ESTIMATION OF GENETIC VARIABILITY AND INTERRELATIONSHIP BETWEEN YIELD AND YIELD CONTRIBUTING CHARACTERS OF BC_1F_7 POPULATION IN *Brassica napus* L.

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DHAKA-1207

DECEMBER, 2020

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By

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REGISTRATION NO: 18-09289

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: JULY-DECEMBER, 2020

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CERTIFICATE

This is to certify that thesis entitled, " ***ESTIMATION OF GENETIC VARIABILITY AND INTERRELATIONSHIP BETWEEN YIELD AND YIELD CONTRIBUTING CHARACTERS Of BC_1F_7 FPOPULATION IN (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* ***Sima Akter*** *Registration No.* ***18-09289*** *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.

(Prof. Dr. Firoz Mahmud)
Supervisor

Dated: December, 2020
Place: Dhaka, Bangladesh


DEDICATED TO
MY
BELOVED PARENTS

ACKNOWLEDGEMENTS

It is my pleasure to acknowledge all people who cooperate with me for the completion of this thesis work. First and foremost, praises and thanks to the Almighty, for giving me motivation, strength, and courage to fulfill my aims and for His showers of blessings throughout my research work to complete the research successfully. I am deeply indebted to my honorable teacher ***Professor Dr. Firoz Mahmud****, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for his scholastic supervision, academic support, unvarying inspiration over the research work to complete this thesis completely.*

Besides my advisor, I would like to express my deepest appreciation to my co-supervisor, professor ***Dr. Md. Ashaduzzaman Siddikee*** *Department of Genetics and plant Breeding, SAU for his helpful support, constructive criticism, and practical suggestion.*

My earnest indebtedness is acknowledged to Professor Dr. Md. Shahidur Rashid Bhuiyan Honorable Vice-Chancellor, Sher-e-Bangla Agricultural University, Dhaka-1207 for providing me with all possible help during my experiment.

I would also like to extend my deepest gratitude to the chairman of the Department, Professor ***Dr. Md. Abdur Rahim*** *and also grateful to Professor Dr. Md. Sarowar Hossain, Professor Dr. Naheed Zeba, Professor Dr. Jamilur Rahman, Professor Dr. Mohammad Saiful Islam, Professor Dr. Kazi M.K. Huda, Dr. Md. Harun-Ur-Rashid, Associate Professor, Dr. Shahnaz Parveen, Associate Professor and all other teachers of the Department of Genetics and Plant Breeding.*

Thank should also go to all the staff of my department for their appreciative helped to me.

I owe my wholehearted thanks and appreciation to my brother and sister for their keen interest and encouragement were a great help throughout my research work.

And I would like to give great thanks to my senior sister as well as my friend Umme Habiba Tonny for her complimentary support. And my joys know no bounds in expressing my cordial gratitude to all of my friends.

Last but not the least, I am indeed and my gratitude sincerely goes to my beloved father and mother who always give me dreams to be an excellent daughter. And their support, unparallel affections gave me the power to complete the work spiritually. I am proud to be the daughter of my parents. And obviously, this thesis is devoted to my adorable parents.

December, 2020 *The Author*

SAU, Dhaka

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ABSTRACT

Thirty genotypes from BC_1F_7 populations of *Brassica napus* L. were evaluated to study the genetic variability, heritability with genetic advanced, correlation and path analysis based on yield and yield component traits. The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka during mid-November 2018 to mid-March 2019. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Analysis of variance revealed significant variations among the genotypes for all the traits studied. Mean difference studies showed significant values for all the traits among the genotypes. Comparatively phenotypic variances and PCV (**Phenotypic Coefficient of Variation)** were higher than the genotypic variances and GCV **(Genotypic Coefficient of Variation)** for all the characters studied. The highest PCV value was observed followed by seed yield per plant (31.20%) number of secondary branches per plant (25.39%) and 1000 seed weight (21.96%) and GCV values were followed by seed yield per plant (23.97%), number of secondary branches per plant (17.68%) and thousand seed weight (12.18%). High heritability values coupled with high genetic advances as percent of mean was noticed for seed yield per plant (37.94%) with heritability (59.04%) and secondary branches per plant (25.36%) with heritability (48.49%). The significant positive correlation with seed yield per plant was found in primary branches per plant (G=0.297, P=0.283), secondary branches per plant (G=0.260 P=0.293), siliqua per plan (G=0.589, P=0.489), seeds per siliqua (G=0.325, P=0.403) and 1000 seed weight (G=0.277, P=0.278). On the other hand, path analysis was exhibited the positive direct effects towards days to 50 % flowering (5.806), plant height (cm) (1.838), primary branches (3.067), siliqua length (cm) (0.789), seeds per siliqua (1.385) and 1000 seed weight (g) (1.102) where negative direct effect was recorded in days to 1st flowering (-5.490), secondary branches per plant (-2.497), siliqua per plant (-0.279). Based on the result of the study, according to seeds yield per plant and other agronomic performance genotypes G_{13} (19.59), G_{24} (17.20), G_{19} (14.05), G_{30} (13.65), G_1 (13.19) and G_{29} (15.13) can be used further for varietal improvement programs and development of higher-yielding variety.

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LIST OF EXPANSIONS AND ACRONYMS

Expansions	Acronyms
Agronomy	Agron.
Agricultural	Agril.
Agriculture	Agric.
At the rate	@
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
By way of	via
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Cultivars	cv.
Centimeter	cm
Degrees of Freedom	df
Days to 50% flowering	D50%F
Days After Sowing	DAS
Days to Maturity	DM
Duncan`s Multiple Range Test	DMRT
Etcetera	etc.
Environmental variance	σ^2 e
Food and Agricultural Organization	FAO
Genotypic variance	σ^2 g
Gram	g
Genotype	G
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Heritability in broad sense	h^2_b
International Center for Agricultural Research in Dry Areas	ICARDA
Indian Agricultural Research Institute	IARI
Journal	J.
Kilogram	kg
Meter	m

LIST OF EXPANSIONS AND ACRONYMS (Cont'd)

Expansion	Acronyms
Mean sum of square	MSS
Muriate of Potash	MP
Number	No.
Primary branches per plant	PBP
Plant height	PH
Percentage of Coefficient of Variation	CV%
Phenotypic variance	σ^2p
Percent	%
Residual Effect	R
Randomized Complete Block Design	RCBD
Science	sci.
Standard Error	SE
Siliqua length	LS
Secondary branches per plant	SBP
Seeds per silique	SPS
Seed yield per plant	SYP
Square meter	m^2
Sher-e-Bangla Agricultural University	SAU
Triple Super Phosphate	TSP
Thousand seeds weight	TSW
The third generation of a cross between two dissimilar homozygous parents	F_3
University	Uni.
Variety	var.

CHAPTER I

INTRODUCTION

Chapter I

INTRODUCTION

Rapeseed (*Brassica napus* L.) is a principal oilseed crop, which plays a vital role in the national economy of Bangladesh. It is a leading oilseed crop belongs to the genus Brassica of the mustard family, Brassicaceae. The Brassicaceae family (Cruciferae) includes around 375 genera and about 3,200 species (Ahuja *et al.*, 2010). The family contains cruciferous vegetables, including species such as *Brassica oleracea* (e. g. Cabbage, broccoli, cauliflower, kale, Brussels sprouts, Chinese Kale, Savoy cabbage, and kohlrabi), *Brassica rapa* (e. g: Chinese cabbage, broccoli too, Chinese mustard and turnip), *Brassica juncea* (e. g: mustard green, head mustard and cut leaf mustard), *Brassica napus* (e.g., rapeseed and rutabaga), and *Raphanus sativus* (radish) (Ishida *et al.*, 2014). The genus Brassica is one of the 51 genera belonging to the crucifer family (Rakow, 2004). Species within the genus would be categorized into oilseed, forage, condiment, and vegetable crops by using their buds, inflorescences, leaves, roots, seeds, and stems (Francisco *et al.*, 2016). The genetic relationships among different Brassica species were established in the classical work done by U (NU, 1935). The so-called U-triangle comprises six species (three basic diploids and three amphidiploids) (Figure 1). The vertices of the triangle include the three diploid species: *Brassica oleracea* L. (2n=18; CC), *Brassica rapa* L. (2n=20; AA), and *Brassica nigra* L. Koch (2n=16; BB), and the edges of the triangle include the three amphidiploid species: *Brassica juncea* L. Czern. (2n =36; AABB), *Brassica napus* L. (2n=38; AACC), and *Brassica carinata* Braun (2n=34; BBCC) (Gómez-Campo, 2003). *Brassica napus* (genome AACC, 2n= 38) is the most ancient amphidiploid in the genus Brassica.

Mainly the rapeseed is cultivated for seeds oil. It has 35-45 % oil which is used for edible purposes. There are two members of Brassica are the major contributors i. e. *Brassica napus* L. and *Brassica rapa* L. for oil and protein supply in the world. Where, *Brassica napus* L. contains more than forty percent oil while in *Brassica rapa* L. this amount is up to thirty-five percent (Nasr *et al.*, 2006). Even the seed oil of *Brassica*

napus is usually used for culinary purposes. It has a wide range of applications such as cooking oil, element of beautifying agents but also pesticides, biofuels, etc. In Iranian traditional medicine, the root parts of this plant were used for therapeutic purposes as a diuretic, anti-scurvy, anti-inflammatory of the bladder, and anti-goat. It also holds from 18 to 22 percent of proteins which consist of different protein units like cysteine, methionine, and lysine. Total consumption of oils and fats was 3.5 million tons in 2019 and import edible oil which cost 1161 million US$ (BER, 2019). In Bangladesh the total production was 311740 metric ton in 667242-acre land in 2018-19 and 351537 metric ton in 759874-acre land in 2017-2018 (Yearbook of Agricultural Statistics-2019). It is required 0.30 million tons of oil equivalent to 0.85 million tons of oil seeds for nourishing people of Bangladesh. According to FAO (2019) rapeseed was globally grown on area of approximately 34.5 million ha with the total production 70 million metric tons. At present, the oil seed production in Bangladesh is about 0.26 million tons, which cover only 30% of the domestic need (BBS, 2011). Bangladesh has been facing acute shortage of edible oil for the last several decades. Therefore, we need to import oil and oilseeds to meet up the deficit. In cereal, the amount of these amino acids is too much low so *Brassica napus* L. is the alternate source to get these proteins (Rashid *et al.,* 2005). And according to (BBS, 2019) it is the most important oilseed crop in Bangladesh and it occupies the 1st position in respect of area and production among the oil crops grown in Bangladesh. But in the world's oilseed market it has the second position after soybean (Hasan *et al.,* 2006).

The improvement of a crop is largely dependent on the nature and magnitude of available genetic variability, heritability, and the transfer of desired characters into new varieties. The success of breeding programmers can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones (Meena and Bahadur, 2013; Meena and Bahadur, 2014; Ranganatha *et al.,* 2013; Yared and Misteru, 2016). Hence, knowledge of key genetic parameters is crucial for any crop improvement program, providing precise information for selection. Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (GA) are useful biometric tools for measuring genetic variability (Aditya *et al.,* 2013).

Generally, correlation coefficients show relationships among independent characteristics and the degree of linear relation between these characteristics. For plant breeders it is thus essential to learn the relationships among pairs of characters in order to make a decision on the proper selection criteria for a breeding program.

The path coefficient analysis has been used by many researchers for a more and complete determination of impact of independent variable on dependent one. The Path coefficient analysis helps the breeder(s) to explain direct and indirect effects and hence has extensively been used in breeding work in different crop species by various researchers (Ali *et al.,* 2013). There must be a thorough knowledge of the existence of genetic variability, heritability, the kind of gene action and the relative magnitude of additive, dominance and total genotypic and phenotypic variances of the population. We had used to 30 hybrid genotypes by crossing between *Brassica napus* L. on growing up to 7^{th} generation to maintain the heterozygosity. And we need to improve our yield potential for develop the high yielding Varity (HYVs). For them we need to study among the BC_1F_7 advanced line.

Keeping in mind the available genetic variability and widely practiced breeding programs for developing variety for any trait, the present study was undertaken to achieve the following objectives:

- To study the genetic variability in BC_1F_7 segregating populations,
- To understand the correlation co-efficient and the path co-efficient pattern of different characters and
- To select the best promising lines for systematic trial.

CHAPTER II

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Wide evaluation and researches on Brassica breeding have been attained in many countries for its improvement in respect of yield and yield contributing characters. A large number of literatures are available on variability, heritability, correlation and path analysis of yield and yield contributing characters of *Brassica* grown under a particular environment. The triangle of U is described on the tri-angular diagram (Figure 1). It shows how three of the *Brassica spp*. were derived from three linear genomes and those are denoted by the letters AA, BB, or CC. Each and every one of these diploid genomes produces a common Brassica species.

