GENETIC DIVERSITY AND CHARACTERS ASSOCIATION ANALYSIS OF ADVANCED LINE OF *Brassica napus* L.

AZIZA KHATUN

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

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BY

AZIZA KHATUN

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Approved by:

Dr. Firoz Mahmud	**Dr. Md. Shahidur Rashid Bhuiyan**
Professor	Professor
Supervisor	Co-supervisor

Professor Dr. Jamilur Rahman
Chairman
Examination Committee

DEDICATED

TO

MY BELOVED PARENTS

AND

MY DAUGHTER

Dr. Firoz Mahmud
Professor
Department Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh

Mob: +8801552432589
E-mail: fmahmud08@gmail.com

CERTIFICATE

This is to certify that thesis entitled, ***"Genetic Diversity And Characters Association Analysis of Advanced Line of Brassica napus L."*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***AZIZA KHATUN****, Registration No.* ***12-04942*** *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.

June, 2018
Dhaka, Bangladesh

(Dr. Firoz Mahmud)
Professor
Supervisor

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SAU, Dhaka

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ABSTRACT

A field experiment was conducted with 26 BC_1F_6 genotypes of *Brassica napus* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the Genetic diversity and characters association analysis of advanced line of *Brassica napus* during November 2017 to March 2018. The populations were found significantly variable for all the characters. Comparatively phenotypic variances were higher than the genotypic variances for all the characters studied. PCV was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied. Higher estimates of PCV than GCV were observed for all the traits. PCV ranged from 1.32% for Days to maturity to 28.46% for Secondary branches per plant and GCV from 0.95% (Days to maturity) to 17.88% (seed yield per plant) The high PCV value was observed for number of secondary branches per plant (28.46%), siliqua per plant (15.43%), 1000 seed weight (13.39%). Seed yield per plant showed high broad base heritability (61.07). The significant positive correlation with seed yield per plant was found with days to flowering (0.319 and 0.070) and siliqua length (0.068 and 0.015). Path coefficient analysis revealed that days to flowering (1.180), plant height (0.009), secondary branches per plant(0.210), number of siliqua per plant (0.493), siliqua length (0.498) and seeds per siliqua (0.005) had the positive direct effect on yield per plant. By genetic divergence analysis Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes (29.70%) and three PCA account for (61.00%) of the total variation The genotypes were grouped into five clusters. Cluster II contained the large no. of genotypes (11) and cluster III contained only one (1). The cluster V had higher intra cluster distance (2.44) that indicates the highest amount of genetic divergence within the group. The maximum inter cluster distance was observed between genotypes of cluster III and IV (16.453) followed by clusters II and III (11.693). Under cluster III genotypes possessed early maturity, highest plant height, more primary and secondary branches per plant, more siliqua per plant and short siliqua. Considering group distance and other agronomic performance genotypes G1, G2, G13, G15, G18, G19, G21 and G24 might be suggested for future hybridization program.

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LIST OF ABBREVIATIONS

Full name	Abbreviation
Percent	%
Degree Celsius	^{0}c
At the rate	@
Phenotypic variance	δ^2_p
Genotypic variance	δ^2_g
Environmental variance	$\delta^2 e$
Heritability in broad sense	h^2b
Agro Ecological Zone	AEZ
Analysis of variance	Anova
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Percentage of Coefficient of Variation	CV%
Cultivars	cv.
Degrees of Freedom	Df
And others	*et al.*
Etcetera	etc.
Food and Agricultural Organization	FAO
Gram	g
Genotype	G
Genetic Advance	GA
Genotypic coefficient of varience	GCV
Genetics and plant breeding	GEPB
Harvest Index	HI
Indian Agricultural Research Institute	IARI

International Center for Agricultural Research in Dry Areas	ICARDA
Journal	J.
Kilogram	Kg
Centimeter	cm
Mean sum of square	MS
Murate of potash	MP
Ministry of Agriculture	MoA
Square meter	m^2
Phenotypic coefficient of Variation	PCV
Randomized Complete Block Design	RCBD
Triple Super Phosphate	TSP

Chapter 1

INTRUDUCTION

The genus *Brassica* L. holds the most economically valuable position in the tribe Brassiceae, which is a part of family Brassicaceae. This genus consists of a versatile batch of species that includes major oilseed crops and vegetables. There are different species in *Brassica* family i.e, turnip, cauliflower, broccoli, brusssels sprouts, cabbage, weeds and various mustards which are so much important due to their presence in different food, feed and edible oil etc.

Due to their agricultural importance, Brassica plants have been the subject of much scientific interest. Six economically valuable species are comprises in this genus with huge genetic and morphological variation and is cultivated in all over the world. Among these, three species are diploid (*Brassica oleracea*, 2n = 18; *Brassica rapa*, 2n = 20; *Brassica nigra*, 2n = 16), and three are amphidiploid (*Brassica napus*, 2n = 38; *Brassica juncea*, 2n = 36; *Brassica carinata*, 2n = 34). Rapeseed-mustard (*Brassica napus, Brassica campestris and Brassica juncea*) are grown all over the world as an important source of edible oil as described by the Triangle of U theory (Abideen *et al*. 2013).

They provide the most concentrated source of energy and also help to absorb vitamins A, D, E and K. It is the second highest source of edible oils supply in the world after soybean (FAO, 2014). Rapeseed is one of the most important oil and protein rich annual crops in the world. Oilseed provides oil both for industrial and culinary purpose. Vegetable oils and fats lipids constitute an important component of human diet. Oils from plant origin are nutritionally superior to that of animal origin. Therefore, vegetable oil has been always considered as a major component for food preparation.

Bangladesh produces good number of oil seed crop like mustard, sesame, groundnut, linseed, niger, safflower, sunflower, sunflower, soybean , castor etc. Brassica oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2013). Mustard and rapeseed seeds contain 42% oil, 25% protein (Khaleque, 1985). The oil cake contains proteins of high biological value and applicable quantities of calcium and phosphorus. It is used as a very good animal feed as well as organic manure for various crops.

The average yield of local varieties and high yielding varieties are 600-1000 kgha^{-1}and 1400-2000 kg ha^{-1} respectively which contributes to 52% of the total production and 61.2% of the oilseed production of Bangladesh (Anonymous, 2010). Now-a-days *Brassica napus* production in Bangladesh accounts for approximately 23,667 metric tonnes which is grown in almost 20,580 hactre of lands (BBS, 2014-2015). Brassica napus lines have become more important to the western world through breeding for better oil quality and improved processing techniques (Hachey *et al*. 1991)

Bangladesh required 0.30 million tons of oil equivalent to 0.85 million tons of oil seed for nourishing her people. At present, the oil seed production is about 0.26 million tons, which covers only 30% of the domestic need (BBS, 2011). About 70% of requirement of oil has been imported every year by spending huge amount of foreign currency involving Tk.2951core (BBS, 2011). Per capita consumption of edible oil is the lowest in Bangladesh from the world (11g/head/day) which is one fifth of the recommended requirement for a balanced diet (FAO, 2014).

In Bangladesh the seed yield of mustard/rapeseed is about 740 kg ha^{-1}, which is very low in comparison to other developed countries (2400 kg ha^{-1}) (FAO, 2014). The most of the released mustard cultivars are generally long in duration and thus, did not fit well for cultivation in cropping pattern. If we can develop new lines which would be successfully cultivated between Aman and Boro rice rotation

without affecting present cropping pattern, since after Aman rice harvest and before the transplantation of Boro rice 70-80 days are available for cultivating gap filling crop. So, it is urgent to analyze the genetic diversity and its response for the selection of good mustard genotypes for increasing our cropping intensity. Crop improvement program through plant breeding, as a result, occurs through selection operating on genetic variability. Selection by plant breeders or by farmers can be intense and has resulted in major improvements. Importance of genotypic and phenotypic variability, heritability and character association have proved by many scientists (Ali *et al*. 2002; Lekh *et al*. 1998) for further genetic improvement. Gosh and Gulati (2001) also showed that the traits showing high heritability are under the control of additive genes and can be successfully utilized for plant selection on the basis of phenotypic performance.

