). It was also found non-significant but negative correlation with primary branches/plant (P=-0.192) (Table 6). Azadgoleh *et al.*, (2009) reported that Plant height had significantly correlated with number of siliqua per plant and seeds per siliqua at both genotypic and phenotypic levels.

Table 6. Genotypic and phenotypic correlation of 10 characters of *B. napus*

Characters		**DFFF**	**DM**	**PH**	**PB**	**SB**	**SP**	**SL**	**SS**	**TSW**
DM	r_g	-0.152								
	r_p	-0.083								
PH	r_g	0.053	-0.040							
	r_p	0.060	-0.017							
PB	r_g	0.333**	0.051	-0.303**						
	r_p	0.294**	0.051	-0.192						
SB	r_g	-0.254*	0.019	0.005	-0.271**					
	r_p	-0.181	-0.015	0.003	-0.175					
SP	r_g	0.177	0.323**	0.471**	-0.013	0.346**				
	r_p	0.142	0.273**	0.433**	0.009	0.325**				
SL	r_g	-0.051	-0.081	0.242*	-0.445**	0.240*	0.186			
	r_p	0.006	-0.113	0.131	-0.300**	0.207*	0.154			
SS	r_g	-0.277**	0.010	-0.506**	0.403**	-0.174	-0.384**	-0.502**		
	r_p	-0.141	0.009	-0.337**	0.246*	-0.126	-0.262**	-0.248*		
TSW	r_g	0.053	-0.026	0.444**	-0.295**	0.388**	0.304**	0.715**	-0.409**	
	r_p	0.052	0.001	0.327**	-0.222*	0.344**	0.272**	0.591**	-0.246*	
SYP	r_g	0.110	-0.106	0.401**	-0.359**	0.491**	0.365**	0.699**	-0.685**	0.850**
	r_p	0.112	-0.112	0.311**	-0.283**	0.453**	0.346**	0.711**	-0.439**	0.768**

DFF= Days to 50% flowering. DM= Days to Maturity, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SP = Siliqua per plant, SL = Siliqua length (cm), SS = Seeds per siliqua, TSW = thousand seed weight (g) and SYP= seed yield per plant (g).

4.3.4 Primary Branches/Plant

Primary branches/plant showed highly significant and positive correlation with seed per siliqua (G=0.403, P=0.246). It also expressed highly significant but negative correlation with secondary branches/plant (G=-0.271), siliqua length (cm) (G=-0.445, P=-0.300), thousand seeds weight (g) (G=-0.295, P=-0.222) and seed yield/plant (g) (G=-0.359, P=-0.283). It was found non-significant and positive correlation with siliqua/plant (P=0.009). It was also found non-significant but negative correlation with secondary branches/plant (P=-0.175) and siliqua/plant (G=-0.013) (Table 6). Basalma (2008) noticed significant positive correlation of branches per plant with siliqua per plant. Gangapu *et al.*, (2009) noticed that number of primary was highly and significantly correlated with seed yield per plant at both genotypic and phenotypic levels.

4.3.5 Secondary Branches/Plant

Secondary branches/plant showed highly significant and positive correlation with siliqua/plant (G=0.346, P=0.325), siliqua length (cm) (G=0.240, P=0.207), thousand seeds weight (g) (G=0.388, P=0.344) and seed yield/plant (g) (G=0.491, P=0.453). It was also found non-significant but negative correlation with seed per siliqua (G=-0.174, P=0.126) (Table 6). Chowdhary *et al.* (1987), Nagaraja (1990), Srivastava and Singh (2002) observed positive significant correlation of seed yield with number of secondary branches.

4.3.6 Siliqua/Plant

Siliqua/plant showed highly significant and positive correlation with thousand seeds weight (g) (G=0.304, P=0.272) and seed yield/plant (g) (G=0.365, P=0.346). It also expressed highly significant but negative correlation with seed per siliqua (G=-0.384, P=-0.262). It was also found non-significant and positive correlation with siliqua length (cm) (G=0.186, P=0.154) (Table 6). Uddin *et al.* (2013) recorded high significant positive correlation of yield per plant with secondary branches per plant and siliqua per plant at both genotypic and phenotypic levels.

4.3.7 Siliqua Length

Siliqua/plant showed highly significant and positive correlation with thousand seeds weight (g) (G=0.715, P=0.591) and seed yield/plant (g) (G=0.699, P=0.711). It also expressed highly significant but negative correlation with seed per siliqua (G=-0.502, P=-0.248) (Table 6).

4.3.8 Seed per Siliqua

Siliqua/plant showed highly significant but negative correlation with thousand seeds weight (g) (G=-0.409, P=-0.246) and seed yield/plant (g) (G=-0.685, P=-0.439) (Table 6). Gangapu *et al.,* (2009) found that number of seeds per siliqua had high and significant correlation with seed yield per plant at both genotypic and phenotypic levels.

4.3.9 Thousand Seeds Weight

Siliqua/plant showed highly significant and positive correlation with seed yield/plant (g) (G=0.850, P=0.768) (Table 6). Kumar and Kakroo (2009), recorded 1000 seed weight had positive correlation with seed yield.