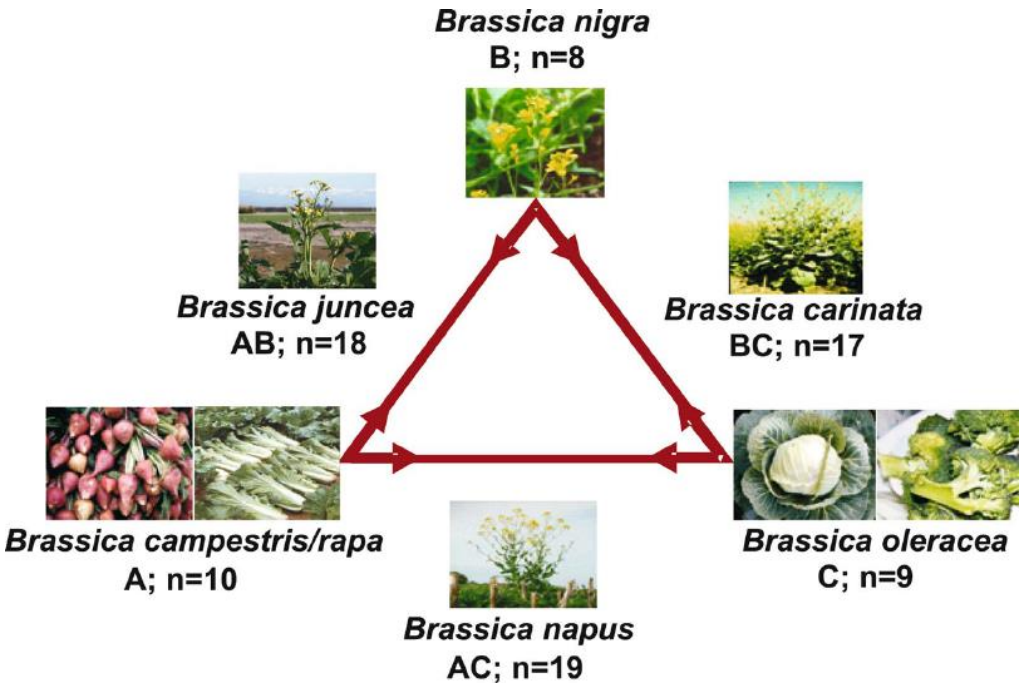


Figure 1. The "triangle of "U" diagram, representing the genetic relationships among the six species of the genus Brassica.

An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely –

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation among different characters

2.3 Path co-efficient analysis

2.1 Genetic variability, heritability and genetic advance

Genetic variability is a prerequisite for initiating a successful breeding program aiming to develop high-yielding varieties. Large numbers of literatures concerning the variability in the Brassica spp. are available. These literatures are outlined here.

The present finding about genetic similarity range were also comparable with that of Shinwari *et al.,* (2013) who observed 60% to 100% genetic similarity among the genotypes of *Eruca sativa* L. Similar result was found through during characterization of *Brassica carinata* by Zada *et al.,* (2013) also found comparable agreement with present findings. They found the genetic similarity within the range of 50% to 100%. During the present study *Brassica napus* L. genotypes were found to have the similarity within the range of 83 to 98%. The present study was found in close agreement with that of Turi *et al.,* (2010) who recorded similarity up to 98% during their characterization of Brassica genotypes.

An experiment was conducted by Belete *et al.,* (2012) to estimate various genetic parameters for some agronomic traits of introduced Ethiopian mustard (*Brassica carinata* A. Brun) genotypes was undertaken. The experiment was laid out in randomized complete block design with three replications at Holetta Research Center, Ethiopia. Analysis of variance showed significance difference among the genotypes for traits studied except plant height and seed yield. Phenotypic coefficient of variation and genotypic coefficient of variation ranged from 1.2- 10.2% and 1.9-6.8%, respectively. The highest heritability values had shown by oil content (99.8%) followed by days to flowering (96.5%) and days to maturity (89.1%). High heritability along with high

genetic advance (as percent of mean) was recorded for days to flowering and oil content. Days to flowering, days to maturity and oil content are important traits to be considered for further variety development program.

Zebarjadi *et al.,* (2011) carried out an experiment to study some traits and to estimate genetic parameters in 16 rapeseed genotypes in two conditions (irrigation and non-irrigation). Statistical analysis showed significant differences among the genotypes based on the data for 13 different characters, including chlorophyll content (SPAD), sugar solution (SS), stem size (SS), plant height, oil percent, oil yield etc. In stress condition heritability was maximum oil percentage, whereas low genetic advance was observed for thousand kernel weights.

Sheikh *et al.,* (2009) guided the induction of genetic variability in Ethiopian mustard (*Brassica carinata*) for quality traits through interspecific hybridization was studied by them. The result revealed that interspecific hybridization was used to enhance the spectrum of genetic variability in mustard for oil and meal quality traits from quality lines of *Brassica juncea.*

Mahak *et al.,* (2004) conducted an experiment on genetic variability, heritability, genetic advance and correlation for eight quantitative characters (days to flowering, days to maturity, plant height, number of primary branches, length of main raceme, seed yield per plant, 1000-seed weight and oil content) in 21 hybrids of Indian mustard and their seven parents (Varuna, Pusa Bold, Basanti, Maya, NDR-850I, RH 30 and Kanti) grown during Rabi 2002/03 in Kanpur, Uttar Pradesh, India. High heritability coupled with high genetic advance as percentage of mean was observed for days to flowering, followed by 1000-seed weight, days to maturity and plant height.

Genetic variability for nine traits in 25 genotypes study by Pant and Singh, (2001) analysis of variance revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. All traits showed high heritability, with the highest value estimated for seed yield per plant. The estimates of genetic advance were comparatively low for oil content and days to

flowering. The genotypic 7 coefficient of variation and heritability estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

In a study, Lekh *et al.,* (1998) reported that secondary branches showed the highest genotypic co- efficient of variation. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering. Thousand seed weight is also an important trait of Brassica oil crops, where the highest consideration is on the seed yield. This trait has been found to vary widely from genotype to genotype and from environment to environment including macro and micro environments. The coefficient of variation was high for thousand seed weight. pod length and number of seed per pod for both genotypic and phenotypic variability.

Generally high number of seeds per siliqua is desirable. On the variability of this trait a good number of literatures are available. Significant variability in number of seeds per siliqua in oleaceous Brassica materials of diverse genetic base was observed by Kumar and Singh (1994). Similar significant variability in the genotypes of *Brassica napus*, *Brassica campestris* and *Brassica juncea* were studied by them.

In every breeding program yield is the important character among various traits for oil crops. It is a complex trait which is influenced by various factors of production. A good number of literatures are available on the variability of this trait. High variability in different genotypes of *Brassica rapa* was reported by Sharma *et al.,* (1994).

Diwakar and Singh (1993) while working with segregating populations of yellow seeded Indian mustard (*Brassica juncea* L. Czern and Coss).

High variability in different genotypes of *Brassica napus* was found by Khera and Singh (1988). An experiment conducted by Varshney *et al.,* (1986) to estimate high heritability and genetic advance for number of siliquae per plant in *Brassica rapa* and *Brassica juncea* but they found high heritability and genetic advance for plant height in all the three species. Thakral (1982) also reported significant genetic variability in genotypes of *Brassica napus*.

Bhardwaj and Singh (1969) observed GCV value of 35.85% in case of *Brassica campestris* genotypes.

2.2 Correlation between yield and yield contributing characters

Meena *et al.,* (2017) illustrated identical results of highly positive and significant impacts of correlation of height of plant on yield of seed, weight of 1000 seeds, oil contents, seeds of a silique and primary and secondary branches. There was noticed positive and significant relationship among height of plant and protein and positive and non-significant relationship with primary branches, yield of seed, linolenic and erucic acid proportion. Negative and non-significant effects occurred between height of plant and seeds of a silique. Singh *et al.,* (2016) elaborated the positive significant correlation of weight of seeds and silique of plant, oil percentage and yield of seed.

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

Ara *et al.,* (2013) reported the same results that plant height possessed highly positive and significant correlation impacts on yield of seed, weight of 1000 seeds, oil contents, seeds of a silique and primary and secondary branches. There was noticed positive and highly significant relationship among height of plant and secondary branches, silique of plant, oil proportion and oleic acid proportion. While height of plant had high significant and negative correlation with weight of 1000 seeds. Height of plant was positively correlated with protein and possessed positive and non-significant relation with primary branches, yield of seed, linolenic and erucic acid proportion. Negative and non-significant effects occurred between height of plant and seeds of a silique.

Uddin *et al.,* (2013) conducted an experiment with seven parental and twenty-one F2 progenies of *Brassica rapa* to study correlation among different yield component and found that yield per plant had high significant positive correlation with number of primary branches per plant, number of secondary branches per plant and siliqua per

plant at both phenotypically and genotypically and significant positive correlation at genotypically in days to flowering and days to maturity.

Khan *et al.,* (2013) was noticed positive and highly significant relationship among primary branches and seed of silique, protein proportion and yield of seed. While it had non-significant negative correlation with weight of 1000 seeds, oleic acid, linolenic acid and erucic acid Proportion. Primary branches possessed positive and non-significant relation with silique of plant. Seed yield and primary branches were also positively correlated with primary branches in this work.

Rameeh (2012) aimed at finding out the planting date effect on yield associated traits and also determining the variations of correlations among the traits in different planting dates of rapeseed genotypes. Significant planting dates and genotypes effect for phonological traits, yield components, seed yield and oil percentage revealed significant differences of planting dates genotypes for these traits. The variation of correlation between duration of flowering and pods per plant was less than the correlation of duration of flowering to other traits in different planting dates.

Golparvar (2011) also notified the significant positive relationship among silique of a plant with seed yield. They concluded that selection of this parameter of yield could be fruitful for improvement of yield.

Chen *et al*., (2008) estimated that differential expression of the genes, specifically of the QTL regions involved in seed yield, plays a significant role in seed yield heterosis in *Brassica napus*. Hybrid performance has been recently related to the difference in gene expression between the hybrid and its parental lines.

A study was conducted by Hosen, (2008) using five parental genotypes of *Brassica rapa* and their ten F3 progenies including reciprocals. He found yield per plant showed the 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 siliquas per plant.

In an experiment Mahmud, (2008) found highly significant positive association of seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of siliquas per plant.

Quijada *et al.,* (2006), Udall *et al.,* (2006), Radoev *et al.,* (2008) and Rahman *et al.,* (2017) found that more than 90% of the inbred lines derived from the Rutabaga × spring canola crosses gave lower seed yield than their spring canola parent; however, few (5+2 = 7 lines of the two crosses) gave higher seed yield as compared to the spring canola parent. Quijada also found low seed yield in a majority of the spring *Brassica napus* lines derived from European winter × spring and Chinese semi-winter × spring *Brassica napus* crosses. Seed yield in *Brassica napus* is controlled by several QTL from both the A and C genomes therefore, variation for seed yield observed in the inbred lines derived from the Rutabaga × spring canola crosses apparently resulted from variable combination of the Rutabaga and spring canola alleles generated through segregation of these two types of alleles. The higher seed yield in the few inbred lines, apparently, resulted from favorable combination of Rutabaga and spring canola alleles. This agrees with Rahman that exotic allele of the primary gene pool can be used to increase seed yield in spring canola; however, undesired alleles often get introduced into the breeding population which would need repeated cycle of breeding for removal.

Khan *et al.,* (2006) studied correlation for some quantitative traits relating to yield and quality. The results indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

Pankaj *et al.,* (2002) undertaken an experiment of four parental cultivars and the F_4 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of

the characters. The number of siliquae per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliqua and test weight at both levels. The number of seeds per siliqua was positively associated with siliqua length and yield per plant at both levels.

The number of siliquas per plant had the highest direct effect on seed yield followed by 1000 seed weight, number of primary branches per plant and plant height. Most of the characters had an indirect effect on seed yield was observed by Shalini *et al.,* (2000) while studied path analysis of Indian mustard germplasm.

According to Kumar *et al.,* (1999) genotypic correlation co-efficient were higher in magnitude than corresponding phenotypic correlation co-efficient for most characters. The plant height, siliquae on main shoot, siliquae per plant and thousand seed weight were positively correlated with seed yield.

The number of siliquae per plant, number of seeds per siliqua and plant height was significantly positively correlated with seed yield was observed by Masood *et al.,* (1999) while studied seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* to calculate correlation co-efficient.

Zajac *et al.,* (1998) studied on phenotypic correlation between yield and its component and reported that strong positive correlation occurred between seeds per siliqua and actual yield. Positive but a weaker correlation was observed between seed yield and siliqua per plant. The number of seeds per siliqua had the greatest influence and number of siliquae per plant had the smallest effect on yield.

Nanda *et al.,* (1995) studied correlation analysis with 65 strains of *Brassica juncea*, *Brassica rapa* and *Brassica napus* and observed that positive association between yield and siliqua filling period.

Zaman *et al.,* (1992) studied on several yield contributing traits of Swedish advanced rape lines and reported that number of seeds per siliqua negatively correlated with siliqua per plant.