Determination of correlation co-efficient between the characters has a considerable importance in selecting breeding materials. The path co-efficient analysis has been found to give more specific information on the direct and indirect influence of each of the component characters upon seed yield (Behl *et al*. 1992). Path-coefficient technique splits the correlations, coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an efficient selection strategy (Sabaghnia *et al.* 2010).

Genetic diversity is the basic for genetic improvement. It is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding ((Mukhtar *et al*. 2002). It is very important factor for any hybridization program aiming at genetic improvement of yield especially in self pollinated crops (Joshi and Dhawan, 1966). Different methods have been used to assess genetic diversity. This can be obtained from pedigree analysis, morphological traits or using molecular markers. With the development of advanced biometrical method such as multivariate

analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics and Ward's no-hierarchical squared Eucalidean distance method have become possible to quantity magnitude of diversity among germplasm for their evaluation in respect of breeding program.

Therefore the present study was, executed with the objectives of estimating the genetic variability, correlation, path analysis and diversity seed yield and its related traits of twenty six *Brassica napus* populations.

Objectives:

- To compare the yield potential and yield contributing characters among the twenty six populations of *Brassica napus.*
- To assess the interrelationships among the populations.
- To identify short durated mustard varieties suitable for Bangladesh to increase our cropping intensity.

Chapter 2

REVIEW OF LITERATURE

Brassica is a genus of plants in the mustard family (Brassicaceae). This family includes about 334 genus and about 3708 species. The members have a cosmopolitan distribution around the world. The members of the genus are collectively known as cruciferous vegetables, cabbages, or mustards.

2.1 Origin and geographical distribution

Due to their agricultural importance, *Brassica* plants have been the subject of much scientific interest. Six particularly important species (*Brassica carinata, B. juncea, B. oleracea, B. napus, B. nigra* and *B. rapa*), from which (*B. carinata, B. juncea, B. napus)* are derived by combining the chromosomes from three earlier species, as described by the Triangle of U theory. But the edible oil is obtained from *B. napus, B. juncea* and *B. campestris.*

The genus is native in the wild in Western Europe, the Mediterranean and temperate regions of Asia. In addition to the cultivated species, which are grown worldwide, many of the wild species grow as weeds, especially in North America, South America, and Australia.

Brassica is the most important oil crops of Bangladesh and many countries of the world. The crops have received much attention by a large number of researchers on various aspects of its production and utilization. Identification of suitable parental lines on the basis of their genetic parameters, nature and magnitude of genetic variability and the correlation of different yield attributing characters is important for successful *Brassica* breeding programs. Yield in *Brassica* is associated with many yield contributing characters and in addition there are other characters plant height, primary and secondary branches, siliqua per plant, siliqua

length, seeds per plant and thousand seeds weight etc. which also contribute to *Brassica* yield. Reviewing the information and knowledge on performance of different genotypes, variation for genetic divergence, relationship between yield and yield contributing characters, heritability, genetic diversity based analysis in *Brassica* for yield and yield contributing characters is important for future breeding program for developing high yielding varieties.

A large number of literatures are available on genetic diversity, variability, correlation and path analysis of yield and yield contributing characters of *Brassica* grown under a particular environment (latest to older from 2018 to 1999). 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 -

- Genetic variability, heritability and genetic advance
- Correlation among different characters
- Path co-efficient analysis
- Genetic Diversity 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.

Abideen *et al.* (2013) carried out an experiment to study the genetic variability and correlation among different traits in *Brassica napus*. Results revealed that highly significant differences among the genotypes for most of the traits. Non significant differences were observed among the genotypes for primary branches and pods.

Zebarjadi *et al.* (2011) carried out an experiment to study some traits and to estimate genetic parameters in sixteen 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 the maximum for oil percentage, whereas low genetic advance was observed for thousand kernel weight.

Aytac and Kinaci (2009) conducted an experiment with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for two years. They observed maximum broad sense heritability get genetic advance seed yield followed.

Aytac *et al.* (2008) reported highest genotypic and phenotypic variances for seed yield per plant followed by seed yield and high heritability of seed yield per plant, seed yield, pods per main stem coupled with high genetic advance revealed that additive gene effects are important in determining these characters and could be improved through mass selection.

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

Hosen (2008) conducted a study by using five parental genotype of *Brassica rapa* and their ten F_3 progenies including reciprocals. There are large numbers of variations present among all the genotypes used in the experiment. The plant

height, days to 50% flowering, and number of siliqua per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

An experiment was carried out by Mahmud (2008) with 58 genotypes of *Brassica rapa* to study inter genotypic variability. Significant variation was observed among all the genotypes for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in percentage of mean were obtained for days to 50% flowering, seed per siliqua and siliqua length.

Nanda *et al.* (1995) observed that days to first flowering varied both by genotypes and date of sowing, while working with 65 strains of *B. napus, B. juncea, B. carinata* and *B. rapa.* Many other researchers like Kumar and Singh (1994), Kumar *et al.* (1996), Kachroo and Kumar (1991), Andrahernnadi (1991), Lebowitz (1989), Biswas (1989), Singh *et al.* (1987), Yadava (1983) and Thakral (1982)

Dominance gene action was important in the expression of days to flowering was found by Jain *et al.* (1988). Significant genetic variability in days to 50% flowering in *B. napus* and *B. rapa* was observed by Singh *et al.* (1991).

Katiyar *et al.* (1974) observed high genetic co-efficient of variation for days to first flowering, plant height (cm) and seed yield per plant (g) where as low values were observed for other characters like days to maturity and number of primary branches per plant, while observing on genetic variability and genetic advance of seed yield and its components in Indian mustard.

Chandola *et al.* (1977) worked on 30 varieties of *B. campestris* and reported that the varietal differences were highly significant for plant height, due to varieties and growing conditions. They also found highly significant varietal differences for yield and six other yield components.

According to Tyagi *et al.* (2001) variation was the highest in parents and their hybrids for plant height. The seed yield per plant exhibited the highest co-efficient of variation (41.1%). Significant genetic variability was observed for this character by many workers like Andarhennadi *et al.* (1991), Gupta and Labana (1989), Malik *et al.* (1995), Kumar and Singh (1994), Yadava *et al.* (1993), Lebowitz (1989), Chaturvedi *et al.* (1988), Gupta *et al.* (1987), Chauhan and Singh (1985) and Sharma (1988) among different genotypes of B. napus, B. rapa and B. juncea.

The highest genotypic co-efficient of variation was calculated for secondary branches. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering among 10 genotypes for each of *Brassica campestris*, *Brassica carinata* and *Brassica napus* and 24 genotypes of *Brassica juncea* by Lekh *et al.* (1998).

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/siliqua in oleiferous Brassica materials of diverse genetic base was observed by Kudla (1993) and Kumar and Singh (1994). Similar significant variability in the genotypes of *Brassica napus*, *B. campestris* and *B. juncea* were studied by them.

Bhardwaj and Singh (1969) observed GCV value of 35.85% in case of *Brassica campestris* genotypes. High co-efficient of variation for thousand seed weight, pod length and number of seeds per pod for both genotypic and phenotypic level was found by Masood *et al.* (1999) while working with seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* to study genetic variability.

Higher seed yield is the result of higher number of siliqua. Large variation is involved for this trait. High genetic variation in number of siliqua was observed by Yin (1989) while working with 8 cultivars of *Brassica napus*. Kumar *et al.* (1996) also observed and reported similar results of high variation for this trait.

Singh *et al.* (1987) observed variable results of GCV (25.41%) and PCV (29.15%) in *Brassica campestris* for siliqua number higher and the seed yield, GCV was reported to be also as 18.85% by Yadava (1973) and Bhardwaj and Singh (1969) reported 97.3% of GCV. Number of siliquae per plant is one of the most important traits of *Brassica* spp. This trait has high variation and a considerable part of which appeared to be environmental. High genetic variation was found by Kudla (1993). Similar results was also found by Andraherinadi *et al.* (1991), Biswas (1989), Jain *et al*. (1988), Chowdhury *et al*. (1987), Alam *et al.* (1986) and Thakral (1982).