4.4 Path Coefficient Analysis

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering ten characters viz. Days to 50% flowering. Days to maturity, plant height, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliqua and 1000 seeds weight to seed yield per plant. Seed yield being the complex outcome of different characters, was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters are shown in Table 7.

Table 7. Path coefficient analysis of 10 characters of *B. napus*

Traits	DFF	DM	PH	PB	SB	SP	SL	SS	TSW	SYP
DFFF	**-0.0761**	0.0200	-0.0095	0.0127	-0.0285	0.0121	0.0028	0.1387	0.0379	0.112
DM	0.0116	**-0.1316**	0.0072	0.0019	0.0021	0.0220	0.0044	-0.0050	-0.0187	-0.112
PH	-0.0041	0.0053	**-0.1782**	-0.0115	0.0006	0.0320	-0.0132	0.2539	0.3157	0.311**
PB	-0.0253	-0.0067	0.0539	**0.0380**	-0.0304	-0.0009	0.0242	-0.2019	-0.2095	-0.283**
SB	0.0193	-0.0025	-0.0010	-0.0103	**0.1121**	0.0235	-0.0131	0.0870	0.2756	0.453**
SP	-0.0135	-0.0425	-0.0839	-0.0005	0.0388	**0.0679**	-0.0101	0.1925	0.2165	0.346**
SL	0.0039	0.0107	-0.0431	-0.0169	0.0269	0.0126	**-0.0544**	0.2515	0.5083	0.711**
SS	0.0211	-0.0013	0.0902	0.0153	-0.0195	-0.0261	0.0273	**-0.5014**	-0.2906	-0.439**
TSW	-0.0041	0.0035	-0.0791	-0.0112	0.0434	0.0207	-0.0389	0.2048	**0.7113**	0.768**
Residual effect 0.08										

DFF= Days to 50% flowering. DM= Days to Maturity, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SP = Siliqua per plant, SL = Siliqua length (cm), SS = Seeds per siliqua, TSW = thousand seed weight (g) and SYP = seed yield per plant (g).

4.4.1 Days to 50% Flowering

Path co-efficient analysis revealed that days to 50% flowering had a negative direct effect (-0.0761) on yield/plant (g). Days to 50% flowering had positive indirect effect on days to maturity (0.0200), primary branches/plant (0.0127), siliqua/plant (0.0121), siliqua length (cm) (0.0028), seed per siliqua (0.1387) and thousand seeds weight (g) (0.0379) while negative indirect effect on plant height (cm) (-0.0095) and secondary branches/plant (-0.0285). It showed that non-significant and positive genotypic correlation (0.112) with yield/plant (g) (Table 7).

4.4.2 Days to Maturity

Path co-efficient analysis revealed that days to maturity had a negative direct effect (-0.1316) on yield/plant (g). Days to maturity had positive indirect effect on days to 50% flowering (0.0116), plant height (cm) (0.0072), primary branches/plant (0.0019), secondary branches/plant (0.0021), siliqua/plant (0.0220) and siliqua length (cm) (0.0044) while negative indirect effect on seed per siliqua (-0.0050) and thousand seeds weight (g) (-0.0187). It showed that non-significant but negative genotypic correlation (-0.112) with yield/plant (g) (Table 7).

4.4.3 Plant Height (Cm)

Path co-efficient analysis revealed that plant height had a negative direct effect (-0.1782) on yield/plant (g). Plant height had positive indirect effect on days to maturity (0.0053), secondary branches/plant (0.0006), siliqua/plant (0.0320), seed per siliqua (0.2539) and thousand seeds weight (g) (0.3157) while negative indirect effect on days to 50% flowering (-0.0041), primary branches/plant (-0.0115), and siliqua length (cm) (-0.0132). It showed that highly significant and positive genotypic correlation (0.311) with yield/plant (g) (Table 7).

4.4.4 Primary Branches/Plant

Path co-efficient analysis revealed that primary braches/plant had a positive direct effect (0.0380) on yield/plant (g). Primary braches/plant had positive indirect effect on plant height (0.0539), siliqua length (cm) (0.0242) while negative indirect effect on days to 50% flowering (-0.0253), days to maturity (-0.0067), secondary branches/plant (-0.0304), siliqua/plant (-0.0009), seed per siliqua (-0.2019) and thousand seeds weight (g) (-0.2095). It showed that highly significant but negative genotypic correlation (-0.283) with yield/plant (g) (Table 7). Uddin *et al.* (2013) and Alam (2010) also found primary branches per plant showed direct positive association with seed yield per plant.