Chaudhury *et al.,* (1990) observed seed yield was positively correlated with siliqua length when evaluated seven of *Brassica juncea*, two of *Brassica carinata* cultivars and one cultivar each of *Brassica campestris* and *Brassica turneries*.

Ramanujam and Rai (1963) observed significant positive correlations between yield and all the yield components in *Brassica rapa* cv. yellow sarson. Zuberi and Ahmed (1973) observed similar results in *Brassica rapa* cv. toria. Campbell and Kondra (1978) observed positive correlation between yield and the yield components in rape seed (*Brassica napus*).

2.3 Path co-efficient analysis

Balalić *et al.,* (2017) also evaluated negative effects on oil content. Protein proportion directly and positively affected the yield of seed of plant. Negative indirect effects occurred through siliques of a plant, seeds of a silique, oil contents, oleic acid and linolenic acid proportion. While all other characters had positive and direct effects.

Ali *et al.,* (2017) and Ahmad *et al.,* (2015) showed negative effects of oleic acid on oil, linolenic acid, erucic acid proportion. Erucic acid proportion directly and negatively affected the yield of seed of plant. The indirect negative effects of erucic acid proportion occurred through primary branches and linolenic acid proportion. Negative indirect effects occurred through primary branches, siliques of a plant, seeds of a silique, oil, linolenic acid and erucic acid proportion. While all other characters had positive indirect effects.

Ejaz-Ul-Hasan *et al.,* (2014) conducted an experiment on *Brassica napus* and studied path coefficient. The result revealed that the highest direct positive effect of seeds per plant on yield followed by days to maturity, days to flowering, seeds per siliqua, siliqua length and thousand seed weight while plant height had direct negative effect on the yield per plant.

Yadava *et al.,* (2011) identified that, path coefficient analysis was an effort to access the magnitude of contribution of various traits to the yield in the form of cause and effect. It was simply called standardized partial regression coefficient. It estimated the

direct impacts of various variables on one another. It split the coefficient of correlation into direct and indirect effect. In this method there was occurrence of cause and effects between different variables. The direction of the experiment required casual system related to evidence of experiment. So, in this way, selection of the best performing traits could be possible in breeding program. The work was presented the direct and in direct impacts between the variables that resulted from path coefficients analysis of present breeding material. Height of plant directly and positively affected the yield of seed of plant. While height of plant showed indirect and negative effects on yield through silique of a plant, seeds in a silique and proportion of oil, protein, oleic acid and linolenic acid. While height of plant exhibited indirect and positive effects through the left-over parameters of yield.

The path co-efficient analysis by Hosen, (2008) exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F3 progenies including reciprocals.

Siddikee, (2006) conducted and experiment on oleaceous *Brassica campestris* L. to study the path analysis and revealed that thousand seed weight had the highest positive direct effect on seed yield per plant.

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

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

Khulbe and Pant (1999) studied path co-efficient analysis in eight Indian mustard (*Brassica juncea*) parents and their 28 F1 hybrids. The results revealed that harvest index, 22 siliqua lengths, seeds per siliqua, siliqua per plant, thousand seed and days to initial flowering were the major traits influencing seed yield.

Uddin *et al.,* (1995) studied path analysis in 13 Indian mustard (*Brassica juncea*) and observed that seeds per siliqua and thousand seed weight had high positive direct effect on seed yield per plant. Chauhan and Singh (1995) observed that plant height, siliqua per plant and seeds per siliqua had high positive direct effect on seed yield.

Yadava *et al.,* (1993) when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed that number of siliquae per plant had the highest positive direct effect on seed yield.

Kachroo and Kumar (1991) studied path co-efficient analysis in *Brassica juncea* and found that thousand seed weight had positive direct effect but days to flowering and number of primary branches had negative indirect effect via seeds per siliqua on seed yield.

Dhillon *et al.,* (1990) reported that the plant height had the highest positive direct effect on seed yield per plant in *Brassica juncea*, but *Singh et al.,* (1978) also found negative direct effect of the trait on seed yield.

CHAPTER III

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

The experiment was done with the 30 genotypes. It was conducted following Randomized Complete Block Design (RCBD) with three replications at the experimental farm of the department of Genetics and Plant Breeding, Sher-e Bangla Agricultural University. Data were recorded on ten randomly chosen plants of each genotype for each replication for different characters, such as days to first flowering, days to 50 % flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, seeds per siliqua, number of seeds per pod, 1000-seed weight (g) and seed yield per plant (g). This chapter consists of a short explication of position of the experimental site, materials used in the experiment, soil characteristics, layout and design of the experiment, plot preparation, seed sowing, manuring and fertilizing, intercultural practices, harvesting, data recording procedure and statistical analysis etc. which are submitted as follows:

3.1 Experimental site and duration

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during mid-November to mid-March. The location of the experimental site was situated at 230 74' N latitude and 900 35' E longitude with an elevation of 8.6 meter from the sea level. Photograph showing the experimental site (Appendix II).

3.2 Plant Materials

The experiment was conducted with 30 genotypes. The 30 genotypes of BC_1F_7 populations were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University. The materials of experiments are as follows (table 1).

Table 1. **Materials used for the experiment**

Genotype	BC_1F_7	Source
G_1	(Nap205×Nap0130) × Nap0130	SAU
G_2	(Nap108×Nap0130) × Nap108	SAU
G_3	(Nap108×Nap2066) × Nap2066	SAU
G_4	(Nap9905×Nap9901) × Nap9905	SAU
G5.	(Nap9908×Nap2066) × Nap9908	SAU
G6.	(Nap9908×Nap2066) × Nap9908	SAU
G7.	(Nap108×Nap9908) × Nap108	SAU
G8.	(Nap9905×Nap9908) × Nap9908	SAU
G9.	(Nap2066×Nap0130) × Nap2066	SAU
G10.	(Nap9905×Nap9908) × Nap9908	SAU
G11.	(Nap9906×Nap205) × Nap205	SAU
G12.	(Nap9905×Nap0130) × Nap9905	SAU
G13.	(Nap2066×Nap205) × Nap205	SAU
G14.	(Nap108×Nap9908) × Nap108	SAU
G15.	(Nap9905×Nap0130) × Nap0130	SAU
G16.	(Nap205×Nap0130) × Nap205	SAU
G17.	(Nap9906×Nap9901) × Nap9906	SAU
G18.	(Nap9905×Nap108) × Nap9905	SAU
G19.	(Nap108×Nap2066) × Nap108	SAU
G20.	(Nap9905×Nap2066) × Nap9905	SAU
G22.	(Nap108×Nap205) × Nap108	SAU
G23.	(Nap9901×Nap203) × Nap9901	SAU
G24.	(Nap2066×Nap0130) × Nap0130	SAU
G25.	(Nap9908×Nap0130) × Nap9908	SAU
G26.	(Nap2066×Nap205) × Nap2066	SAU
G27.	(Nap108×Nap0130) × Nap108	SAU
G28.	(Nap9908×Nap0130) × Nap0130	SAU
G29.	(Nap9905×Nap0130) × Nap9905	SAU
G30.	(Nap108×Nap0130) × Nap108	SAU

3.3 Climate and soil

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agroecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish-brown mottles. The pH was 5.47 to 5.63 and organic carbon content is 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.4 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 56m X 14m = 784 m^2. Each replication size was 56m X 3.5m, and the distance between replication to replication was 1m. Replication size and interspace between line to line was 1m and 30 cm. The spacing between row-to-row distance was 30 cm and distance between plant-to-plant distance was 30 cm. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that there were no clods on the seeds.

3.5 Methods

3.5.1 Land preparation

It was a well leveled land with proper drainage facility. Land preparation was done by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilt. Plot was leveled entirely. Rock, stubbles and weeds were dispelled gingerly. Finally, the plot was prepared for the seed sowing on date 10th November, 2018.

3.5.2 Fertilizer uses

Emphasis was given on basal application of FYM at the rate of 2-3 t/ha and N, P and K 50+30+30 kg/ha respectively. Organic and inorganic fertilizer viz. cow dung, Urea, TSP and MP fertilizers are required for mustard cultivation. Chemical fertilizers were applied at the rate of 220- 140-80-150-5 kg/ha of urea, Triple Super Phosphate (TSP), Muriate of Potash (MP), Gypsum and Zinc sulphate respectively. Cow dung was applied at the rate of five ton per hectare. The whole amount of TSP, MP, Gypsum, Zinc sulphate and 50% urea were applied as basal dose. The remaining 50% urea was applied as top dressing at flower initiation stage.

3.5.3 Sowing of seeds

Seeds of 30 lines were sown in separate line in the experimental field on mid-November, 2018 was the best time to sowing the Mastered seed. The measurement of sowing was perfect. The row spacing was 30cm having plant spacing 15 cm within the row. Variety to variety distance in each replication was 60 cm. Distance between replication was 50 cm. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds The seedlings emerged within four days.

Plate 1. Photograph showing the land preparation with *Brassica napus* L. in the experimental plot

Plate 2. Photograph showing the sowing the seeds of *Brassica napus* L. in the experimental plot

3.5.4 Irrigation and drainage

One pre-sowing irrigation was given in the field area. One irrigation either at 50% flowering was needed as dry field. One post sowing irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of soil to assure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period.

Plate 3. Photograph showing the irrigation of *Brassica napus* L. in the experimental plot

Plate 4. Photograph showing the drainage system of *Brassica napus* L. in the experimental plot

3.5.5 Weed management

Hand weeding was effective to control the weeds. Application of Isoproterenol at the rate of 0.75 kg ai/ha and Pendimethalin at the rate of 1.0 kg ai/ha to control the rabi weeds.

3.5.6 Intercultural operation, Insect and disease control

Thinning was accompanied with hoeing and weeding after 15-25 days of sowing to maintain plant population and plant growth. Also, Intercultural operation was needed to control disease and insect. It was done during the crop period to ensure normal growth and development of the plants. Thinning and 1st weeding were done after 15 days of sowing (plate 5). Top-dressing, weeding and necessary thinning were done after 25 days of sowing. Malataf was sprayed two times one just before flowering and the other of the middle of flowering for protecting the crop from the attack of aphids and Rovral-50 WP was sprayed at the rate of 20-g/10 L water first one at the time of siliquae setting of fruiting and second one after 15 days of 1st spraying to control Alternaria leaf spot. No remarkable disease attack was observed.

Plate 5. Photograph showing the thinning stage of *Brassica napus* L. in the experimental plot

3.5.7 Harvesting of sample plants

Harvest of the crop was early in the morning when 75-85 % siliqua was turned golden yellow in color. Then bundles and stack was in sun for 7-8 days. Threshing was done by separate seeds by winnowing. Then it was in store room when it showed moisture content about 8 percent. Harvesting was done in 10 March, 2019 and different dates was recoding according to the maturity (plate 7). when 80% of the plants showed symptoms of maturity i.e., straw color of siliqua, leaves, stem and desirable seed color in the matured siliqua, the crop was assessed to attain maturity. Ten plants were selected at randomly from BC_1F_7 populations in each replication. the sample plants were harvested by uprooting and then they were tagged properly. All parameters were recorded according to the ten number of plants characters (plate 6). In each replication, 10 plants were selected at randomly from the middle row of each plot.

3.6 Data Collection

Ten yield and yield components traits were taken into consideration for studying different genetic parameters. Data were recorded on ten randomly selected plants for each genotype.

(A) (B)

(C) (D)

Plate 6. A pictorial view observation and data collection (A. Seedling stage, B. Growth stage, C. Days to 50% flowering, and D. Siliquae formation stage,) in the experimental field of *Brassica napus* L.

(A)

(B)

Plate 7. Photograph showing (A. Pre-harvesting and B. The harvesting stage) of *Brassica napus* L. in the experimental plot

Quantitative traits:

During the present study data was recorded on 10 qualitative traits which are given in the following:

i. Days to first flowering: Days to 1st flowering was recorded when the 1st flowering plants had at least one open flower in each line. Flowering stage was shown in Plate 3.

ii. Days to 50% flowering: Days to 50% flowering were recorded from sowing date to the date of 50% flowering of every entry.

iii. Plant height (cm): Plant height was measured in centimeter (cm) from the base of the plant to the tip of the longest inflorescence and it was taken after harvesting.

iv. **Number of primary branches per plant:** Primary branches per plant was taken randomly from ten plants one by one. When primary branches arisen from the main stem, from the base of the plant to the starting point of the main raceme of the plant. And then average of the five plants was taken.

v. Number of secondary branches per plant: Number of branches originated from the primary branch from 10 randomly selected plants from each line at maturity.

vi. Number of siliquae per plant: Total number of siliquae of each plant was counted and considered as the number of siliques per plant.

vii. Siliquae length (cm): This measurement was taken in centimeter (cm) from the base to the tip of a siliqua of the five-representative siliqua.

viii. Number of seeds per siliqua: All siliqua from the sample plants was collected and 10 siliqua was randomly selected. Seeds obtained from them, were counted and average numbers of seeds per siliqua was recorded.

ix. 1000-seed weight (g): Weight in grams of randomly counted thousand seeds of each entry was recorded.

x. Seed yield per plant(g): All the seeds produced by a representative plant was weighed in g and considered as the seed yield per plant.