Siliqua length is another important character for the development of fruits in oil seed crops like mustard and rape seed. Peduncle, beak as well as siliqua length varies due to difference in genotypes. High genetic variability was found by Olsson (1990) for this character. Lebowitz (1989) found similar results while working with *B. rapa* for siliqua length. Thurling (1983) reported that selection for increased siliqua length is an effective strategy for yield improvement through raising seed weight per siliqua.

Thousand seed weight is a very important character of rape seed and mustard, where highest consideration is on the seed yield. This character has been found to vary widely from genotypes to genotypes and from environment to environment. A good number of literatures are available on the variability of this trait.

According to Kumar and Singh (1994) in *B. juncea,* Kudla (1993) in rapeseed, Andarhennadi *et al.* (1991) in brown mustard, Biswas (1989) in *Brassica campestris*,

Lebowitz (1989) in *B. rapa*, Yin (1989) in *B. rapa* and Chowdhury *et al.* (1987) in *B. rapa* found different degrees of significant variations among the genotypes for thousand seed weight.

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 *B. rapa* was reported by Sharma *et al*. (1994). Thakral (1982) also reported significant genetic variability in genotypes of *B. napus*. Similar high variability in different genotypes of *B. napus* was found by Khera and Singh (1988).

High degrees of variation for seed yield per plant in *B. rapa* was observed by Yin (1989) and Kudla (1993) in *B. napus* and Kumar et al. (1996) in *B. juncea*. Bhardwaj and Singh (1969) found GCV value of 96.99% among different strains of *B. rapa.* Yadava (1973) found 48.76% GCV value among 29 strains of *B. juncea*. While Singh *et al.* (1987) found GCV and PCV values of 44.04% and 46.9% in *Brassica juncea.*

High heritability coupled with high genetic advance for seed yield per plant, number of secondary branches per plant, siliqua per plant, 1000 seed weight (g) and number of primary branches per plant was observed by Sheikh *et al*. (1999) while working with 24 genotypes of toria.

Lekh *et al.* (1998) carried out an experiment with 24 genotypes of *B. juncea* and 10 genotypes each of *B. campestris*, *B. carinata* and *B. napus* and observed highest genetic advance and high genotypic and phenotypic co-efficient of variation for days to 50% flowering and high heritability for other yield contributing characters.

Both additive and dominance genetic components were important for seed yield and yield components in *B. campestris* var. toria, and higher heritability for days to maturity and thousand seed weight while studied 8x8 diallel analysis (excluding reciprocals) was reported by Yadava *et al.* (1993).

Malik *et al.* (2000) observed very high broad sense heritability (h^2b>90%) for number of primary branches per plant, days to 50% flowering and oil content while working with different strains of *B. napus.* They also observed low heritability ($h^2$1, 50%) for plant height, number of siliqua/plant, number of seeds siliqua and seed yield. But high heritability for all these characters were found by Lodhi *et al.* (1979) while working with 55 genotypes *of B. napus, B. rapa* and *B. juncea.*

High heritability and genetic advance for number of siliqua per plant in *B. rapa* and *B. juncea* were observed by Varshney *et al.* (1986), but they found high heritability and genetic advance for plant height in all the three species. High narrow sense heritability and genetic advance for days to flowering and plant height were reported by Diwakar and Singh (1993) while working with segregating populations of yellow seeded Indian mustard (*B. juncea* L. Czern and Coss).

High heritability and genetic advance for number of seeds per siliqua and seed yield per plant was reported by Singh (1986) while working with 22 genotypes of *B. napus, B. campestris* and *B. juncea.*

Low heritability for yield per plant was observed by Malik *et al.* (1995), Kumar et al. (1988) and Yadava *et al.* (1993). Chen *et al.* (1983) and Wan and Hu (1983) found high heritability and genetic advance for days to flowering, number of primary branches per plant and plant height.

Singh *et al.* (1987) studied 179 genotypes of Indian mustard and found high heritability for seed yield per plant and oil content and the lowest heritability for number of primary branches per plant. In a study of variability and correlations in some varieties of *brown sarson,* reported high heritability for siliqua length, number of seeds per siliqua and thousand seed weight was observed by Chaudhury *et al.* (1990).

Kwon *et al.* (1989) and Rao (1977) reported high heritability (h > 90%) for siliqua length, but Kachroo and Kumar (1991), Sharma (1988) and Yadava *et al.* (1978) reported low to medium for this trait.

Plant height and number of seeds per siliqua were highly heritable whereas siliqua length, number of primary branches per plant were less heritable was observed by Labana *et al.* (1980) while working with 104 mutants of Indian mustard *B. juncea* L. Czern and Coss. Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *B. rapa.*

Paul *et al.* (1976) found in his study that a good genetic advance was expected from a selection index comprising seed yield, number of seeds per siliqua, number of primary branches per plant and number of siliquae per plant.

Katiyar *et al*. (1974) reported heritability in the broad sense was associated with high genetic advance for number of siliquae on the main shoot and seed yield per plant while working with *B. campestris* L. var. *sarson*. In a study of genetic variability, heritability and genetic advance of Indian mustard Katiyar *et al.* (1974) reported high heritability for days to flowering, plant height, number of primary branches and seed yield per plant, moderate for days to maturity and low for the number of secondary branches. He also reported low genetic advance for number of primary branches and high values for days to flowering, plant height and seed yield per plant.

According to Yadava (1973) high heritability in the broad sense and genetic advance for days in maturity, plant height and number of node on the main shoot among the nine traits studied in 29 varieties. The most important feature in winter rape plant selection for seed yield and number of branches was reported by Teresa (1987).

According to Knott (1972), Seitzer and Evans (1978) and Whan *et al.* (1982), selection for yield in early segregating generations was effective in developing

high yielding cultivars of selfpollinated crops. Selection for bold seed size from F_2 to F_5 generations was highly effective was observed by Gupta and Labana (1985) in Indian mustard.

Chatterjee and Bhattacharyya (1986) found higher efficiency with index selection than selection based on yield alone. The efficiency increased with an increase in the number of characters in the index. The index comprising plant height, thousand seed weight and yield per plant was considered effective from the practical point of view.

2.3 Correlation among different characters

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.

Esmaeeli Azadgoleh *et al.* (2009) mentioned positively significant correlation of seed yield with number of pod per plant, number of pods in sub branches and number of seeds per pod. An experiment was conducted by Basalma (2008) in Ankara conditions using 25 winter oil seed rape cultivars. Correlation analysis showed a high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, thousand seed weight and oil ratio.

Rashid (2007) carried out an experiment with 40 oleiferous Brassica species to estimate correlation and observed that, highly significant positive association of yield per plant with number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and number of siliqua per plant.

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

An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee (2006) to study the correlation analysis. The results revealed that yield per plant had highest significant positive correlation with number of siliquae per plant.

Pankaj *et al.* (2002) studied 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 siliqua per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per 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.

Srivastava and Singh (2002) studied correlation in Indian mustard [*Brassica juncea* L. Czern and Coss] for 10 characters was conducted with 24 strains of Indian mustard along with two varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and oil percent were positively associated with seed yield.

Shalini *et al*. (2000) evaluated 81 genotypes of Indian mustard for the magnitude of association between their quantitative characters of secondary branches, plant

height, number of siliqua and seeds per siliqua were highly associated with seed yield.

Khulbe and Pant (1999) carried out a study of correlation in 8 Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids and revealed that the number of siliqua per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and harvest index were positively associated 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 *B. campestris* and standard cultivar of *B. napus* to calculate correlation co-efficient.

Thakaral *et al.* (1999) studied correlation co-efficient on seed yield and yield contributing characters in 8 Indian mustard (*Brassica juncea*) parents and their 28 F1 hybrids grown at Hisar. The data indicated that higher seed yield could be obtained by selecting for increased plant height.