4.4.5 Secondary Branches/Plant

Path co-efficient analysis revealed that secondary braches/plant had a positive direct effect (0.1121) on yield/plant (g). Secondary braches/plant had positive indirect effect on days to 50% flowering (0.0193), siliqua/plant (0.0235), seed per siliqua (0.0870) and thousand seeds weight (g) (0.2756) while negative indirect effect on days to maturity (-0.0025), plant height (-0.0010), primary branches/plant (-0.0103) and siliqua length (cm) (-0.0131). It showed that highly significant and positive genotypic correlation (0.453) with yield/plant (g) (Table 7). Gangapu *et al.*, (2009) found that number of secondary branches per plant had positive direct effects towards seed yield which match with this finding.

4.4.6 Siliqua/Plant

Path co-efficient analysis revealed that siliqua/plant had a positive direct effect (0.0679) on yield/plant (g). Siliqua/plant positive indirect effect on secondary braches/plant (0.0388), seed per siliqua (0.1925) and thousand seeds weight (g) (0.2165) while negative indirect effect on days to 50% flowering (-0.0135), days to maturity (-0.0425), plant height (-0.0839), primary branches/plant (-0.0005) and siliqua length (cm) (-0.0101). It showed that highly significant and positive genotypic correlation (0.346) with yield/plant

(g) (Table 7). Alam (2010) observed primary siliqua per plant had direct positive association with seed yield per plant that supported this finding.

4.4.7 Siliqua Length (Cm)

Path co-efficient analysis revealed that siliqua length had a negative direct effect (-0.0544) on yield/plant (g). Siliqua length positive indirect effect on days to 50% flowering (0.0039), days to maturity (0.0107), secondary braches/plant (0.0269), siliqua/plant (0.0126), seed per siliqua (0.2515) and thousand seeds weight (g) (0.5083) while negative indirect effect on plant height (-0.0431) and primary branches/plant (-0.0169). It showed that highly significant and positive genotypic correlation (0.711) with yield/plant (g) (Table 7). Uddin *et al.* (2013) found siliquae length had direct positive association with seed yield per plant.

4.4.8 Seed per Siliqua

Path co-efficient analysis revealed that seed per siliqua had a negative direct effect (-0.5014) on yield/plant (g). Seed per siliqua positive indirect effect on days to 50% flowering (0.0211), plant height (0.0902), primary branches/plant (0.0153) and siliqua length (0.0273) while negative indirect effect on days to maturity (-0.0013), secondary braches/plant (-0.0195), siliqua/plant (-0.0261) and thousand seeds weight (g) (-0.2906). It showed that highly significant but negative genotypic correlation (-0.439) with yield/plant (g) (Table 7).

4.4.9 Thousand Seeds Weight (G)

Path co-efficient analysis revealed that thousand seed weight had a positive direct effect (0.7113) on yield/plant (g). thousand seed weight positive indirect effect on days to maturity (0.0035), secondary braches/plant (0.0434), siliqua/plant (0.0207) and seed per siliqua (0.2048)while negative indirect effect on days to 50% flowering (-0.0041), plant height (-0.0791), primary branches/plant (-0.0112) and siliqua length (-0.0389). It showed that highly significant and positive genotypic correlation (0.768) with yield/plant (g) (Table 7). Hosen (2008) and Siddikee (2006) noticed that thousand seed weight had the highest positive direct effect.

4.4.10 Residual Effects

The residual effect (R) of path co-efficient analysis was 0.08 which revealed that the traits under study contributed 92% of the seed yield per plant (g). It is said that there were some other factors those contributed 8% to the seed yield per plant (g) those are not included in the present study could have significant effect on seed yield per plant (g) (Table 7).

4.5 Selection:

The purposes of the study were to identify short duration and high yielding population of *Brassica napus* L. which can be released as a promising variety in the Aman-Mustard-Boro cropping system. Mean performance was observed for most of the characters of five advanced populations such as G20 (), G12 (), G15 (), G22 () and G5 () were selected from the 33 populations based on the variability. Selection of most promising populations from different cross combinations of *Brassica napus* L. based on mean performance is presented:

G20 [Nap (9901 × 2066)]:

Seed yield per plant of G20 was recorded as 9.59 g which was highest among the other advanced populations. On the other hand, thousand seeds weight of G20 was recorded as 5.80 and siliqua length as 9.59 cm which both of which were higher than other advanced populations. Besides this, data recorded for days to maturity (91.00days), secondary branches/plant (5.08) and siliqua/plant (182.93) was also moderately high (Table 4).

G12 [Nap (9906 × 205)]:

Average seed yield per plant of G12 was recorded as 9.19 g (Table 4). G12 had highest average thousand seeds weight (5.80 g). Besides, it was also noticed that secondary branches/plant (5.13) and seliqua length (9.19 cm) were moderately high. On the other side, days to maturity (32.33 days) was lower than many others population in G12 (Table 4).

G15 [Nap (108 × 9901)]:

Average seed yield per plant of G15 was recorded as 7.45 g. It was also observed that days to 50% flowering (43.00 days) were higher in G15 than other population. Besides, days to maturity (90.67 days), thousand seeds weight (5.19 g) and siliqua/plant as 152.53 were moderately higher than the others in G15 (Table 4).