3.7 Statistical analysis

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTATC software program and then phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955). Path co-efficient analysis was done following the method outlined by Dewey and Lu (1995).

3.8 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula of Johnson *et al.*, (1955).

Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replications

Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$= Genotypic variance,

$\delta^2 e$ = Environmental variance = Mean square of error

3.9 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the following formula Burton (1952).

$$GCV = \frac{\sigma^2 g \times 100}{\bar{x}}$$

$$PCV = \frac{\sigma^2 p \times 100}{\bar{x}}$$

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population means

3.10 Estimation of heritability

Broad-sense heritability (h^2) was estimated by the ratio of the genotypic variance to the phenotypic variance. The heritability gives information on transmission of traits from parents to off springs hence aiding in selection.

$$h^2_b(\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, h^2_b = broad sense heritability

and σ^2_p = phenotypic variance and

σ^2_g = genotypic variance

3.11 Estimation of genetic advance

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

$$GA = \frac{\sigma^2 g}{\sigma^2 p} . K . \delta_p$$

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic standard deviation of the original population

K = Selection differential which is equal to 2.06 at 5% selection intensity.

3.12 Estimation of genetic advance in percentage of mean (%)

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Rabinson (1952).

Genetic Advance in percentage of mean = (Genetic advance/mean) × 100

3.13 Estimation of correlation co-efficient

Correlation is defined in so many ways but Simple correlation co-efficient (r) was estimated with the following formula Singh and Chaudhary (1985)

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{[\{\sum x^2 - \frac{(\sum x)^2}{N}\}\{\sum y^2 - \frac{(\sum y)^2}{N}\}]}}$$

Where, $\sum$ = Summation, x and y are the two variables correlated

N = Number of Observation

3.14 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1995) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992) using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable. In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yx1} = P_{y\times1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$

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

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

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

Total correlation, say between 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):

$P^2_{RY} = 1 - \sum P_{iy}. Riy$

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

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

R_{iy} = Correlation of the character with yield.

CHAPTER IV

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among 30 materials of *Brassica napus* L. genotypes and also to study the correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different characters such as days to 1st flowering, 50% flowering, plant height (cm), primary branches, secondary branches, siliqua per plant, seeds per siliqua, 1000 seed weight, seed yield per plant. The data were analysis and results obtained are following headings:

4.1 Estimation of variability, heritability and genetic advance of characters

4.2 Correlation coefficient analysis

4.3 Path coefficient analysis

4.1 Estimation of variability, heritability and genetic advance of characters

The results are pertained to analysis of variance (ANOVA), range, grand mean, CV%, mean performance, genotypic and phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2 b) and expected genetic advance as per cent of mean (GA) for all the ten traits are furnished in Table 2 to Table 5. Out of the ten traits studied, plant height, no. of primary branches per plant, no. of secondary branches per plant are considered as growth attributing characters. Days to 50% flowering and days to maturity were regarded as earliness attributes. No. of siliqua per plant, length of siliqua, no. of seeds per siliqua and 1000 seed weight were considered as reproductive traits. Yield per plant was the economic trait. The character wise details of these variability are discussed below of the genotypes evaluated for ten characters are presented in below.

Table 2. Estimation of genetic parameters for different characters in *Brassica napus* L.

Parameters	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	h^2	GA (5%)	GA (%mean)
Days to first flowering	2.49	0.93	1.56	5.61	3.43	37.33	1.21	4.32
Days to 50% flowering	5.21	2.39	2.82	7.10	4.81	45.92	2.16	6.72
Plant height (cm)	610.58	179.65	430.94	20.18	10.95	29.42	14.98	12.23
Primary branches	0.52	0.19	0.32	18.87	11.59	37.69	0.56	14.65
Secondary branches	0.47	0.23	0.24	25.39	17.68	48.49	0.68	25.36
Siliqua per plant	1042.04	316.49	725.55	20.91	11.53	30.37	20.20	13.08
Siliqua length (cm)	0.79	0.24	0.55	10.61	5.86	30.54	0.56	6.67
Seeds per Siliqua	13.62	7.48	6.14	16.44	12.18	54.92	4.18	18.60
1000 seed weight (g)	0.76	0.26	0.50	21.96	12.84	34.15	0.61	15.45
Seed yield per plant(g)	11.23	6.63	4.60	31.20	23.97	59.04	4.07	37.94

Where, σ^2_p = Phenotypic variance
σ^2_g = Genotypic variance
σ^2_e = Environmental variance
h^2 = Heritability
GCV = Genotypic Coefficient of Variation
PCV = Phenotypic Coefficient of Variation
GA (5%) = Genetic Advance (5%)
GA (% mean) = Genetic Advance (% mean)

Table 3. Analysis of variance for different characters in *Brassica napus* genotypes

Parameters	Mean sum of square		
	Replications (df=2)	**Genotypes (df=29)**	**Error (df=58)**
Days to first flowering	1.48	4.34*	1.56
Days to 50% flowering	2.98	9.99**	2.82
Plant height (cm)	472.68	969.87*	430.94
Primary branches	0.73	0.91*	0.32
Secondary branches	0.17	0.92**	0.24
Siliqua/plant	1355.78	1675.01*	725.55
Siliqua length (cm)	0.23	1.27**	0.55
Seeds/Siliqua	0.05	28.59**	6.14
1000 seed weight (g)	0.33	1.28*	0.50
Seed yield per plant(g)	7.38	24.48**	4.60

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

4.1.1 Days to 1st flowering

The genotypes revealed the significant variation in days to 1st flowering (4.34**) (Table 3). The data range was recorded from 26.33 to 30.33 for this trait (Table 4). The maximum days to 1st flowering was observed in 5 genotypes (Table 5). The (Nap-9905×Nap-0130) × Nap-9905 showed the first flowering for the minimum time of 26.33 days and the maximum 30.33 days was found in the genotypes (Nap-9906×Nap-205) × Nap-205, (Nap-2066×Nap-205) × Nap-205, (Nap-108×Nap-9908) × Nap-108, and in the (Nap-2066×Nap-205) × Nap-2066(Table 5). Sing *et al.* (2001) studied different morpho-physiological characters of 29 genotypes of *Brassica napus* grown under normal and stress condition of production. They found the existence of significant genetic variability for days to 50% flowering.

The genotypic variance (0.93) was lower than phenotypic variance (2.49) along with the environmental differences (1.56) (Table 2). Thus, genes controlling this trait possessed considerable influence of environment on the expression of the character. The range of PCV (5.61) was higher than the GCV (3.43) (Table 2) for 1st flowering which indicated that the character was influenced by genotypes and environment both.

The days to 1st flowering exhibited moderate heritability (37.33%) with low genetic advanced (1.21%) and genetic advanced in percentage of mean (4.32%) indicated that this trait was controlled by non-additive gene (Table 2).

Table 4. Range, mean, CV (%) and standard deviation of ten characters of *Brassica napus* L.

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Days to first flowering	26.33	30.33	28.09	4.44	1.57	0.72
Days to 50% flowering	29.33	35.33	32.14	5.22	2.27	0.97
Plant height (cm)	98.15	183.07	122.42	16.96	24.65	11.99
Primary branches	3.06	5.47	3.81	14.90	0.72	0.33
Secondary branches	1.4	4.0333	2.70	18.22	0.68	0.28
Siliqua per plant	120.13	223.87	154.36	17.45	32.39	15.55
Siliqua length (cm)	7.07	9.49	8.38	8.84	0.88	0.43
Seeds per Siliqua	17.31	30.453	22.45	11.04	3.65	1.43
1000 seed weight (g)	3.1	5.4	3.97	17.82	0.87	0.41
Seed yield per plant(g)	7.027	19.593	10.74	19.97	3.34	1.24

CV (%) = coefficient of variation, SD= standard deviation and SE= standard error

4.1.2 Days to 50% flowering

Dayes of 50% flowering was observed with substantial contrast among 30 genotypic characters. Data mentioning days to 50% flowering showed significant difference amongst the breeding materials (9.99**) (Table 3). The range of data was found from 29.33 to 35.33 (Table 4). Genotype (Nap-9905×Nap-0130) ×Nap- 9905 showed the 50% flowering for the lowest 29.33 days and the highest 35.33 days in the genotype (Nap-9908×Nap-2066) ×Nap- 9908 (Table 5). The days to 50% flowering were observed in varieties 39.33 days in BARI-8. Singh *et al.,* (2005) obtained earliness on YSK-S501 × SS-2 in *Brassica campestris/rapa*. Singh *et al.,* (1997) observed earliness in PR-1108 × BJ1235 in *Brassica juncea* L.

The genotypic variance (2.39) was lower than phenotypic variance (5.21) with environmental differences (1.56) (Table 2). This result suggested that the possibility of predominance of additive gene, which have an extensive scop to promote. The range of PCV (7.10) was higher than the GCV (4.81) (Table 2) for 50% flowering which indicated that, there was a moderate influence of environment on the expression of the gene. The days to 50% flowering exhibited moderate heritability (45.92%) with low genetic advanced (2.16%) and genetic advanced in percentage of mean (6.72%) indicated that this trait was controlled by non-additive gene (Table 2). In the contrary, Niraj and Srivastava (2004) and Hosen (2008) reported that days to 50% flowering showed high heritability with genetic advance in percentage of mean. The flowering trait of the plant is moderate sensitive and influenced by the environmental temperature fluctuation which is reflected in the present study.

Table 5. Mean performance of 30 genotypes of *Brassica napus* L. in BC_1F_7 population

Genotypes	Dayes to first flowering	Dayes to 50% Flowering	Plant height (cm)	Primary branches	Seconda-ry branches	Siliqua/pla-nt	Siliqua length (cm)	Seeds/Sil-iqua	1000 seed weight (g)	Seed yield per plant(g)
G1	28.33a-f	34.33abcd	102.90ef	3.73c-g	2.63cdef	184.93abcd	8.15b-i	25.00b-f	3.27g	13.19cdef
G2	27.00def	30.33gh	149.72abc	3.10fg	2.83bcde	168.43cde	8.35a-h	17.31j	3.30g	9.16ghij
G3	27.00def	31.00efgh	98.15f	3.23efg	2.13e-i	120.13f	7.97c-i	27.59abc	4.13b-g	8.93ghij
G4	27.00def	31.00efgh	114.27def	3.77c-g	3.13bcd	141.76def	8.16b-i	20.77hij	4.80abcd	8.36ij
G5	29.00abcd	35.33a	111.18def	3.06g	2.60c-g	135.27ef	9.12abc	21.57e-i	4.74a-e	10.53e-j
G6	27.00def	29.67gh	127.16cdef	3.70c-g	2.37d-h	149.31cdef	7.08i	23.61c-h	3.61efg	10.63d-i
G7	29.33abc	33.33a-f	108.51def	3.80c-g	3.23abc	136.67ef	9.21ab	25.68bcd	3.48fg	9.38ghij
G8	26.67ef	29.33h	116.87cdef	3.90c-g	2.63cdef	162.81cdef	8.82a-e	19.51ij	3.67defg	10.08f-j
G9	28.00b-f	32.00c-h	118.23cdef	4.53bc	1.67hi	138.53ef	7.46ghi	20.61hij	3.87c-g	8.83ghij
G10	28.33a-f	31.67d-h	113.27def	3.77c-g	2.97bcd	154.03cdef	8.89a-e	20.67hij	4.10c-g	8.19ij
G11	29.67ab	33.67a-e	119.98cdef	3.93c-g	3.13bcd	150.10cdef	8.91a-e	20.4hij	3.60efg	9.06ghij
G12	26.33f	30.00gh	123.20cdef	3.33efg	2.10e-i	151.20cdef	7.90d-i	22.59d-i	3.37fg	10.36e-j
G13	29.67ab	34.67abc	116.52cdef	3.40defg	3.20bc	152.17cdef	8.72a-f	30.45a	5.40a	19.59a
G14	29.67ab	34.33abcd	120.22cdef	4.30bcd	2.70b-f	147.50cdef	7.31hi	22.28d-i	3.63efg	9.83f-j
G15	29.33abc	34.33abcd	132.90cde	3.83c-g	2.70b-f	172.22bcde	7.59fghi	19.45gij	4.17b-g	12.06c-h
G16	30.33a	34.67abc	120.92cdef	3.83c-g	3.37abc	186.57abc	7.82d-i	20.93ghij	3.44fg	12.23c-g
G17	29.67ab	35.00ab	107.97def	3.87c-g	1.97fghi	128.33ef	9.02abcd	20.77hij	3.33fg	7.03j
G18	27.67b-f	31.67d-h	119.60cdef	3.73c-g	2.57c-g	170.43bcde	7.92c-i	25.08bce	3.93c-g	10.90d-i
G19	27.00def	31.67d-h	114.17def	4.00cdef	2.63cdef	136.83ef	8.50a-h	28.40ab	3.30g	14.05bcd