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, siliqua on main shoot, siliqua per plant and thousand seed weight were positively correlated with seed yield. Gurdial and Hardip (1998) carried out and experiment with gobhi sarson (*B. nigra*) and reported that dwarf plant gave higher yield.

Zajac *et al.* (1998) studied 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 siliqua number per plant had the smallest effect on yield.

Das *et al.* (1998) carried out an experiment with 8 genotypes of Indian mustard (*B. juncea*) and reported that the length of siliqua, seeds per siliqua had high positive genotypic correlation with seed yield per plant. The number of siliqua par plant, seed weight per plant and thousand seed weight were positively correlated with seed yield per plant were observed by Dileep *et al.* (1997).

Tyagi *et al.* (1996) carried out and experiment with six yield components in three cultivars of mustard and observed that plant height, siliqua per plant, siliqua length, seed weight, and seeds per siliqua had positive and significant effects on seed yield per plant.

Uddin *et al.* (1995) while studied correlation analysis in 13 Indian mustard (*B. juncea)* and reported that seed yield per plant had high positive arid significant correlations with plant height and thousand seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

Arthamwar *et al.* (1995) studied correlation and regression in *B. juncea.* Results revealed that weight of siliqua per plant showed the highest correlation with seed yield followed by number of siliqua per plant, number of seeds per siliqua and thousand seed weight.

Malek *et al.* (2000) studied correlation analysis and reported that days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. He also reported that number of branches per plant and number of siliqua per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight.

Nanda *et al.* (1995) studied correlation analysis with 65 strains of *B. juncea, B. rapa* and *B. napus* and observed that positive association between yield and siliqua filling period. Similar results also found by Olsson (1990) in *B. napus.* He also observed positive correlation between siliqua density and yield.

Kumar *et al.* (1996) studied 12 genotypes of *B. juncea* for correlation analysis and found flowering time and plant height negatively correlated with number of primary branches per plant.

Labana *et al.* (1980) also found that number of primary branches per plant was negatively correlated with plant height and siliqua length. Shivahare *et al.* (1975) observed days to flowering were positively correlated with primary branches per plant and plant height.

Singh et al. (1987) observed number of primary branches per plant negatively correlated with siliqua length and 1000 seed weight, but positively correlated with number of siliqua per plant.

Gosh and Mukhopadhyay (1994) studied Tori-7 *(B. campestris var. toria*) for evaluation of seed yield and five seed yield contributing characters and found that plant height, siliqua per plant, seeds per siliqua and thousand seed weight was significant and positively correlated with seed yield.

Nasim *et al.* (1994) studied correlation analysis in *B. rapa* and found 1000 seed weight was significantly and positively correlated with seed yield per plant and number of siliqua per plant but significantly and negatively correlated with siliqua length and number of seeds per siliqua.

Das *et al.* (1984) observed thousand seed weight had high significant genotypic and phenotypic correlation with seed yield.

Ahmed (1993) worked with eight cv. of *B. campestris* and *B. juncea* for study of nature and degree of interrelationship among yield components and observed that siliqua length, number of siliqua per plant, number of seeds per siliqua and seed weight per siliqua was positively and linearly associated with seed yield per plant. He also observed that seed oil content was positively correlated with seed weight, but negatively correlated with number of seeds per siliqua.

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

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

Reddy (1991) studied correlation analysis in Indian mustard (*B. juncea*) and reported that positive and significant correlation between seed yield and number of primary branches per plant, number of secondary branches per plant, siliqua per plant and seeds per siliqua.

Swain (1990) studied correlations of yield components in 15 genotypes of brown sarson (*B. campestris var. dichotoma*) and found that number of siliqua per plant was the most important characters to yield.

Labana *et al.* (1980) observed plant height negatively correlated with siliqua length and seeds per siliqua. Chowdhury *et al*. (1987) studied 179 genotypes of Indian mustard and observed positive correlation of plant height with number of siliqua per plant, number of primary branches per plant and seeds per siliqua. Positive association of plant height with these three traits in eight strains of yellow sarson was also found by Banerzee *et al.* (1968).

Increasing the number of branches is a means of increasing yield, since the number of primary and secondary branches have a significant positive correlation with seed yield (Katiyar and Singh, 1974).

Srivastava *et al.* (1983) observed in *B. juncea* the number of primary branches per plant and secondary branches per plant, plant height and days to maturity showed significant positive association with the seed yield per plant. The number of primary branches showed positive and significant association with the number of

secondary branches per plant, plant height and days to maturity. Plant height showed positive and significant correlation with the number of secondary branches and days to maturity.

Banerjee (1968) reported significant correlation between number of siliqua per plant and number of seeds per siliqua in *yellow sarson.* But negative genotypic correlation between number of siliqua per plant and number of seeds per siliqua in brown sarson and toria varieties was observed by Tak (1976) when studied with B. rapa.

Chay and Thurling (1989) studied the inheritance of siliqua length among several lines of *B. napus* and reported that the siliqua length when increased there was an increase in the number of seeds per siliqua and thousand seed weight. The siliqua length was positively correlated with both number of seeds per siliqua and thousand seed weight was observed by Singh *et al*. (1987) in *B. rapa*, Chowdhury *et al.* (1987), Lebowitz (1989) and Lodhi *et al*. (1979) in *B. juncea.*

In *B. juncea* Chowdhury *et al.* (1987) and Yadava *et al.* (1978) observed thousand seed weight positively associated with days to 50% flowering and days to 80% maturity, but negative correlation was observed by Singh *et al.* (1987) and Shivhare *et al.* (1975).

Chowdhury *et al.* (1987) and Yadava *et al.* (1978) also reported that thousand seed weight negatively correlated with plant height, number of primary branches per plant and number of siliquae per plant.

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

2.4 Path co-efficient analysis

When more characters are involved in correlation study it becomes difficult to ascertain the traits which really contribute towards the yield. The path analysis under such situation helps to determine the direct and indirect contribution of these traits towards the yield.

Rashid (2007) carried out an experiment with 40 oleiferous Brassica species to estimate path analysis and observed that yield per plant had the highest direct effect on days to maturity, number of seeds per siliqua, number of siliqua per plant and number of primary and secondary branches per plant.

An experiment was conducted by Parveen (2007) with F_2 population of *Brassica rapa* to study the path analysis and observed that number of seeds per siliqua showed highest direct effect on yield per plant.

Siddikee, (2006) conducted and experiment on oleiferous *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.

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

Shalini *et al.* (2000) studied path analysis of Indian mustard germplasm and observed that number of siliqua 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.

Khulbe and Pant (1999) studied path co-efficient analysis in eight Indian mustard (*B. juncea*) parents and their 28 F_1 hybrids. The results revealed that harvest index,

siliqua length, seeds per siliqua, siliqua per plant, thousand seed and days to initial flowering were the major traits influencing seed yield.

The number of seeds per siliqua exerted the highest effect on seed yield was observed by Masood *et al.* (1999) when they studied seven genotypes of *B. campestris* and standard cultivar of B. napus.

Sheikh *et al.* (1999) worked with 24 diverse genotypes of toria for assess the direct and indirect effect of seven quantitative and developmental traits on seed yield. Results revealed that thousand seed weight and siliqua per plant had highly positive direct effect on seed yield.

Yadava *et al.* (1996) when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed that number of siliqua per plant had the highest positive direct effect on seed yield.

Uddin *et al.* (1995) studied path analysis in 13 Indian mustard (*B. 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. Kachroo and Kumar (1991) studied path co-efficient analysis in B. *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.

Han (1990) studied *B. napus* and observed negative direct effect of number of siliquae per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield. Dhillor *et al*. (1990) observed the highest positive direct effect on seed yield per plant. Kudla (1993) reported that 1000 seed weight had positive direct effect on seed yield.