G22 [Nap (108 × 9901)]:

Average seed yield per plant of G22 was recorded as 7.25 g. It was also observed that, days to maturity (89.00 days) and thousand seeds weight (5.29 g) were moderately higher than the others in G22 (Table 4).

G5 [Nap (9901 × 0130)]:

Average seed yield per plant of G5 was recorded as 7.24 g. It was also observed that, days to maturity (90.67 days), plant height (126.10 cm) and thousand seeds weight (5.17 g) were moderately higher than the others in G5 (Table 4).

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with the objective to assess the selection of superior genotypes from 33 *B. napus* L. genotypes through study the genetic variation among the genotypes for improvement of yield. The experiments were performed at the experimental Farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangaldesh during the period from November 2019 to February 2020. The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. Data on different morphological characters were recorded time to time and analyzed statistically. The results of the studies have been summarized as follows:

The analysis of variance showed highly significant differences among the genotypes for all the characters. From the mean performance it was observed that days to 50% flowers was recorded higher in G15 (43.00 days) and minimum was in G33 (30.33 days). Maximum days to maturity were observed in G1 (93.00 days) whereas G10 showed the minimum (76.67 days). Plant height was observed the highest in G7 (127.93 cm) and the lowest in G25 (84.56 cm). The maximum number of primary branches/plants was observed in G15 (5.73) and the minimum was found in G5 (1.33). The G5 performed the highest secondary branches/plant (7.53) and lowest by the G6 (1.23). Highest siliquae/plant was found by the G33 (186.00) whereas the lowest siliquae/plant was observed in G12 (66.67) and G19 (67.67). The longest length of siliqua was recorded for G20 (9.59) while the shortest length was found in G19 (5.36). Maximum seeds per siliqua were observed in G2 (24.26) and minimum was noticed in G22 (13.87). Highest value for thousand seed weight was found in G12 (5.80 g) and lowest value was recorded in G14 (2.80 g).

Yield/plant was observed maximum for G20 (9.59 g) and minimum yield/plant was found in G1 (3.23 g). Phenotypic variance was considerably higher than the genotypic variance for all the studied characters. Differences between the genotypic and phenotypic variances were low in all characters except plant height (cm) and siliqua/plant. Low differences indicating low environmental influence on them. High differences between the genotypic and phenotypic variances of plant height (cm) and siliqua/plant were observed which indicating significant environmental influences on them.

High phenotypic coefficient of variation was noticed for all the studied characters over genotypic coefficient of variations. Low genotypic and phenotypic coefficients of variations were found in days to maturity. Moderate genotypic and low phenotypic coefficients of variations were noticed in plant height. Moderate genotypic and phenotypic coefficients of variations were observed for days to 50% flowering, sliqua length (cm) and seeds per siliqua. High genotypic and low phenotypic coefficients of variations were observed in primary branches/plant, secondary branches/plant, siliqua/plant, thousand seeds weight (g) and yield/plant (g).

High heritability coupled with high genetic advance was recorded in siliqua/plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. High heritability coupled with low genetic advance was found in days to 50% flowering, days to maturity, primary branches/plant, secondary branches/plant, siliqua length (cm), thousand seeds weight (g) and yield/plant (g) indicating the non-effective selection of the populations for these traits.

Positive significant genotypic and phenotypic association with seed yield per plant was observed in plant height (cm), secondary branches/plant, siliqua/plant, siliqua length (cm) and thousand seeds weight (g) suggesting that genotypes with high partitioning efficiency gave increase in seed yield per plant. On the other hand, significant negative association with seed yield per plant was recorded in primary branches/plant and seeds per siliqua.

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering ten characters. It was expressed that primary branches/plant, secondary branches/plant, siliqua/ plant and thousand seeds weight (g)had positive and direct effect on yield per plant indicating them as most important

contributors to seed yield per plant which could be taken in consideration for future hybridization programme. On the other hand, negative and direct effects were observed in days to 50% flowering, days to maturity, plant height (cm), siliqua length and seeds per siliqua.

Selection was performed among 33 populations of *B. napus* based on their yield and yield contributing characters. Based on the variability and as per our objectives, the highest seed yield per plant was noticed in G20, with highest thousand seed weight and siliqua length. On the basis of other character including day of maturity and with moderate high yield G12, G15, G22 and G5 were also selected. They performed best among the studied genotypes and selected as a potential candidate for future hybridization program in Bangladesh.

RECOMMENDATION

- It may be considered that the advanced population G20, G12, G15, G22 and G5 had the potentiality for future hybridization program.

CHAPTER VI

REFERANCES

Abideen, S.N.U., Nadeem, F. and Abideen, S.A. (2013). Genetic variability and correlation studies in *Brassica napus* L. genotypes. *Int. J. Innov. Appl. Stud*. **2**:574-581.

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): 20 1-226.

Afrin, T. (2014).Variability and comparative analysis in F_4 Populations of *Brassica rapa* L. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Afrin, T., Bhuiyan, M.S.R. and Parveen, S. (2016). Variability and comparative analysis among advanced generations of *'Brassica rapa'* L. *Plant Knowl. J*. **5**(1): 18

Ahmad, B., Muhammad, S., Ali, J. and Ali, I. (2013). Genetic variability studies of some quantitative traits in advance mutant lines of winter rapeseed (*Brassica napus* L). *Life Sci. J*. **10**(12): 103-108.