Table 5. (Cont'd)

Genotypes	Dayes to first flowering	Dayes to 50% flowering	Plant height	Primary branches	Secondary branches	Siliqua/Plant	Siliqua length(cm)	Seeds/Siliqua	1000 seeds weight	Seed yield per plant(g)
G20	27.67b-f	30.67fgh	119.23cdef	3.83c-g	1.40i	144.00cdef	8.61a-g	20.98f-j	4.94abc	10.21e-j
G21	27.00def	30.67fgh	115.67def	4.31bcd	2.97bcd	153.24cdef	8.37a-h	19.80hij	3.90c-g	10.22e-j
G22	28.67a-e	33.67abcde	169.84ab	3.20efg	2.63cdef	152.40cdef	9.01abcd	24.84b-g	3.10g	7.92ij
G23	26.67ef	32.00b-h	115.49def	3.591deg	1.81ghi	134.67ef	9.49a	26.19bcd	3.83c-g	8.66hij
G24	29.33abc	32.33b-g	123.65cdef	5.46a	2.73b-f	223.87a	9.21ab	20.74hij	5.28ab	17.20ab
G25	29.67ab	34.00abcd	114.79def	3.10fg	3.47ab	122.27f	8.95a-e	24.88b-g	4.48a-f	9.99f-j
G26	27.33cdef	30.33gh	129.63cdef	4.03cde	2.90bcde	147.07cdef	7.50ghi	19.91hij	4.83abc	8.77ghij
G27	28.00b-f	30.67fgh	119.78cdef	3.73c-g	3.00bcd	145.63cdef	9.01abcd	20.41hij	4.73a-e	7.77ij
G28	26.67ef	30.67fgh	183.07a	3.47defg	2.70b-f	155.07cdef	7.78e-i	19.91hij	3.18g	10.29e-j
G29	27.00def	30.67fgh	106.59def	3.50defg	2.74b-f	151.54cdef	8.64a-g	23.27d-i	4.11c-g	15.13bc
G30	27.67b-f	30.67fgh	139.02bcd	5.20ab	4.03a	213.73ab	7.99c-i	19.93hij	3.61efg	13.65cde
Maximum	30.33	35.33	183.07	5.46	4.03	223.87	9.49	30.45	5.40	19.59
Minimum	26.33	29.33	98.15	3.06	1.4	120.13	7.07	17.31	3.1	7.02
LSD (0.05)	0.2213	1.3704	16.950	0.4634	0.4015	21.993	0.5050	1.0234	0.5780	2.073

4.1.3 Plant height (cm)

Plant height was significantly influenced by different genotypes (969.87*) (Table 3). The regarding data was ranged from 98.15 to 183.07 (Table 4). The highest height of the plant was recorded in (Nap-9905×Nap-0130) × Nap-99051 (183.07) (183.07) and the lowest height was recorded in (Nap-205×Nap-0130) × Nap-0130 (98.15) (Table 5). The nearest result was also found by Iqbal *et al.,* (2014), Ali *et al.,* (2003) and Ivanovska *et al.,* (2007) elaborated the highest genotypic and phenotypic values of variances for plant height. Analysis of variance showed highly significant results for plant height among different genotypes. The range of plant height means lied between 240.67 cm and 77.23 cm. Plant height mean value of Napus-2 was maximum while Rainbow accession had the minimum value of mean of plant height. There was significant relation of Napus-2 with all other accessions.

The genotypic variance (179.65) was lower than phenotypic variance (610.58) with environmental differences (430.94) (Table 2). The range of PCV (20.18) was higher than the GCV (10.95) (Table 2) for plant height which indicated that, there was a moderate influence of environment on the expression of the gene.

Among the 30 genotypes, the trait plant height exhibited moderate heritability (29.42%) with low genetic advanced (14.98%) and genetic advanced in percentage of mean (12.23%) indicated that selection (Table 2). Which revealed that the character was influenced by the environmental effects with predominance of additive gene action in the inheritance of this trait and it could be enhanced through selection process.

4.1.4 Number of primary branches per plant

Regarding to 30 number of materials, the number of primary branches per plant was observed. The number of primary branches per plant was significantly influenced by different genotypes (0.91**) (Table 3). The range was from 5.47 to 3.06 (Table 3). The highest number of primary branches was found in the (Nap-2066×Nap-0130) × Nap-2066 (5.47) (Table 5) among the 30 numbers of genotype and two genotypes had shown the lowest number of primary branches in (Nap-108×Nap-0130) × Nap-108 and another (Nap-2066×Nap-205) × Nap-2066 to obtaining (3.06) (Table 5). Khan *et al.,* (2000) Was illustrated the significant variation between primary branches of a plant and seed yield in different genotypes in the analysis of variance. Where means for primary

branches of different accessions are arranged in descending sequence from 6.6667 was the maximum value of mean of accession while 4.000 was the minimum value of mean of Zn-M-9 accession.

The genotypic and phenotypic variance was observed as 0.19 and 0.52 respectively. Whereas, the phenotypic co-efficient of variation (PCV) (18.87) was higher than the genotypic co-efficient of variation (GCV) (11.59) (Table 2). Which indicated that there was a moderate influence of environment on the expression of the genes. According to Mekonnen *et al.,* (2014) assessed that number of primary branches per plant exhibited comparatively high genotypic and phenotypic coefficient of variation.

The number of primary branches exhibited moderate heritability (37.69%) with low genetic advanced (0.56%) and genetic advanced in percentage of mean (14.65%) indicated that this trait was controlled by non-additive gene (Table 2), which proved that the additive gene has the lower possibility to predominance in the inheritance of this trait.

4.1.5 Number of Secondary branches per plant

Among the 30 genotypes, the number of secondary branches per plant was observed. The number of secondary branches per plant was significantly influenced by different genotypes (0.92^{**}) (Table 3). The range was from 4.03 to 1.4 (Table 4). Among the materials the highest number of secondary branches was observed in the (Nap-9905×Nap-9901) × Nap-9905 for obtaining the highest number 4.30 (Table 5) and the lowest number of secondary branches was observed in the (Nap-9905×Nap-2066) × Nap-9905 for acquiring the lowest value 1.4 (Table 5). Means for secondary branches were ranged from 19.333 to 3.000. Zn-M-6 genotype had the maximum range of mean, while Cyclone genotype had minimum range of mean value. Sadat *et al.,* (2010) and Ullah *et al.,* (2015) computed significant variation for secondary branches among various genotypes.

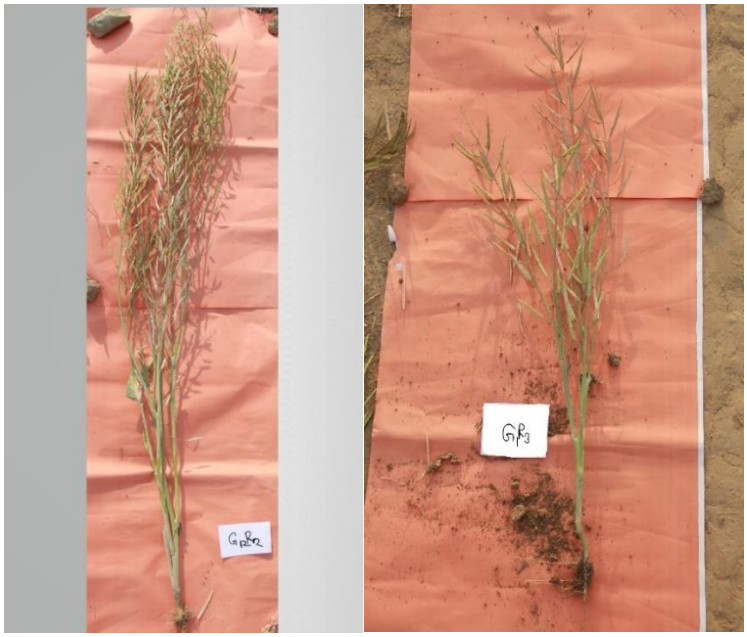
The genotypic and phenotypic variance for the number of secondary branches per plant was observed 0.23 and 0.47 respectively. The value of PCV was higher than GCV were found as 25.39 and 17.68, respectively (Table 2). Which indicated that a slight environmental influence was shown for the expression of this character. High GCV and PCV also observed for number of secondary branches per plant by Choudhary *et al.,* (2003).

The high heritability (37.69%) for this trait with low genetic advanced (0.68%) and moderate genetic advanced in percentage of mean (25.36%) (Table 5), which revealed that the high heritability with low genetic advance and moderate genetic advance as percent of mean indicates that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. In contrary, Parveen (2007), Ghosh and Gulati (2001) found the high heritability coupled with high genetic advance for this trait.

4.1.6 Number of siliquas per plant

Numbers of siliqua per plant was significantly influenced by different genotypes (1675.01**) (Table 3). The range of this trait was observed from 223.87 to 120.13 (Table 4). Among the 30 materials, the highest number of siliquas per plant was observed in the (Nap-9908×Nap-0130) × Nap-9908 line (Table 5) for getting the range of maximum number of siliqua 223.87 and the second highest for number of siliquas per plant was found in the (Nap-9905×Nap-9901) × Nap-9905 line (213.73) (Table 5). The lowest number of siliquas per plant was observed in the (Nap-108×Nap-2066) × Nap-2066 for the minimum range of (120.13) (Table 5). Where the almost nearest value was found by Shiralee accession had maximum mean of 357 while Zm-21 accession had minimum mean value of 137. Awal *et al.,* (2015) and Rout *et al.,* (2018) elaborated the highest genotypic and phenotypic values of variances for plant height.

The genotypic and phenotypic variance for the number of siliquae per plant was observed 316.49 and 1042.04 respectively with large environmental differences (725.55) (Table 2). The value of PCV was higher than GCV were found as 20.91 and 11.53, respectively (Table 2) indicated existence of variation among the materials. Similar result was also reported by Khan *et al.,* (2013). Mekonnen *et al.,* (2014) observed comparatively high PCV for this trait.



G12 **G1**

(Nap-9905×Nap-0130) × Nap-9905 **(Nap-205×Nap-0130) × Nap-0130**

Plate 8. Photograph showing variation between highest and lowest number of plant height

G9 **G7**

(Nap-2066×Nap-0130) × Nap-2066 **(Nap-108×Nap-0130) × Nap-108**

Plate 9. Photograph showing variation number of primary branches per plant

G4 **G20**

(Nap-9905×Nap-9901) × Nap-9905 **(Nap-9905×Nap-2066) × Nap-9905**

Plate 10. Photograph showing variation number of secondary branches per plant

G7 **G24**

(Nap-108×Nap-2066) × Nap-2066 **(Nap-9908×Nap-0130) × Nap-9908**

Plate 11. Photograph showing variation numbers of siliqua per plant

The high heritability (30.37%) for this trait with moderate genetic advanced (20.20%) and genetic advanced in percentage of mean (13.08%) (Table 2) that, the high heritability with moderate genetic advanced indicating the trait performance could be enhanced through selection process and the character was influenced by the environmental effects. So, these traits could be exploited for further improvement through selection procedures. It was also reported by Alam *et al.,* (2010) founded that, the pods per plant had moderately high GCV and genetic advance and high heritability.

4.1.7 Length of siliqua (cm)

This trait was significantly influenced by different genotypes (1.27^{**}) (Table 3). And the range of this trait was observed from 9.49 to 7.07(cm) (Table 4). The maximum length 9.49 cm was found in the (Nap-2066×Nap-0130) × Nap-0130 (Table 5) and the second maximum length was found in two genotypes followed by (Nap-108×Nap-9908) × Nap-108 (Table 5) and (Nap-9908×Nap-0130) × Nap-9908 (Table 4) for gaining the value 9.12 (cm). And the lowest length was audited in the (Nap-9908×Nap-2066) × Nap-9908 (Table 4) by obtaining value 7.08 (cm) (Table 5). Where almost the nearest value was found by Shiralee accession had maximum mean of 357 while Zm-21 accession had minimum mean value of 137. Awal *et al.,* (2015) and Rout *et al.,* (2018) elaborated the highest genotypic and phenotypic values of variances for plant height.

The genotypic and phenotypic variance for the number of siliquae per plant was observed 0.24 and 0.79 respectively with environmental differences (0.55) (Table 2). The value of PCV was higher than GCV were found as 10.61 and 5.86, respectively (Table 2) indicated existence of variation among the materials.

The moderate heritability (30.54%) for this trait with low genetic advanced (0.56%) and genetic advanced in percentage of mean (6.67%) (Table 2) indicated that, non-additive gene controlled this trait. Labowitz (1989) studied *Brassica campestris* population for pod length and observed high genetic variation on this trait. Olsson (1990) found high genetic variability for this trait.