Chowdhury *et al.* (1987) worked with 42 strains of mustard and observed that siliqua length had highest positive direct effect and number of primary branches per plant had the highest negative direct effect on seed yield. On the other hand, Gupta *et al.* (1987) observed that primary branching and thousand seed weight had the direct effect on seed yield.

Kumar *et al.* (1984) also worked with *B. juncea* and found negative indirect effect of days to flowering via plant height and siliqua length, but negative direct effect of these traits was observed by Singh *et al.* (1978).

Varshney (1986) worked with several strains of *B. rapa* and observed that plant height, siliqua per plant and thousand seed weight had the negative direct effect on yield.

But many scientists like Das and Rahman (1989) in *B. rapa,* Alam *et al.* (1986) in *B. juncea,* Singh *et al.* (1985) in *B. juncea,* Chen *et al.* (1983) in *B. napus* and Srivastava *et al.* (1983) in *B. juncea* observed that plant height, days to maturity, siliqua per plant, seeds per siliqua and thousand seed weight had positive direct and indirect effect on seed yield.

Chaudhary *et al.* (1990) observed that days to 50% flowering and plant height indirectly contributed to plant yield.

Kachroo and Kumar (1991) studied several strains of *B. juncea* and found that thousand seed weight had positive direct effect, but days to 50% flowering and primary branches had negative indirect effect via seeds per siliqua on seed yield. Kumar et al. (1988) found the indirect positive effect of days to 50% flowering on seed yield.

Kumar *et al.* (1984) worked with *B. juncea* and observed negative indirect effect on seed yield of days to flowering via plant height and siliqua length on seed yield.

Chauhan and Singh (1995) found high positive direct effect of days to 50% flowering, plant height, primary branches per plant, siliquae per plant and seeds per siliqua on seed yield while working with several strains of *B. juncea.*

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

2.5 Genetic Diversity analysis

The genetic diversity of 22 rapeseed (*Brassica napus*) advanced genotypes was studied by Mahmud *et al*. (2008) using principal component analysis non-hierarchical clustering and canonical vector analysis. The genotypes were grouped into four clusters. Cluster II contained the maximum number of genotypes (9) and cluster III contained the lowest (2). The highest inter cluster distance was found between cluster I and cluster III and the lowest between cluster I and cluster II. The highest intra cluster distance was noticed for cluster III and the lowest for cluster II. Cluster I had the highest mean values for siliqua length and thousand seed weight. Cluster III had the lowest cluster mean values for the number of days to 50% flowering and the number of days to maturity with moderate seed yield. Crosses between genotypes belonging to cluster II with those of cluster I and cluster IV might therefore produce high heterosis in yield as well as earliness.

Goswami et al. (2006) reported the moderate genetic diversity between parents had the good general combining ability (GCA) effect and high specific combining ability (SCA) and high mean values in F_2, had the highest frequency of transgressive segregates in F_2 and the magnitude of transgression were high in Indian Mustard.

Choudhary and Joshi (2001) determined genetic diversity among the 88 entries including eighty F_4 derivatives i.e. 20 each selected from *Brassica* crosses viz. B.

juncea B. napus, B. juncea B. rapa var. toria, B. juncea B. rapa var. yellow sarson and B. *tournefortii B. juncea,* and eight parent genotypes through multivariate analysis (D^2 statistic). The genetic distances calculated among different Brassica species revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus, B. rapa var. toria* and *B. rapa* var. yellow sarson. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. The characters, namely, plant height, secondary branches per plant, days to flowering and 1000-seed weight was contributed maximum towards genetic divergence.

Nath *et al.* (2003) conducted and experiment with varieties, inter-variety and interspecies hybrids of Brassica oil crop to determine genetic divergence. The divergence study indicated that parent, inter-variety and inter-species hybrids almost clearly form five groups indicating that they are divergent and might be of value for future breeding program. Based on the study on genetic divergence of the Brassica, the varieties having the performance and located in the distant clusters could be utilized for hybridization program to develop desired high yielding varieties.

A study of genetic divergence using Mahalanobis D^2 statistic was conducted by Rawhat and Anand (1981) on 27 strains of Indian brown mustard (*Brassica juncea* L. Czern and Coss) for seven characters related to yield and fitness. The various strains were grouped in seven clusters on three diverse lines. Parallel variation was observed between clusters III, IV and VII on one line, and I, II and V on the other, with cluster VI diverging from the rest. The geographical diversity of strains was found not to be related with the genetic diversity. The characters that contributed maximally to divergence were days to flowering, plant height and 1000-seed weight in that order.

Nadaf *et al.* (1986) conducted multivariate analysis using Mahalanobis D^2 statistic to group 83 genotypes on the basis of yield/plant and six other agronomic characters of bunch groundnut. They reported nine clusters, which were not related to the grouping formed by geographical origin. They also observed that variation in pod yield.

accounted for 88% of the total variation between clusters but number of developed pods, days to 50% flowering and 1000 seed weight were important in accounting for divergence with clusters.

The D^2 analysis allowed the 36 genotyped/variety of linseed to be identified into five distinct clusters by Begum *et al.* (2007). The cluster I included 11 genotypes that had medium mean values for 1000-seed weight (g) and seed yield/plant. The cluster II contained six genotypes, which had the highest mean values for number of seeds/capsule, number of branches/plant and seed yield/plant. They also showed the highest mean value for plant height. It is also related with medium mean values for rest of the characters. The cluster IV included three genotypes having the highest mean values for number of capsules/plant and days to maturity. The cluster V included single genotype, which had the lowest mean values for days to maturity and plant height. The highest inter cluster distance was observed among clusters V, IV and II, while the lowest between III and I. The highest intra cluster distance was observed in cluster III that revealed maximum variability within the clusters. In this study, two traits such as number of branches/plant and number of seeds/capsule contributed the maximum towards divergence in the existing germplasm.

Islam and Islam (2000) reported the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were grouped into four clusters. The inter-cluster distances were larger than the intra-cluster distances. The

characters contributed maximum in divergence analysis is days to 50% flowering, plant height, primary branches/plant and number of siliquae/plant.

Genetic divergence was studied by Dhillon *et al.* (1999) for seed yield and six important yield components in Indian mustard (*Brassica juncea* Czern & Coss) and found 8 clusters. Cluster I comprising of 24 genotypes, whereas clusters VI, VII and VIII comprised of one genotype of each. Seed yield per plant showed maximum divergence followed by number of siliqua on main shoot and minimum by number of primary branches per plant. The inter cluster distance was maximum between clusters V and VIII (713.86) followed by clusters V and III (454.63).

Uddin (1994) conducted an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Thirty one toria genotypes were grown in 12 artificially created environments in order to study genetic divergence by Singh and Gupta (1984). D^2 estimates based on 12 characters were used in obtaining the clustering pattern and inter- and intra-cluster distances. Out of 31 genotypes, on the basis of stability, high yield and divergence six genotypes were found to be suitable for use in a breeding program.

Chapter 3

METERIALS AND METHODS

This chapter describes the information on the subject of materials and methods that were used in conducting the experiment. It consists of a short explanation of locations of the experimental site, soil characteristics, climate, materials used in the experiment, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural practices, harvesting, data recording procedure and statistical analysis etc. which are presented as follows:

3.1 Experimental site

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during November 2017 to February 2018. The location of the experimental site was situated at $23^0$74' N latitude and $90^0$35' E longitude with an elevation of 8.6 meter from the sea level. Photograph showing the experimental site (Appendix I).

3.2 Soil and Climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to the Agro-ecological zone of "The Modhupur Tract" (AEZ-28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH ranges from 5.47 to 5.63 and organic carbon content is 0.82% (Appendix III). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix IV).