Alam, M.F. (2010). Variability studies in F_4 progenies of *Brassica rapa*, obtained through intervarietal crosses. M.S. Thesis. Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Ali N., F. Javidfar, A.A. Attary, 2002 - Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (Brassica napus L.). Pak. J. Bot., 34:145-150.

Al-Jibouri, H., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances and co-variances in an upland cotton cross of interspecific origin. *Agron. J*. **50**(10): 633-636.

Allard, R.W. (1960). Principles of Plant Breeding. John Willey and Sons. Inc. New York. pp. 36.

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.

Ara, S., Afroz, S., Noman, M.S., Bhuiyan, M.S.R. and Zia, M.I.K. (2015). Variability, correlation and path analysis in F2 progenies of inter-varietal crosses of *Brassica rapa* L. *J. Environ. Sci. Nat*. Res. **6**(1): 217-220.

Awasthi, D., Tiwari, V.K. and Kandalk, V.S. (2020). Studies on correlation and path analysis in germplasm of Indian mustard [*Brassica Juncea* (L) Czern and Cross.]. *International J. plant Sci.* 15(2): 101-106.

Aytac, Z. and Kinaci, G. (2009). Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). *African J. Biotech*. **8**(15): 3547-3554.

Azadgoleh E, Zamani M. A. and Yasari E. M. (2009). Agronomical important traits correlation in rape seed (*Brassica Napus* L.) Genotypes, *Res. J. Agril. Biol. Sci*. **5**(5): 798-802.

Bahadur, V., Bharti, L.J., Kumar, A., Kumar, D., Chaudhary, R.P. and Maurya, K.N. (2021). To study on genetic variability for yield and its contributing traits in yellow mustard under sodic soil. The Pharma Innovation Journal; 10(4): 609-613.

Basalma, D. (2008). The correlation and path analysis of yield and yield components of different winter rapeseed (*Brassica napus* ssp. oleifera L.) cultivars. *Res. J. Agric. Biol. Sci.* **4**(2): 120-125.

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

Bilal, M., Khan, S.A., Raza, H., Ali, F., Masaud, S., Khan, N.A., Hussain, I. and Khan, J. (2015). Evaluation of some indigenous rapeseed genotypes for adaptability and yield traits in the agro-climatic conditions of Mansehra. *Int. J. Bio Sci*. **7**(5): 127-135.

Burton, G.W. (1952). Quantitative inheritance in grass pea. *Proc. 6th Grassl.* Cong. 1: 277- 283.

Chowdhary M. A., Miah A. J., Rahman L. and Rahman A. (1987). Correlation and path coefficient analysis of nine important characters of Mustard (*Brassica juncea* L. Czern and Coss). *Bangladesh J. Agric*., 12: 149-154.

Cochran, W.G. and Cox, G. (1957). Experimental design. W.S John, (2nd ed.). New York. pp.615.

Comstock, K. and Robinson, P.R. (1952). Estimation of genetic advance. *Indian J. Hill*. **6**(2): 171-174.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518.

Ejaz-UI-Hadan, 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).

Engida T. S. (2007). Genetic variability for yield and other agronomic traits in seed potato. *J. Agron*. 6: 94-99.

Esmaeeli-Azadgoleh, M.A., Zamani, M. and Esmaeil, Y. (2009). Agronomical important traits correlation in rapeseed (*Brassica napus* L.) genotypes. *Res. J. Agric. Biol. Sci*. **5**(5): 798-802.

FAO. (2019). Food and Agriculture Organization of the United Nations, FAOSTAT.

FAO. (2019). Food and Agriculture Organization of the United Nations, Trade and Market Division. Food outlook.

Fayyaz, L. and Afzal, M. (2014). Genetic variability and heritability studies in indigenous *Brassica rapa* L. accessions. *Pakistan J. Bot.* **46**(2): 609-612.

Gangapur, D.R., Prakash, B.G., Salimath, P.M., Ravikumar, R.L. and Rao, M.S.L. (2009). Characterization and Path analysis in Indian Mustard (*Brassica juncea* L. Czern and Cross). *Karnataka J. Agril. Sci.* **22**(5): 971-977.

Gosh S.K., S.C. Gulati, 2001 - Genetic variability and association of yield components in Indian mustard (Brassica juncea L.). Crop Res. Hisar, 21:345-349

Gomez. K.A. and Gomez, A.A. (1984). Statistical procedure for agricultural research (2nd ed). Wiley. New York. pp. 28-192.

Halder, T. (2013). Variability in advanced lines of *Brassica rapa*. MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Halder, T., Bhuiyan, M. S. R. and Islam, M. S. (2014). Variability and correlation study of some advanced lines of *Brassica rapa*. *Bangladesh J. Plant Breed. Genet.* **27**(1): 25-36.