G24 **G5**

(Nap-2066×Nap-0130) × Nap-0130 **(Nap-9908×Nap-2066) × Nap-9908**

Plate 12. Photograph showing the maximum and minimum length of siliqua

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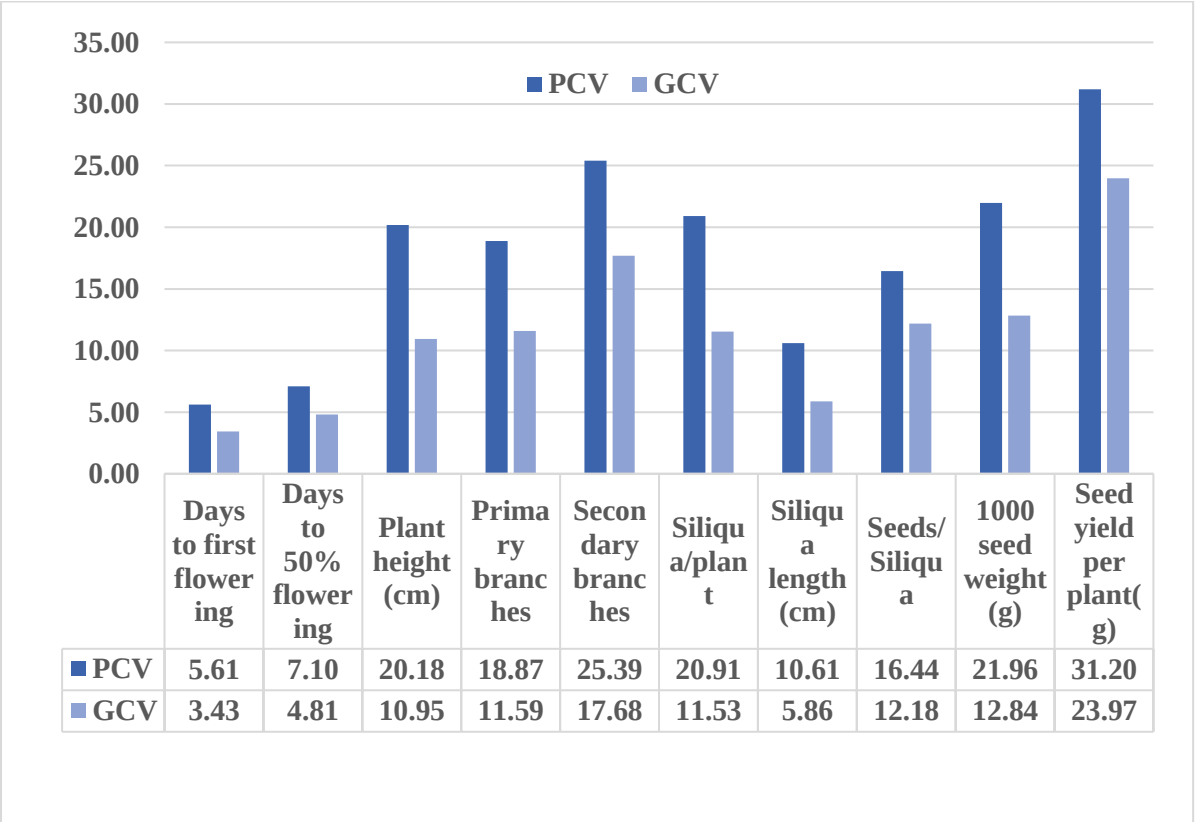

	Days to first flowering	Days to 50% flowering	Plant height (cm)	Primary branches	Secondary branches	Siliqua/plant	Siliqua length (cm)	Seeds/ Siliqua	1000 seed weight (g)	Seed yield per plant(g)
PCV	5.61	7.10	20.18	18.87	25.39	20.91	10.61	16.44	21.96	31.20
GCV	3.43	4.81	10.95	11.59	17.68	11.53	5.86	12.18	12.84	23.97

Figure 2. Genotypic and phenotypic coefficient of variation in *Brassica napus* L.

4.1.8 Number of seeds per siliqua

The data of number of seeds per siliqua was exhibited significantly influenced by different genotypes (28.59**) (Table 3). The range of this trait was observed from 30.45 to 17.31 (Table 4). The number of seeds Per siliqua range was contained from 17.31 to 30.45. As, in most cases the yield depends on the number of seeds per siliqua, so the number of parameters was observed at least at two positions. The highest number of seeds per siliqua was found in the (Nap-2066×Nap-205) × Nap-205 (30.45) (Table 4). The second highest position was found in the (Nap-108×Nap-2066) × Nap-108 (28.40) (Table 5). And the lowest number was observed in the (Nap-108×Nap-0130) × Nap-108 (17.31) (Table 5). The nearest result was found from Mondal *et al.,* (1992), Podder *et al.,* (1996) also reported that the varieties Daulat and Rai-5 were highly responsive and stable under a wide range of sowing time. The maximum seeds per siliqua (24 and 25) were found from Nap-0538.

In the genotypic and phenotypic variance, the range number of seeds per siliqua was observed 7.48 and 13.62 respectively with environmental differences (6.14) (Table 2). The PCV and GCV were found as 16.44 and 12.18, respectively (Table 2) indicated existence of variation among the materials. It indicates that in 30 different genotypes the moderate variation subsisted between them (Table 2).

The high heritability (54.92%) for this trait with low genetic advanced (4.18%) and genetic advanced in percentage of mean (18.60%) (Table 2) indicated that, this character was controlled by additive gene and selection for this trait would be effective. Acharya and Swain (2004) was observed the maximum number of seeds per siliqua in BM 20-12-3×Pusa Bahar in *Brassica juncea.*

4.1.9 Thousand seed weight (gm)

Significant differences were recorded all the genotypes for this trait (1.28**) (Table 3). The number of thousand seed weight's range was observed from 3.1 to 5.4 (Table 4). The maximum thousand seed weight was found in the (Nap-9905×Nap-2066) × Nap-9905 (Table 5) by obtaining the range 4.94(gm). As the seeds weight carry the total number of yields, so the highest number was counted more than one material. So, the second highest position was found in the (Nap-108×Nap-0130) × Nap-108 (4.83gm)

(Table 5). And the third highest position was found in the (Nap-9908×Nap-2066) × Nap-9908 (Table 4) by gaining the range of 4.74 (gm). At last, the lowest number was found in the (Nap-9901×Nap-203) × Nap-9901 (Table 5) by getting the minimum value 3.10(gm) for thousand seed weight. Singh *et al.,* (2000) observed on more seed weight per plant in YSC-68 × SS-2 in *Brassica campestris* L. Chowdhury *et al.,* (2004) obtained the highest seed weight in Dhali × Sampad in *Brassica rapa* L.

Genotypic and phenotypic variance was observed 0.26 and 0.76 respectively with environmental differences (0.50) (Table 2). The phenotypic co-efficient of variation and genotypic co-efficient of variation were found as 21.96 and 12.84, respectively (Table 2) indicating among the materials the differences between PCV and GCV had the major environmental variation of this character (Table 2).

The moderate heritability (34.15%) for this trait with low genetic advanced (0.61%) and genetic advanced in percentage of mean (15.45%) (Table 2) indicated that, the moderate possibility of selecting genotypes for this trait.

4.1.10 Seed yield per plant (gm)

Among the genotypes significant differences were recorded for this trait (24.48^{**}) (Table 3). The range of number of seed yield per plant was recorded from 7.02(gm) to 19.59(gm) (Table 4). As the total yield is fully depends on the seed yield per plant so the data was recorded in more than one material. The highest amount of seed yield per plant was found in the (Nap-2066×Nap-205) × Nap-205 (19.59) gm (Table 5). The second maximum and the third maximum amount was recorded in (Nap-9908×Nap-0130) × Nap-9908(17.20gm), (Nap-108×Nap-0130) × Nap-108 (15.13gm) genotypes (Table 5). And the lowest amount of seed yield per plant was observed in the (Nap-9906×Nap-9901) × Nap-9906 (7.03 gm) genotype (Table 5). Similarly, the highest seed yield was also observed in the hybrid Nap-9905×Nap-205 (107.54 g) which was almost 3 times highest than both its parent. Iqbal *et al.,* (2014) was obtained over dominance in *Brassica rapa*. Farshad far *et al.,* (2011) also reported the effectiveness of over dominance for seed yield per plant in *Brassica napus*.

Genotypic and phenotypic variance was observed 6.63 and 11.23 respectively with environmental differences (0.50) (Table 2) indicated a slight environmental influence for this trait. The PCV and GCV was observed 31.20 and 23.97 respectively with

environmental differences (0.50) (Table 2) indicating among the materials the differences between PCV and GCV had the major environmental variation of this character (Table 2).

The high heritability (59.04%) for this trait with low genetic advanced (4.07%) and high genetic advanced in percentage of mean (37.94 %) (Table 2) indicated that, the lower possibility of selecting genotypes but high genetic advanced in percentage of mean which indicated that possibility of predominance of additive gene, which have an extensive scop to promote.

4.2 Correlation coefficient analysis

The analysis of the relationship among those traits are highly associated with seed yield. Genotypic and phenotypic correlation coefficients among 10 characters were presented in Table 6.

4.2.1 Days to 1st flowering

Among the 30 genotypes the days to 1st flowering was noticed a highly significant and positive correlation with days to 50 % flowering where, (G =0.908**, P = 0.844**) for genotypic and phenotypic correlation, this indicated that if days to 1st flowering increased then days to maturity also increased besides, it noticed the negative and significant correlated with plant height (cm) (G = -0.306) in genotypic correlation and (P = -0.043) in phenotypic correlation (Table 6). As the correlation was significant and negative so the association between two characters was low, indicated that it will not be beneficial for breeders.

It also shown the insignificant and positive correlation with primary branches per plant for genotypic and phenotypic correlation (G = 0.108, P= 0.123) and with siliqua per plant for genotypic and phenotypic correlation (G = 0.015, P= 0.194) (Table 6). Among these traits, insignificant association of these traits indicated that the association between this trait was largely influenced by environmental factors. However, it had significant and positive correlation with secondary branches (G = 0.455**, P= 0.198), siliqua length (G = 0.215*, P= 0.201), 1000 seed weight (G = 0.232*, P= 0.107) and seed yield per plant (G = 0.119*, P= 0.110) (Table 6) indicated that, the traits were governed by same gene and simultaneous improvement would be effective.

Table 6. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus*.

Character		DFF	D50% F	PH (cm)	NPBP	NSBP	NSP	SL (cm)	NSS	TSW(g)	SYP(g)
DFF	r_g	1									
	r_P	1									
D50%F	r_g	0.908**	1								
	r_P	0.844**	1								
PH (cm)	r_g	-0.306**	-0.314**	1							
	r_P	-0.043	-0.074	1							
NPBP	r_g	0.108	-0.193	-0.186	1						
	r_P	0.123	-0.042	0.039	1						
NSBP	r_g	0.455**	0.211*	0.206	0.012	1					
	r_P	0.198	0.075	0.072	0.280**	1					
NSP	r_g	0.015	-0.195	0.313**	0.623**	0.370**	1				
	r_P	0.194	0.065	0.239*	0.607**	0.397**	1				
SL (cm)	r_g	0.215*	0.304**	-0.351**	-0.400**	-0.046	-0.492**	1			
	r_P	0.201	0.187	0.042	-0.042	0.128	0.093	1			
NSS	r_g	-0.006	0.277**	-0.648**	-0.503**	-0.158	-0.643**	0.113	1		
	r_P	0.131	0.249*	-0.124	-0.124	0.005	-0.085	0.232*	1		
TSW (g)	r_g	0.232*	0.051	-0.500**	0.297**	0.092	0.123	0.297**	0.035	1	
	r_P	0.107	-0.004	0.002	0.002	0.013	-0.085	0.138	0.068	1	
SYP (g)	r_g	0.119*	0.106	-0.160	0.297**	0.260*	0.589**	-0.170	0.325**	0.378**	1
	r_p	0.110	0.194	-0.036	0.283**	0.293**	0.489**	0.142	0.403**	0.277**	1

** = Significant at 1%, * = Significant at 5% respectively, NS=Non significant

DFF : Dayes to 1st flowering
D50%F : Days to 50% flowering
PH (cm) : Plant height (cm)
NPBP : Primary branches per plant
TSW(g) : 1000seedweight(g)
NSBP : Secondary branches per plant
NSPP : Siliqua per plant
LS (cm) : Length of siliqua (cm)
NSPS : Seed per siliqua
SYP(g) : Seed yield per plan

4.2.2 Days to 50% flowering

Regarding to 30 number of materials, the days to 50% flowering was a highly significant and positive correlation with seeds per siliqua where, (G =0.277**, P = 0.249*) for genotypic and phenotypic correlation, this indicated that if days to 50% flowering increased then seeds per siliqua also increased besides, it also noticed the significant and negative correlated with plant height (cm) (G = -0.314) for genotypic correlation and (P = -0.074) for phenotypic correlation (Table 6). As the correlation was significant and negative so the association between two characters was low, indicated that it will not be beneficial for breeders.