3.3 Experimental materials:

The healthy seeds of 26 advanced lines of BC_1F_6 of *Brassica napus L*. collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilt. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.4.2 Application of manure and fertilizer

The field was fertilized at the rate of 10 tons of Cowdung, The fertilizers like urea, triple super phosphate, muriate of potash, gypsum and zinc sulphate were applied in quantities of 270, 170, 100, 150 and 5kg ha^{-1}, respectively. The half amount of urea, total amount of Cowdung, TSP, MoP, Gypsum, Zinc Oxide and Boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

3.4.3 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 two 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. The spacing between lines to line was 30 cm. Seeds were sown in lines in the experimental

Table 1. Materials

Genotype	BC_1F_6 population	Source
G1	(205 x130) x 205	GEPB, SAU
G2	(2066x205) x 2066	GEPB, SAU
G3	(2066x0130) x 2066	GEPB, SAU
G4	(9906x205) x 205	GEPB, SAU
G5	(9905x2066) x 9905	GEPB, SAU
G6	(2066x0130) x 0130	GEPB, SAU
G7	(108x2066) x 108	GEPB, SAU
G8	(9905x9908) x 9908	GEPB, SAU
G9	(205x0130) x 0130	GEPB, SAU
G10	(9905x0130) x 9905	GEPB, SAU
G11	(108x01300) x 108	GEPB, SAU
G12	(108x9908) x 108	GEPB, SAU
G13	(9908x0130) x 9908	GEPB, SAU
G14	(9905x0130 x) 0130	GEPB, SAU
G15	(9908x0130) x 0130	GEPB, SAU
G16	(108x205) x 108	GEPB, SAU
G17	(9908x2066) x 9908	GEPB, SAU
G18	(9906x2066) x 9906	GEPB, SAU
G19	(9905x108) x 108	GEPB, SAU
G20	(9906x9901) x 9906	GEPB, SAU
G21	(9905x108) x 9905	GEPB, SAU
G22	(9905x9901) x 9901	GEPB, SAU
G23	(2066x205) x 205	GEPB, SAU
G24	(9901x203) x 9901	GEPB, SAU
G25	(108x2066) x 2066	GEPB, SAU
G26	(9905x9901) x 9905	GEPB, SAU

plots on 24 November 2017. 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. A pictorial view of germinating plot was shown in Plate 1.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart (plate 2). Second weeding was done after 35 days of sowing. Sap sucking insect aphid infestation was found in the crop during the siliqua development stage. Insecticide Malataf 57 EC under Malathion group @ 2 ml/liter of water was applied for controlling aphid. The insecticide was applied in the afternoon. Tagging was done timly. Field inspection was done time to time (Plate 5).

3.4.5 Crop harvesting

The crop was harvested in different dates according to maturity (Plate 7). Harvesting was done in 2 March 2018. When 80% of the plants showed maturity symptoms like straw color of siliqua, leaves, stem and desirable seed color in the matured siliqua, the crop was assessed to attain maturity. The harvesting wad done by my supervision and also present my research supervisor, the photograph shown in Plate 7. Fifteen plants were selected at randomly from BC_1F_7 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants (Plate 8).

Plate 1. Photograph showing the germination stage of *Brassica napus*

Plate 2. a. first thinning stage b. second thinning stage

Plate 3. Photograph showing the flowering stage of *Brassica napus* field

Plate 4. Siliqua formation stage

Plate 5. Field inspection by my respected supervisor

Plate 6. Maturity stage of experimental field

Plate 7. Selected 15 plants are harvested from the each line of the field

3.4.6 Data collection

Ten characters were taken into consideration for studying different genetic parameters, association and genetic diversity. Data were recorded on 15 selected plants for each genotype for each replication on following parameters. The details of data recording are given below on individual plant basis.

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

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

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

iv. **Number of primary branches per plant:** The total number of branches arisen from the main stem of a plant was counted as the number of primary branches per plant.

v. **Number of secondary branches per plant:** The total number of branches arisen from the primary branch of a plant was counted as the number of secondary branches per plant.

vi. **Number of siliquae per plant:** Total number of siliquae of each plant was counted and considered as the number of siliqua 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:** Well filled seeds were counted from five siliquae which was considered as the number of seeds per siliqua.

ix. **1000-seed weight (g):** Weight in grams of randomly counted thousand

.

Plate 8. Photograph showing the data collection from the field

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.

3.5 Statistical analysis

The data were analyzed for different components. 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 Chaudhury (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Simple correlation coefficient was obtained using the formula suggested by Clarke (1973). Singh and Chaudhury (1985) and path coefficient analysis was done following the method outlined by Dewey and Lu (1995).

i) Estimation of genotypic and phenotypic variances:

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

a. **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 replication

b. **Phenotypic variance**, Where, $\delta^2 p = \delta^2 g + \delta^2 e$

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

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

ii) Estimation of genotypic and phenotypic co-efficient of variation:

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

$$GCV = \frac{\delta_g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta_p \times 100}{\bar{x}}$$

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 mean

iii) Estimation of heritability:

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$h^2_b(\%) = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where, h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Penotypic variance

iv) 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).

$$GA = \frac{\delta^2_g}{\delta^2_p} . K . \delta_p$$

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

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

v) Estimation of genetic advance in percentage of mean

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

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{x}} \times 100$$

vi) Estimation of simple correlation co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Clarke, 1973; 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

vii) Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) 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:

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

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

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

Where, r's 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):

$$P^2_{RY} = 1 - \sum P_{iy} \cdot riy$$

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

riy = Correlation of the character with yield.

viii) Estimation of Genetic Diversity

a. Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the

sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jager *et al.* 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

b. Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the point using similarity matrix (Digby *et al.* 1989).

c. Canonical Vector Analysis (CVA)

The canonical vector analysis compute a linear combination of original variability that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variability that can be used to discriminate between groups. Finally a series of orthogonal transformations sequentially maximizing ratio among groups within group variations.

d. Average Intra-cluster Distances

The average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotype included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

e. Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

Chapter 4

RESULTS AND DISCUSSIONS

In the present investigation the data was collected from twenty six diverse *Brassica napus* genotypes on eleven traits related to vegetative, reproductive and yield components parameters emphasizing growth and yield. The data were subjected to biometrical and biochemical analysis and results obtained are following headings:

4.1 Varietal performance and genetic parameters

4.2 Correlation studies

4.3 Path co-efficient analysis

4.4 Genetic diversity

4.1 Varietal performance and genetic parameters

4.1.1 Analysis of variance

The analysis of variance indicated highly significant amount of variability present among the genotypes for all the characters studied viz. Days of 50% flowering, Days of 50% maturity, plant height (cm), primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length (cm), seeds per siliqua, thousand seed weight (g) and seed yield per plant (g) (Table 3). The results clearly revealed that presence of high variability for yield and yield contributing characters among the genotypes studied. Therefore there is a lot of scope for selection for majority of the traits in the genotypes. The mean sum of squares of all the tent characters are presented in Table 3. Significant differences among the genotypes was observed by many researcher like Shalini *et al*. (2000), Pant and

Table 2. Analysis of variance for different characters in *Brassica napus* genotypes

Parameters	Mean Sum of Square		
	Replication (df = 2)	**Treatment (df = 25)**	**Error (df = 50)**
Days to flowering	0.17	4.28**	1.79
Days to maturity	3.55	4.74**	1.12
Plant height (cm)	58.97	113.90**	19.43
Primary branch per plant	0.36	0.41**	0.22
Secondary branch per plant	0.23	0.49**	0.27
Siliqua per plant	79.20	761.79**	108.97
Siliqua length (cm)	0.41	0.95**	0.33
Seeds per Siliqua	7.43	10.86**	6.20
1000 seed weight (mg)	0.21	1.70**	0.29
Seed yield per plant (g)	0.23	2.06**	0.36

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

Singh (2001), Thakra *et al*. (2004), Rukhsana *et al.* (2005), Uddin *et al.* (2005), Khan *et al.* (2006), Parveen (2007), Zebarjadi *et al.* (2011) and Walle *et al*. (2014).

The presence of narrow gap between PCV and GCV for all the characters expect secondary branches per plant under study, suggested that these traits studied had low environmental influence except secondary branches per plant. The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent mean for all the characters were studied and the results are presented in Table 3 and depicted in Figure 1 and 2. The mean performance of Brassica napus BC_1F_7 genotypes for various growth characters and yield components are presented in Table 4.