Halder, T., Bhuiyan, M.S., Islam, M.S. and Hossain, J. (2016). Analysis of relationship between yield and some yield contributing characters in few advanced lines of rapeseed (*Brassica rapa* L.) by using correlation and path analysis. *Adv. Agric. Bot*. **8**(1).

Helal, M.M.U., Islam, M.N., Kadir, M. and Miah, M.N.H. (2014). Genetic variability, correlation and path analysis for selection of mustard (*Brassica spp*.). *Eco-friendly Agril. J.* **7**(12): 176-181.

Hosen, M. (2008). Variability, correlation and path analysis in F_3 materials of *Brassica rapa*. MS Thesis, Department of Genetic and Plant Breeding, SAU, Dhaka.

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

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.

Islam, M.S. and S. Khan. (1991). Variability and character association in tomato (*Lycopersicon esculentum* Mill). *Bangladesh J. Pl. Breed. Genet*. **4**(1&2): 49-53.

Jahan, N., Khan, M.H., Ghosh, S., Bhuiyan, S.R. and Hossain, S. (2014). Variability and heritability analysis in F_4 genotypes of *Brassica rapa* L. *Bangladesh J. Agril. Res*. **39**(2): 227-241.

Jamali, K.H., Mari, S.N., Soomro, Z.A., Soomro, S. and Khanzada, A. (2016). Correlation study on yield and yield contributing traits in *Brassica compestris* L. *Life Sci. Intl. J.* **10**(1): 1-7.

Johnson, R. W., Robinson, H.F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agron. J.* 47: 314-318.

Kadvani, G., Patel, J.A., Patel, J.R., Prajapati, K.P. and Pate, P.J. (2021). Estimation of Genetic variability, heritability and genetic advance for seed yield and its attributes in Sesame (*Sesamum indicum* L.). *IJBSM*; **11**(3):219-224.

Khan, F.A., Sajid-Ali., Amir-Shakeel., Asif-Saeed. and Ghulam-Abbas (2006). Correlation analysis of some quantitative characters in *Brassica napus L*. Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, *Pakistan. J. Agril. Res. Lahore*. **44**(1): 7-14.

Khan, M.H., Bhuiyan, S.R., Rashid, M.H., Ghosh. S. and Paul, S.K. (2013). Variability and heritability analysis in short duration and high yielding Brassica rapa L *Bangladesh I. Agril. Res.* **38**(4): 647-657.

Kumar, P., Yadava, T.P. and Yadav, A.K. (1984). Association of seed yield and its component traits in the F2 generation of Indian mustard. *Indian J. Agric. Sci*. **54**(7): 604-607.

Kumar, S., Snagwan, R. S. and Yadav, I. S. (2009). Correlations studies in Brassica species under dry land conditions. *Cruciferae Newsl.* 21:151-152.

Kumari, S., Kumar, K. and Kumari, K. (2017). Study on correlation among different character pairs and path coefficient analysis in yellow sarson (*Brassica rapa.* Var. Yellow Sarson). *Prog. Agric.* **17**(1): 15-20.

Lodhi, B, Thakral, N. K., Avtar, R. and Singh, A. (2014). Genetic variability, association and path analysis in Indian mustard (*Brassica juncea*), *J. oilseed Brassica*. **5**(1): 26-31.

Mahamood, T., Muhammad, A., Iqbal, S. and Anwar, M. (2003). Genetic variability and heritability estimates in summer mustard (*Brassica juncea* L.). *Asian J. Plant Sci*. **2**(1): 77-79.

Mahmud, M.A. A. (2008). lnter genotypic variability study in advanced lines of *Brassica rapa.* MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

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.

Mili, S.M.S.K. (2014). Genetic variability and character association in F5 population of *Brassica napus* L. M.S. thesis, SAU, Dhaka.

Momena B. (2015). Genetic variability, correlation and path analysis in BC1F5 segregating generation of *Brassica napus* L. MS Thesis. Department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka1207.

Nagaraja T. E. (1990). Genetic variability study in rape seed (*Brassica compestris* L.) and mustard (*Brassica juncea* (L) Czern and Coss). M.Sc. (Agri.) Thesis, Univ. Agric. Sci. Bangalore.

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.

Naznin, S., Kawochar, M.A., Sultana, S., Zeba, N. and Bhuiyan, S. R. (2015). Genetic divergence in *Brassica rapa* L. *Bangladesh J. Agril. Res*. **40**(3): 421-433.

Ousman Yimer, O., Mohammed, W., Teju, E. and Pae, D.H. (2021). Correlation and path coefficient analysis studies in Ethiopian Mustard (B*rassica carinata A. Braun*). *Afr. J. Plant Sci.*. 15(8): 250-256.

Pallvi G. (2020). Rapeseed and Mustard: Origin, Distribution and Production | Agronomy. Agriculture in India.

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.

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 B. Genet*. **26**(2): 15-22.

Parvin, E. (2014). Genetic diversity and character association of *Brassica napus*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka

Parvin, F. (2015). Genetic variability and character association in BC1 F4 genetation of *Brassica napus*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.