It also shown the insignificant and positive correlation with seed yield per plant per (G =0.106, P= 0.194) for genotypic and phenotypic correlation and insignificant and negative correlation with primary branches per plant (G = -0.193, P= -0.042) (Table 6) for genotypic and phenotypic correlation that revealed clearly the independent nature of those characters. However, it had significant and positive correlation with secondary branches per plant (G = 0.211*, P= 0.075) and siliqua length(cm) (G = 0.304**, P= 0.187) (Table 6) indicated that, the traits were governed by same gene and simultaneous improvement would be effective. The insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.,* (1998).

4.2.3 Plant height (cm)

Plant height was a highly significant and positive correlation with siliqua per plant where, (G =0.313**, P = 0.239*) for genotypic and phenotypic correlation, indicated that if plant height increased then the numbers of siliqua per plant also increased and the traits were governed by same gene. Besides, it had negative correlated with siliqua length (cm) (G = -0.351**, P = -0.112), seeds per siliqua (G = -0.648**, P = -0.075) and thousand seed weight (G = -0.500**, P = -0.186) for genotypic correlation and phenotypic correlation (Table 6), as the correlation was significant and negative so the association between two characters was low, indicated that it will not be beneficial for breeders.

However, it had insignificant and positive correlation with secondary branches per plant (G =0.206, P= 0.072) and negative correlation with seed yield per plant (G =-0.160, P= -0.036) for genotypic and phenotypic correlation (Table 6). That revealed clearly the independent nature of those characters. Shalini *et al.,* (2000) also observed that plant height was highly associated with seed yield. A similar result was reported by Srivastava *et al.,* (1983). A significant positive correlation between plant height and seed yield was found by Verma and Sachan (2000). Chaudhary *et al.,* (1990) found a positive correlation of plant height with the number of seed per siliqua, number of siliquas per plant.

4.2.4 Number of primary branches per plant

This trait had the highly significant and positive correlation with siliqua per plant where, (G =0.623**, P = 0.607**) and seed yield per plant (G =0.297**, P = 0.283**) for genotypic and phenotypic correlation indicated that if the number of primary branches per plant height increased then the seed yield per plant numbers of siliqua per plant also increased. Besides, it had negative correlation with siliqua length (cm) (G = -0.400**, P = -0.042), seeds per siliqua (G = -0.503**, P = -0.124) (Table 6). However, it had significant and positive correlation with secondary branches per plant (G = 0.012, P = 0.280**) and thousand seed weight (G = 0.297**, P = 0.002) for genotypic correlation and phenotypic correlation (Table 6) indicated that, the traits were governed by same gene and simultaneous improvement would be effective. Highly significant differences among the genotypes for most of the traits were revealed by Abideen *et al.,* (2013).

4.2.5 Number of secondary branches per plant

Number of secondary branches per plant had shown the highly significant and positive correlation with siliqua per plant where, (G =0.370**, P = 0.397**) and seed yield per plant (G =0.260**, P = 0.293**) for genotypic and phenotypic correlation (Table 6) indicated that if the number of secondary branches per plant increased then the numbers of siliqua per plant also increased. Besides, it had insignificant and positive correlation with thousand seed weight (G =0.092, P = 0.013) indicated that association of these traits indicated that the association between these traits were largely influenced by environmental factors.

4.2.6 Number of siliquas per plant

Among the 30 genotypes of *Brassica napus* L. the number of siliquas per plant had shown the highly significant and positive correlation with seed yield per plant (G =0.589**, P = 0.489**) for genotypic and phenotypic correlation (Table 6) indicated that if the numbers of siliqua per plant increased then the number of seeds per plant must be increased. Besides, it had the negative correlation with seeds per siliqua (G =-0.643**, P = -0.077) (Table 6) for genotypic and phenotypic correlation. So, the association of these traits indicated that the association between these traits were largely influenced by environmental factors. Khan *et al.,* (2000) also notified the significant positive relationship among silique of a plant with seed yield.

4.2.7 Siliqua length (cm)

Siliqua length (cm) had shown the significant and positive correlation with seeds per siliqua (G =0.113, P = 0.232*) and thousand seed weight (G =0.297*, P = 0.138) for genotypic and phenotypic correlation (Table 6) indicated that the trait was governed by same gene and simultaneous improvement would be effective. Nasim *et al.* (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant and positive interaction with seed yield per plant (G = 0.325**, P= 0.403**) indicated that if seeds per siliqua increased than seed yield per plant must be increased. Besides, it had shown the insignificant and positive interaction with thousand seed weight (G = 0.035, P= 0.068) (Table 6) for genotypic and phenotypic correlation. This discussion of positive correlation of seeds of a silique and yield of a plant presented by the Lodhi *et al.,* (2014).

4.2.9 Thousand seeds weight

Among the ten characters, the thousand seed weight showed highly significant and positive interaction with seed yield per plant (G = 0.325**, P = 0.277**) (Table 6) for genotypic and phenotypic correlation indicated that if the thousand seed weight increased than the seed yield per plant must be increased insignificant and positive interaction with primary branches per plant (G = 0.297, P = 0.002) (Table 6). And highly significant and positive interaction had

shown with the siliqua length (G = 0.297) and significant and positive interaction with siliqua length (P = 0.138) (Table 6).

4.2.10 Seed yield per plant

Number of seeds per siliqua showed highly significant and positive interaction had shown with primary branches per plant (G = 0.297, P= 0.283), secondary branches per plant (G = 0.260, P= 0.293), siliqua per plant (G = 0.589, P= 0.489), seeds per siliqua (G = 0.325, P= 0.403), and thousand seeds weight (G = 0.378, P= 0.277) (Table 6).

4.3 Path Co-efficient analysis (PCV)

A path coefficient indicates the direct effect of a variable assumed to be a cause on another variable assumed to be an effect. Path coefficients are standardized because they are estimated from correlations (a path regression coefficient is unstandardized).

Simple correlation does not consider the complex relationships between the various traits related to the dependent variable. Correlation coefficients show relationships among independent variables and the linear relationship between these variables. But it is not sufficient to describe these relationships when the causal relationship among variables is needed. It has been suggested that yield components have either a direct or an indirect effect on seed yield, or both. Therefore, it was essential to determine the effects of yield components on seed yield. Consequently, path coefficient analysis is the most common statistical method used for this purpose. Thus, it is possible to calculate both direct and indirect effects of yield components on seed yield through the other components. Genotypic path was worked out in the present study (Table 7) considering yield per plant as dependent character and its attributes as independent characters viz., days to 1st flowering, days to 50% flowering, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, length of siliqua (cm), no. of seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g). Each component has two path actions viz., direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.3.1 Days to 1st flowering

Path co-efficient analysis exposed that, days to 1st flowering had negative direct effect (-5.490) on yield per plant (Table 7). Even, Plant height (cm) (-0.563), Siliqua per plant (-0.004), seeds per siliqua (-0.008) also had the negative indirect effect on yield per plant. On the other hand, days to 50% flowering (5.269), number of primary branches per plant (0.332), secondary branches per plant (0.736), length of siliqua (cm) (0.170), and thousand-seed weight (gm) (0.256) had positive indirect effect on the part of yield per plant (Table 7). Although the relationship between days to 1st flowering and genotypic correlation of seed yield per plant was (0.119) (Table 7).

4.3.2 Days to 50% flowering

The relationship between days to 50% flowering and genotypic correlation of seed yield per plant was (0.106) (Table 7). This analysis disclosed that, days to 50% flowering had positive direct effect was (5.806) on yield per plant (Table 7). And days to 50% flowering (-4.983), number of primary branches (-0.593), plant height(cm) (-0.578), had negative indirect effect on yield per plant. Besides, the number of secondary branches per plant (0.342), number of siliquas per plant (0.054) and length of siliqua (cm) (0.329), number of seeds per siliqua (0.384) and thousand-seed weight (gm) (0.056) had positive indirect effect on yield per plant (Table 7).

Table 7. Partitioning of genotypic correlation into direct indirect effect of 10 important character by path analysis of *Brassica napus* L.

Trait	DFF	D 50%F	PH (cm)	PBP	SBP	SPP	LS (cm)	SPS	TSW(g)	Genotypic correlation with SYP(g)
DF	**-5.490**	5.269	-0.563	0.332	0.736	-0.004	0.170	-0.008	0.256	0.119
D50%F	-4.983	**5.806**	-0.578	-0.593	0.342	0.054	0.239	0.384	0.056	0.106
PH (cm)	1.683	-1.824	**1.838**	-0.569	0.333	-0.087	-0.277	-0.898	-0.551	-0.160
PBP	-0.593	-1.123	-0.341	**3.067**	0.019	-0.174	-0.316	-0.697	0.328	0.297**
SBP	-2.497	1.227	0.378	0.036	**-2.497**	-0.103	-0.037	-0.218	0.102	0.260*
SPP	-0.082	-1.130	0.576	1.912	0.599	**-0.279**	-0.388	-0.890	0.136	0.589**
LS (cm)	-1.183	1.763	-0.645	-1.228	-0.075	0.137	**0.789**	0.157	0.327	-0.170
SPS	0.031	1.610	-1.191	-1.544	-0.255	0.179	0.089	**1.385**	0.038	0.325**
TSW (g)	-1.274	0.294	-0.919	0.912	0.150	-0.034	0.234	0.048	**1.102**	0.378**

Residual effect: **0.380**** Direct (bold) effect showing **, * = Correlation is significant at the 0.01 and 0.05 level, respectively

DFF : Dayes to 1st flowering
D50%F : Days to 50% flowering
PH (cm) : Plant height (cm)
PBP : Primary branches per plant
TSW(g) : 1000seedweight(g)
SBP : Secondary branches per plant
SPP : Siliqua per plant
LS (cm) : Length of siliqua (cm)
SPS : Seed per siliqua
SYP(g) : Seed yield per plant

4.3.3 Plant height

The relationship between genotypic correlation with yield per plant and plant height was (-0.160) (Table 8). It had positive direct effect (1.838) and days to 1st flowering (1.683), number of secondary branches (0.333) had the indirect positive effect (Table7). Even the negative indirect effect had shown of days to 50% flowering (-1.824), number of primary branches per plant (-0.569), number of siliquas per plant (-0.087), siliquas length(cm) (-0.277), seeds per siliqua (-0.898) and thousand-seed weight (gm) (-0.551) (Table 7). These results were identical to Afrin (2009) observed from path co-efficient analysis that plant height and also others parameters.

4.3.4 Number of primary branches

This character had the positive direct effect (3.067) (Table 7). The relationship between number of primary branches and seed yield per plant as genotypic correlation was positive and highly significant (0.297^{**}). This trait had positive indirect effect on secondary branches per plant (0.019) and thousand seed weight (0.328) (Table 7). And negative indirect effect on Plant height (cm) (-0.341), number of siliquas per plant (-0.174), number of seeds per siliqua (-0.697), days 1st flowering (-0.593), days to 50% flowering (-1.123), length of siliqua (cm) (-0.316) (Table 7).

While primary branches showed indirect and negative effects on yield through height of plant, secondary branches, silique of a plant, yield of seeds and erucic acid proportion. While primary branches exhibited indirect and positive effects through the left-over parameters of yield. These results were identical to those of Akbar *et al*., (2003).

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant showed negative direct effect (-2.4997) (Table7). And it exposed that number of secondary branches had positive indirect effect on days to 50% flowering (1.227), plant height(cm) (0.378), thousand-seed weight (gm) (0.102) and number of primary branches (0.036) (Table 7). On the other hand, negative indirect effect had shown days to 1st flowering (-2.497), number of siliquas per plant (-0.103), length of siliqua (cm) (-0.037) and number of seeds per siliqua (-0.218) (Table 7). Although the relationship between number of secondary branches per plant and genotypic correlation with seed yield per plant was positively significant (0.260) (Table 7). The indirect positive effects of secondary branches occurred through height of plant, weight of seeds, oleic acid and erucic acid

proportion. While all other characters had indirect negative effects on yield through secondary branches. The results were identical to those of Basalma (2008).

4.3.6 Number of siliquas per plant

The negative direct effect of siliquas per plant (-0.279) had shown in path co-efficient analysis. Besides, the negative indirect effect had performed through days to 1st flowering (-0.082), days to 50% flowering (-1.130), length of siliqua (cm) (-0.388), and number of seeds per siliqua (-0.890) (Table 8). Plant height(cm) (0.576), number of primary branches (1.912), number of secondary branch (0.599), and thousand-seed weight (gm) (0.136) had declared the positive indirect effect of this trait (Table 7). Finally, the relationship of numbers of siliqua per plant and seed yield per plant as genotypic correlation was highly significant and positive (0.589^{**}) (Table 7). Almost the same results were found by Sabaghnia *et al.*, (2010).