4.1.1.1 Days to 50% flowering

Considerable variations were observed among 26 BC_1F_7 populations for days to 50% flowering. The minimum days to 50% flowering were observed the (36.00days) in G5, G8 and G19 and the maximum(40.67days) was observed in G20 (Table 4).

Phenotypic and genotypic variance for days to 50% flowering was observed as 2.62 and 0.83 respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The PCV (4.26%) was higher than the GCV (2.40%) (Table 5) which suggested that environment has a significant role on the expression of this trait. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.* (1998).

Significant genetic variability in days to 50% flowering in *B. napus* was also observed by Singh *et al.* (1991).

4.1.1.2 Days to maturity

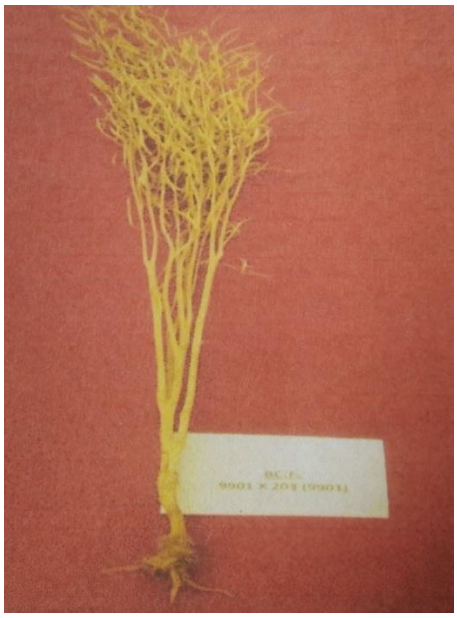
The maximum days to maturity was observed in G25 and G26 (118 days) and the minimum days to maturity was observed in G23 (113.67days) (Table 4). Phenotypic and genotypic variance for days to maturity was observed 2.33 and 1.20 respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The PCV (1.32%) was higher than the GCV (0.95) (Table 5), which suggested that environment has a significant role on the expression of this trait. Higher genotypic variances indicated the better transmissibility of a character from parent to the offspring. Similar result for this trait was also observed by Katiyar *et al*. (1974).

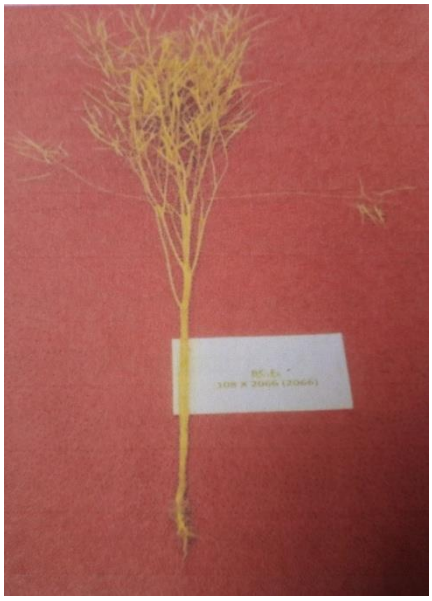
4.1.1.3 Plant height (cm)

In this study the highest plant height was observed in G18 (113.63cm) whereas the minimum plant height was observed in G17 (87.90cm) (Table 3) (Plate 9). Phenotypic variance and genotypic variance were observed as 50.92 and 31.49 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The estimates of PCV (7.33%) and GCV (5.76%) also indicated presence of considerable variability among the genotypes for this trait (Table 5). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al.* (2001).

4.1.1.4 Number of primary branches per plant

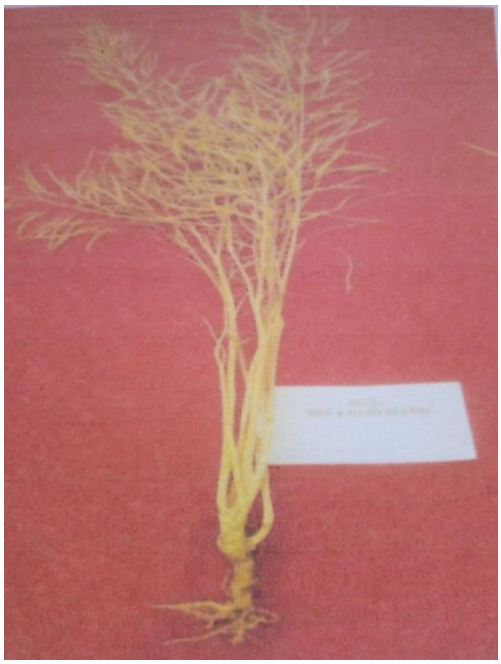
Among the 26 BC_1F_7 populations the highest number of primary branches per plant was observed in G20 (4.42) whereas the minimum number of primary branches/plant was observer in G19 (3.06) (Table 3). Relatively large differences between them indicating large environmental influences on these character and relatively high difference between PCV (14.05%) and GCV (6.66%) value indicating the apparent variation not only due to genotypes but also due to the large influence of environment.

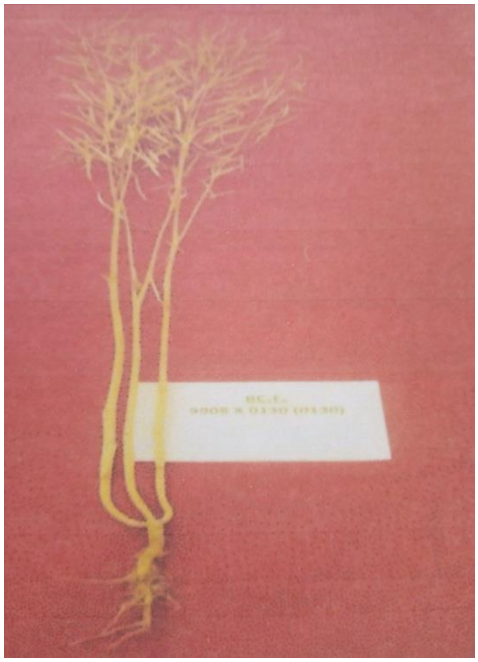




A. G18 **B . G17**

Plate 9. Photograph showing the maximum (A) and the minimum (B) plant height





C. G20 **D. G19**

Plate 10. Photograph showing the maximum (C) and the minimum (D) no. of primary branches of plant

Table 3. Range, mean, CV (%) and standard deviation of 26 *Brassica napus* genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Days to flowering	36.00	40.67	37.99	3.53	1.34	0.51
Days to maturity	113.67	118.00	116.05	0.91	1.06	0.40
Plant height (cm)	87.90	113.63	97.39	4.53	4.41	1.67
Primary branch per plant	3.06	4.42	3.77	12.37	0.47	0.18
Secondary branch per plant	1.20	2.95	2.06	25.20	0.52	0.20
Siliqua per plant	66.21	144.28	95.61	10.92	10.44	3.95
Siliqua length (cm)	6.63	9.21	7.86	7.33	0.58	0.22
Seeds per Siliqua	18.57	25.92	22.43	11.10	2.49	0.94
1000 seed weight (mg)	3.77	6.59	5.04	10.62	0.54	0.20
Seed yield per plant (g)	2.53	5.86	4.21	14.27	0.60	0.23

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

Table 4. Mean performance of different characters of 26 *Brassica napus* genotypes