Patel, P.J. and Vyas, S.R. (2011). Heritability and genetic advance for yield and quality traits in Indian mustard (*Brassica juncea* L.) Czern and Coss. *Adv. Res. J. Crop Improv*. **2**(2): 212-214.

Rameeh, V. (2011). Correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. *J. Oilseed Brassica* **2**(2):56-60.

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 *Brassica* species. M.S. thesis, Sher-e-Bangla Agricultural University, Department of Genetics and Plant Breeding, Dhaka, Bangladesh. pp. 34-63.

Rashid, M.H.U., Parveen, S. and Bhuiyan, M.S.R. (2015). Morphological attributes species identification of oleiferous *Brassica sp.* and better parents selection criteria for *Brassica Juncea. Intl. J. Curt. Res.* **7**(9): 19847-19854.

Robinson, H.F., Comstock, R.E. and Harvey, P. (1966). Quantitative genetics in relation to breeding on the centennial of mendelism. *Indian J. Genetics*. 26: 171-177.

Rout, S., Kerkhi, S.A. and Chauhan, C. (2018). Character Association and Path Analysis among Yield Components in Indian Mustard [*Brassica juncea* (L.) Czern and Coss]. *Int.J.Curr.Microbiol.App.Sci:* **7**(1): 50-55.

Roy, S.K., Haque, S., Kale, V.A., Asabe, D.S. and Dash, S. (2011). Variability and character association studies in rapeseed-mustard (*Brassica sp.*) *J. Crop Weed.* **7**(2): 108-112.

Saleh, M.A., (2009). Variability analysis and selection from F_2 materials generated through inter-varietal crosses of *Brassica juncea*. M.S. thesis, SAU, Dhaka

Seyoum, M., Alamerew, S. and Bantte, K. (2012). Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits inupland rice. *J. Plant Sci.*; **7**(1): 13-20.

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.

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.

Shalini, T.S. Sheriff, R.A., Kulkarni, R.S. and Venkataramana, P. (2000). Variability studies in Indian mustard [*Brassica juncea* L. Czern and Coss*]. Res. Crops*. **12**(3): 230-234.

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

Siddika, K.S. (2015). Genetic variability, correlation and path analysis in F2 segregating generation of *Brassica napus*. MS thesis, Dept. of Genetics and plant Breeding, SAU, Dhaka.

Siddikee, M.A. (2006). Heterosis inter genotypic variability, correlation and path analysis of quantitative characters of oleiferous *Brassica campestris* L. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Sikarwar, R.S., Satankar, N., Kushwah, M.K. and Singh, A.K. (2017). Genetic Variability, Heritability and Genetic Advance Studies in Yellow Sarson (*Brassica rapa* Var. Yellow Sarson). *Int. J. Agric. Innov. Res*. **5**(5): 23191473.

Singh, H. N., Srivastava, J. P. and Prasad, R. (1977). Genetic variability and correlation studies in bitter gourd. *Indian J. Agri. Sci.*; **47**(12): 604-607.

Singh, M., Singh, S.P. and Dhirendra, S. (2011). Genetic analysis for seed yield and its genotypes in yellow sarson (Brassica compestris L.). *Indian J. Agril. Sci.* **70**(9): 624-626

Singh, R.K. and Chaudhary. B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. India. p. 56.

Singh. S.K. and Singh. A.K. (2010). Inter-relationship and path analysis for seed yield in Indian mustard. *Indian J. Ecol*. **37**(1):8-12.

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agril. J.* 60:1093-1096.

Sohail, A., Zabta, K., Malik, A. R. and Sabbir, H. (2017). Assessment of quantitative agro-morphological variations among Brassica rapa diverse populations. *Pakistan J. Bot.* **49**(2): 561-567.

Srivastava, M. K. and Singh, R. P. (2002). Correlation and path analysis in Indian mustard. Crop Res. Hisar, Dept. of Genetics and Plant Breeding. *Indian Univ. Agril. Tech.* **23**(3): 517-521.

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.

Thakral, N.K. (2004). To study the association of some morphophysiological attributes with yield in toria. *Thesis Abst.* **8**(11): 66-67.

Tollenaar, M.F., Ahmaedzedahand, A. and Lee, E.A. (2004). Physiological basis of heterosis for grain yield in maize. *Crop Sci.* 44: 2086–2094.

Twenty four mantra Organic. (2021). Retrieved from the Nutritional facts & Composition Breakdown of Mustard oil**.**

Uddin, M.J., Chowdhury, M.A.Z. and Miah, M.F.U. (2005). Genetic variability, character association and path analysis in Indian mustard (*Brassica juncea* L.). *Bangladesh Ann. Agric.* **5**(1): 51-52.