4.3.7 Length of siliqua

Significantly negative (-0.170) value was estimated genotypic correlation through the relationship between siliqua length and seed yield per plant (Table 7). That the analysis revealed that length of siliqua had direct positive effect (0.789) (Table 7). And indirect negative effect on days to 1st flowering (-1.183), number of secondary branch (-0.075), plant height (cm) (-0.645), number of primary branches (-1.228) (Table 7). On the other hand, it showed indirectly positive effect on days to 50% flowering (1.763), and number of seeds per siliqua (0.157), number of siliquas per plant (0.137) and thousand-seed weight (gm) (0.327) (Table 7). Hence, selection should be practiced for this trait which had longer siliqua in order to improve seed yield. Han (1990) was reported that siliqua length had negative direct effect on yield per plant.

4.3.8 Number of seeds per siliqua

Through the path coefficient analysis, the relation of this trait with seed yield per plant was highly significant (0.325) as genotypic coefficient correlation. It revealed that number of seeds per siliqua had direct positive effect (1.385). This trait had also indirect positive effect on days to 1st flowering (0.031), days to 50% flowering (1.610), thousand seed weight (0.038), length of siliqua (cm) (0.089), number of siliquas per plant (0.179) and length of siliqua (cm) (0.089) (Table 7). Besides, the number of secondary branches per plant (-0.255), plant height (cm) (-1.191), number of primary branches per plant (-1.544), had shown the indirect negative

effect (Table 7). The negative direct effect was mainly counter balanced by indirect positive effect of different characters. Rashid (2007) reported that number of seeds per siliqua had direct positive effect on yield per plant.

4.3.9 Thousand seed weight

Among the 30 genotypes, the thousand seed weight had positive direct effect (1.102) (Table 7). And it revealed that the negative indirect effect had shown on the days to 1st flowering (-1.274), plant height (-0.919), number of siliquas per plant (-0.034) (Table 8). But the positive indirect effect had performed on the number of secondary branch (0.150), siliqua length (0.234), number of seed per siliqua (0.912), days to 50% flowering (0.294), and number of primary branches per plant (0.912) (Table 7). Although the genotypic correlation between thousand seed weight and seed yield per plant was highly significant and positive (Table 7). Kachro and Kumar (1991) reported that thousand seed weight had positive direct effect on seed yield.

4.3.10 Residual effect(R)

The magnitude of residual effect (0.380) identified that traits included in the path analysis explained about 62% of the variation in seed yield. However, the remaining variation in seed yield (38%) can be attained by incorporating other yield related characters in the path analysis as far as studies involving association of traits is concerned.

CHAPTER V

SUMMARY AND CONCLUSION

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Under 30 genotypes of *Brassica napus* L. the research was guided at the Sher-e-Bangla Agricultural University Farm, Dhaka, Bangladesh during mid-November 2018 to mid-March 2019 for a study on genetic variability and interrelationship between yield and yield contributing characters in the BC_1F_7 population of *Brassica napus* L. The field experiment was placed upon on the main field in Randomized Complete Block Design (RCBD) with three replications. Based on ten parameters, days to 1st flowering, days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquas per plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g) were recorded through the different analysis. All the above circumstances, the result of the present studies has been presented as bellow:

Regarding 30 population, the observed value of ten characters was recorded through analysis of variance (ANOVA), estimation of variability, heritability and genetic advance of characters, Correlation coefficient analysis and Path coefficient analysis.

The analysis of variance indicated highly significant among the genotypes for all the characters studied. Significant variation was existed in different characters like, days to 1st flowering, 50% flowering, number of primary branches per plant, secondary branches per plant, seeds per siliqua, thousand seed weight and seed yield per plant.

For days to 1st flowering, the highest days (30.33) was recorded in G_{16} whereas the lowest days (26.33) was observed in the G_{29}. Days to 50% flowering was recorded for the highest value (35.33) in the population G_6 whereas, the lowest value (29.33) was recorded in G_{29}. The population G_{29} showed the highest plant height (183.07 cm) whereas, the lowest height (102.90 cm) was found in G_{15}. The maximum number of primary branches (5.46) was found in G_9 and the minimum number of primary branches (3.06) was found in G_5. The highest number of secondary branches (4.30) was observed in G_4whereas, the lowest number of secondary branches (1.40) was observed in G_{20}. The highest value (223.87) was counted in G_{25} for the number of siliquas per plant and the lowest value was counted in G_3 (120.13). The maximum length of siliqua (9.49 cm) was found in G_{24} whereas, the minimum length (7.08cm) was found in G_6. The highest

number of seeds per siliqua was found in G_{11}(30.45) whereas, the lowest number (17.31) was observed in G_2. The maximum weight of thousand seeds (4.94 gm) was counted in G_{20} whereas, the lowest amount of thousand seed weight (3.10gm) was found in G_{23}. The highest amount of seed yield per plant (19.59 gm) was noticed in G_{13}. And the second maximum amount(17.20gm) was observed in G_{25} population.

Among the 30 genotypes, the analysis from the mean performance showed meaningful differences for all the characters. Least significant was required difference level of probability (0.05%) between the means. Where statistically significant value was shown in days to 50% flowering, plant height, primary branches per plant, siliqua per plant, thousand seeds weight and seed yield per plant. needed

Analysis of variance had performed for both phenotypic and genotypic coefficient of variation. However, the phenotypic variance and phenotypic coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under present study. Where the highest phenotypic variance 1042.04% and genotypic variance 316.59% was found in plant height (cm). For most of the characters the genotypic variance and phenotypic variance were close to days to 1st flowering, days to 50% flowering, primary branches per plant, seeds per siliqua and seed yield per plant. On the other hand, plant height (g), siliqua per plant, siliqua length (cm) and thousand seed weight showed least differences between phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Maximum heritability was found in seed yield per plant (g) (59.04) while plant height (29.42) exhibits the minimum value of heritability. Highest value was noticed as heritability in days to 1st flowering, days to 50% flowering, primary branches per plant, secondary branches per plant, seeds per siliqua and thousand seed weight. High heritability with high genetic advanced was noticed for plant height (14.98) and siliqua per plant (20.20). On the other hand, high heritability with high genetic advance of mean was observed in secondary branches per plant (25.36), seeds per siliqua (18.60) and seed yield per plant (37.94) indicated that these traits were under additive gene control and selection for genetic improvement for this would be effective and beneficial. These results revealed the possibility of the predominance of additive gene

action in the inheritance of these traits. Therefore, the traits could be improved through the selection process.

To determine the relationship between yield and yield contributing characters the correlation coefficient among the traits were studied. In general, most of the characters showed that the genotypic correlation co-efficient were lower than the corresponding phenotypic correlation co-efficient due to effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. Highly significant positive correlation with seed yield per plant was recorded in primary branches per plant (G=0.297**, P= 0.283**), secondary branches per plant (G=0.260**, P= 0.293**), siliqua per plant (G=0.589**, P=0,489**), seeds per siliqua (G=0.325, P= 403**) and thousand seed weight (G=0.378**, P= 0.277**). On the other hand, significant positive and insignificant and positive correlation was found in days to 1st flowering (G=0.119, P= 0.220*) and days to 50% flowering (G=0.106, P=0.194).

Among the 30 genotypes, the analysis from the mean performance showed meaningful differences for all the characters. Least significant difference between the means at the required level of probability (0.05). Where statistically significant value was shown in days to 50% flowering, plant height, primary branches per plant, siliqua per plant, thousand seeds weight and seed yield per plant. needed

Path co-efficient analysis performed those days to 50% flowering, plant height (cm), number of primary branches per plant, siliqua length, seeds per siliqua, 1000 seeds weight (gm) had the positive direct effect on yield per plant where the highest positive direct effect was a pound in days to 50% flowering (5.806). The path coefficient studies proved that plant height (cm), the number of primary branches per plant, siliqua length, seeds per siliqua, 1000 seeds weight (gm) were the most important contributors to seed yield per plant which could be taken into consideration for future hybridization program.

Depending on all the above explanations the traits like plant height (cm), number of primary branches per plant, siliqua length (cm) and 1000 seed weight (g) showed high heritability coupled with high genetic advance in percent of mean, the selection would be effective for those traits and including genotypes G13 (19.59), G24 (17.20), G19 (14.05), G30 (13.65), G1 (13.19), and G29 (15.13) can be further used for varietal improvement programs and development of high yielding variety.

Recommendation:

Among the populations, the highest seed yield per plant (19.59g) was noticed in G_{13} (Nap2066×Nap205) × Nap205 with longest length of siliquae (8.72cm), maximum number of seeds/siliquae (30.45) and highest thousand seed weight (5.40g). The second highest (17.20g) was noticed in G_{24} (Nap2066×Nap0130) × Nap0130 with short days to 50% flowering (32.33 DAS), number of primary branches per plant (5.46), number of seeds per plant (223.87), longest siliqua length (9.21cm) and highest 1000 seed weight (5.28 g) which has the probability to release as the most population that might be used in future breeding programs.

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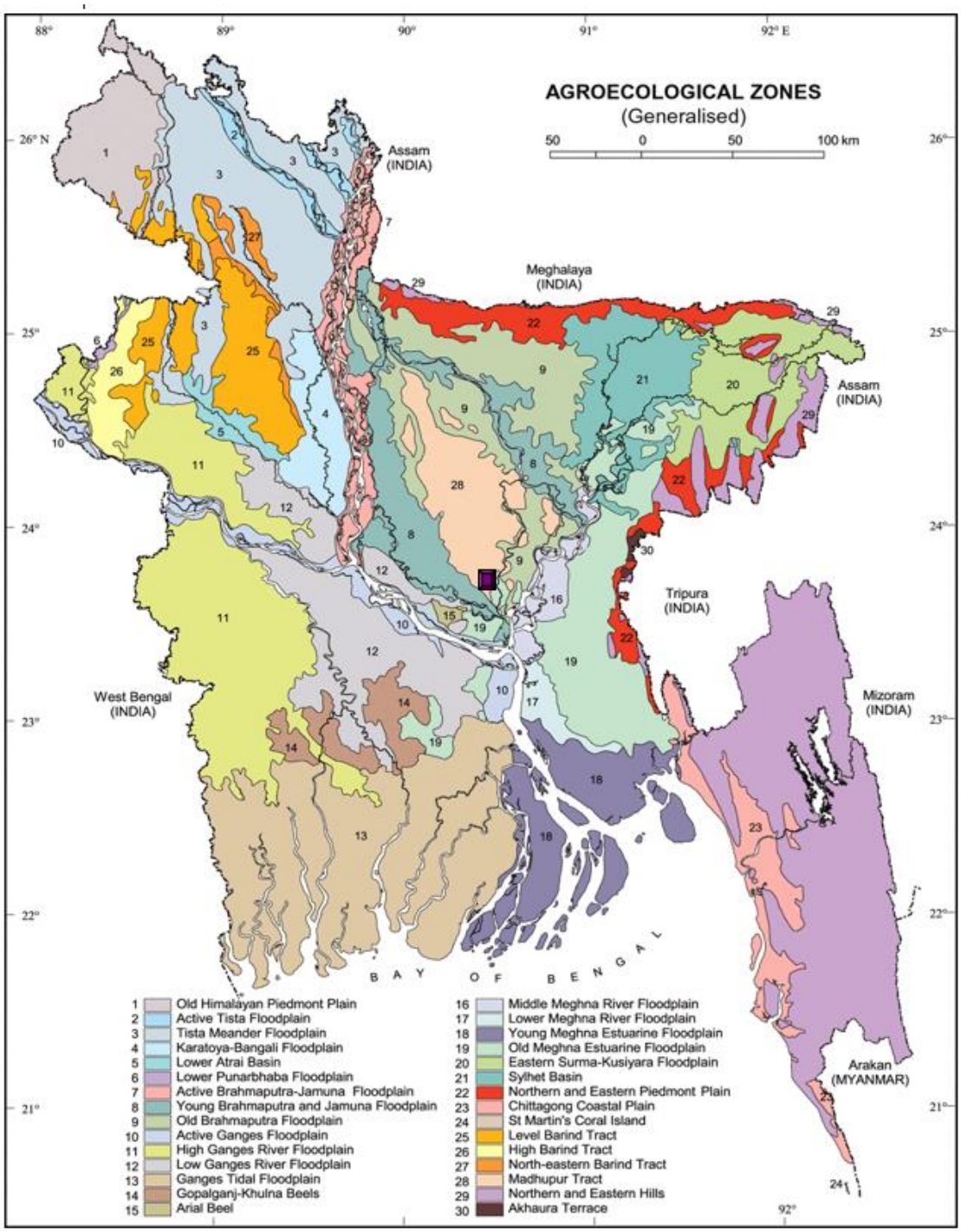
APPENDICES

Appendix I. Map showing the experimental site under the study



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

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

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

Appendix III. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site the period from mid-November, 2018 to mid-March, 2019

Month	Air temperature (^{o}c)		Relative Humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
Mid-November, 2018	34.7	15.0	76	225	**3.9**
December, 2018	29.1	14.4	72	1	**5.7**
January-February, 2019	28.1	13.1	69	0	**3.4**
Mid-March, 2019	**26.1**	**12.1**	**65**	**1**	**3.8**

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