Uddin, M.S. (2008). Variability study in F2 progenies of *Brassica rapa*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

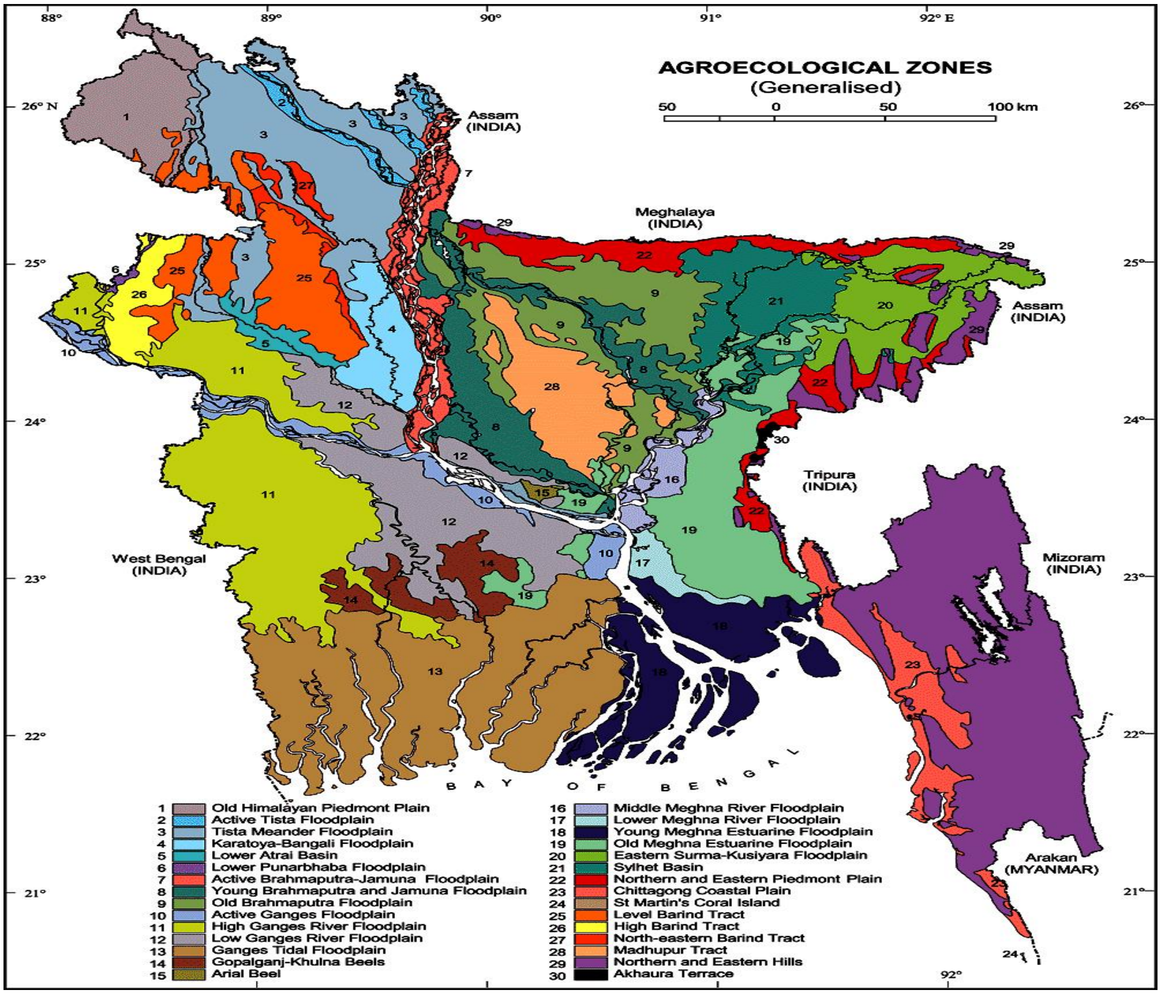
Uddin, M.S., Bhuiyan, M.S.R., Mahmud, F. and Kabir, K. (2013). Study on Correlation and Path Co-efficient in F_2 Progenies of Rapeseed (*Brassica rapa*). *Acad. J. Plant Sci*. **6**(1): 13-18.

USDA, (2019). United States Dept. Of Agriculture. Office of global analysis. International production assessment division.

Zare, M. and Sharafzadeh, S. (2012). Genetic variability of some rapeseed (*Brassica napus* L.) cultivars in Southern Iran. *African J. Agric. Res*. **7**(2): 224-229.

APPENDICES

Appendix I. Map showing the experimental site under the study



🟨 **Legend showing the research site**

Appendix II: Physical and chemical characteristics of initial soil depth of the experimental site.

A. Physical composition of the soil:

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

B. Chemical composition of the soil:

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

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

Appendix III: Monthly average temperature, average relative humidity and total rainfall and total sunshine of the experimental site during the period from November, 2019 to February, 2020.

Month	Air temperature	Relative humidity (%)	Total rainfall (mm)	See level pressure
November, 2019	24.9	74	37	1011.5
December, 2019	19.3	74	5	1015.2
January, 2020	18.5	76	21	1014.7
February, 2020	21.6	59	1	1014.5

Source: https://www.timeanddate.com/weather/bangladesh/dhaka/climate