Genotype	DF	DM	PH (cm)	PBP	SBP	SPP	SL (cm)	SPS	TSW (g)	SYP (g)
G1	38.00	114.00	107.24	4.12	2.33	144.28	7.10	21.22	5.02	4.45
G2	36.67	114.00	100.39	4.07	2.95	91.79	8.43	25.69	4.56	3.85
G3	38.00	114.67	98.31	3.88	2.43	104.72	7.84	21.20	4.57	4.01
G4	38.00	115.33	100.17	3.75	2.39	91.38	7.70	22.13	5.55	3.73
G5	36.00	115.33	97.05	4.03	2.43	89.11	7.49	22.67	4.54	3.47
G6	39.67	116.00	98.11	4.07	2.50	89.72	8.09	24.70	6.00	5.20
G7	38.00	115.00	97.20	3.53	2.27	94.98	7.91	23.73	5.67	2.53
G8	36.00	116.67	92.88	3.37	1.57	88.87	7.86	23.70	4.88	3.55
G9	38.00	116.33	91.40	3.37	1.97	67.32	6.63	20.67	4.36	4.73
G10	39.67	116.00	102.47	3.31	1.95	97.28	7.48	23.27	3.77	3.75
G11	39.33	116.33	92.76	3.89	1.97	105.27	7.10	19.08	4.47	4.77
G12	38.00	116.67	89.78	3.64	2.13	96.35	8.02	20.33	5.54	3.49
G13	37.33	115.00	98.80	3.52	1.87	97.46	7.30	19.58	6.59	4.76
G14	38.00	116.67	90.06	3.40	1.85	103.88	7.89	18.57	5.72	4.27
G15	37.33	116.00	91.19	3.66	1.87	66.21	7.77	22.57	5.52	5.86
G16	36.67	118.00	92.50	3.77	1.53	92.23	7.68	21.72	4.52	3.78
G17	37.67	116.67	87.90	3.17	1.53	75.07	8.25	23.40	5.51	4.89
G18	37.00	117.33	113.63	3.47	1.60	99.76	7.73	23.87	5.01	3.64
G19	36.00	115.67	92.57	3.06	1.47	76.80	7.43	21.33	3.89	4.34
G20	40.67	117.67	100.57	4.42	2.19	100.47	7.60	23.09	4.68	3.07
G21	38.67	117.33	102.14	4.30	2.17	96.65	8.83	25.92	5.62	3.91
G22	39.00	116.00	100.43	4.17	2.30	122.34	7.71	23.21	3.77	5.72
G23	38.00	113.67	107.93	4.00	2.40	104.45	8.43	23.68	5.31	3.75
G24	39.33	115.00	96.23	3.97	2.20	90.07	9.21	24.63	6.45	5.68
G25	38.67	118.00	92.62	3.77	1.20	89.19	8.51	21.23	4.77	4.57
G26	38.00	118.00	97.90	4.27	2.42	110.25	8.30	22.12	4.83	3.58

DF : Days to flowering
DM : Days to maturity
PH (cm) : Plant height (cm)
PBP : Primary branch per plant
SBP : Secondary branch per plant
SPP : Siliqua per plant
SL (cm) : Siliqua length (cm)
SPS : Seeds per Siliqua
TSW (g) : 1000 seed weight (g)
SYP (g) : Seed yield per plant (g)

Table 5. Estimation of genetic parameters for different characters in *Brassica napus* genotypes

Traits	σ^2p	σ^2g	$\sigma^2 e$	PCV	GCV	h^2	GA (5%)	GA (% mean)
Days to flowering	2.62	0.83	1.79	4.26	2.40	31.61	1.05	2.78
Days to maturity	2.33	1.20	1.12	1.32	0.95	51.72	1.63	1.40
Plant height (cm)	50.92	31.49	19.43	7.33	5.76	61.84	9.09	9.33
Primary branch per plant	0.28	0.06	0.22	14.05	6.66	22.48	0.25	6.51
Secondary branch per plant	0.34	0.07	0.27	28.46	13.24	21.65	0.26	12.69
Siliqua per plant	326.58	217.61	108.97	18.90	15.43	66.63	24.81	25.94
Siliqua length (cm)	0.54	0.21	0.33	9.32	5.76	38.23	0.58	7.34
Seeds per Siliqua	7.76	1.55	6.20	12.41	5.55	20.02	1.15	5.12
1000 seed weight (mg)	0.76	0.47	0.29	17.25	13.59	62.07	1.11	22.06
Seed yield per plant (g)	0.93	0.57	0.36	22.87	17.88	61.07	1.21	28.78

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

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

h^2 b : Broad sense heritability
GA (5%) : Genetic advance (5%)
GA (% mean) : Genetic advance (% mean)

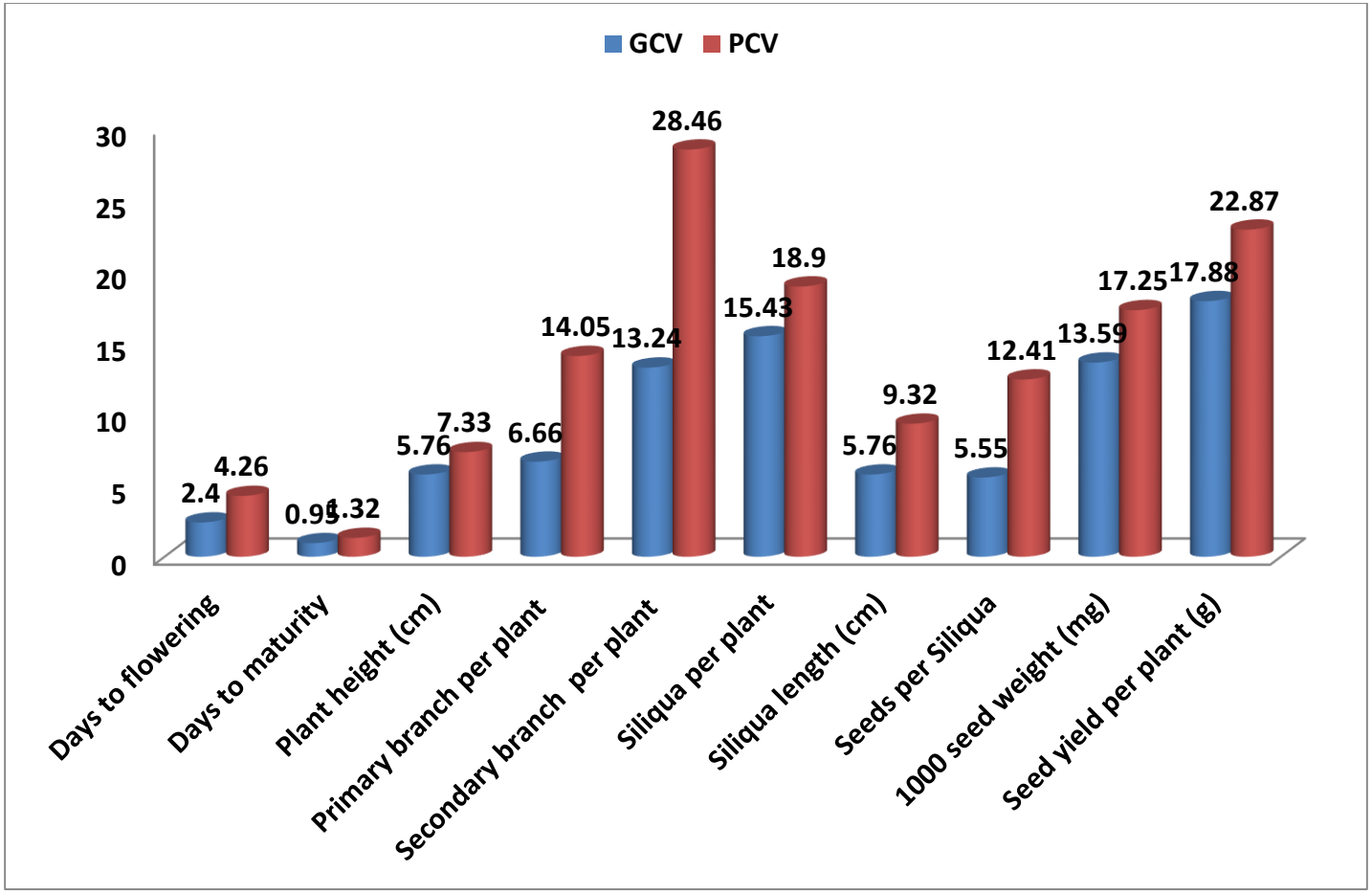


Figure 1: Genotypic and phenotypic variability in *Brassica napus*

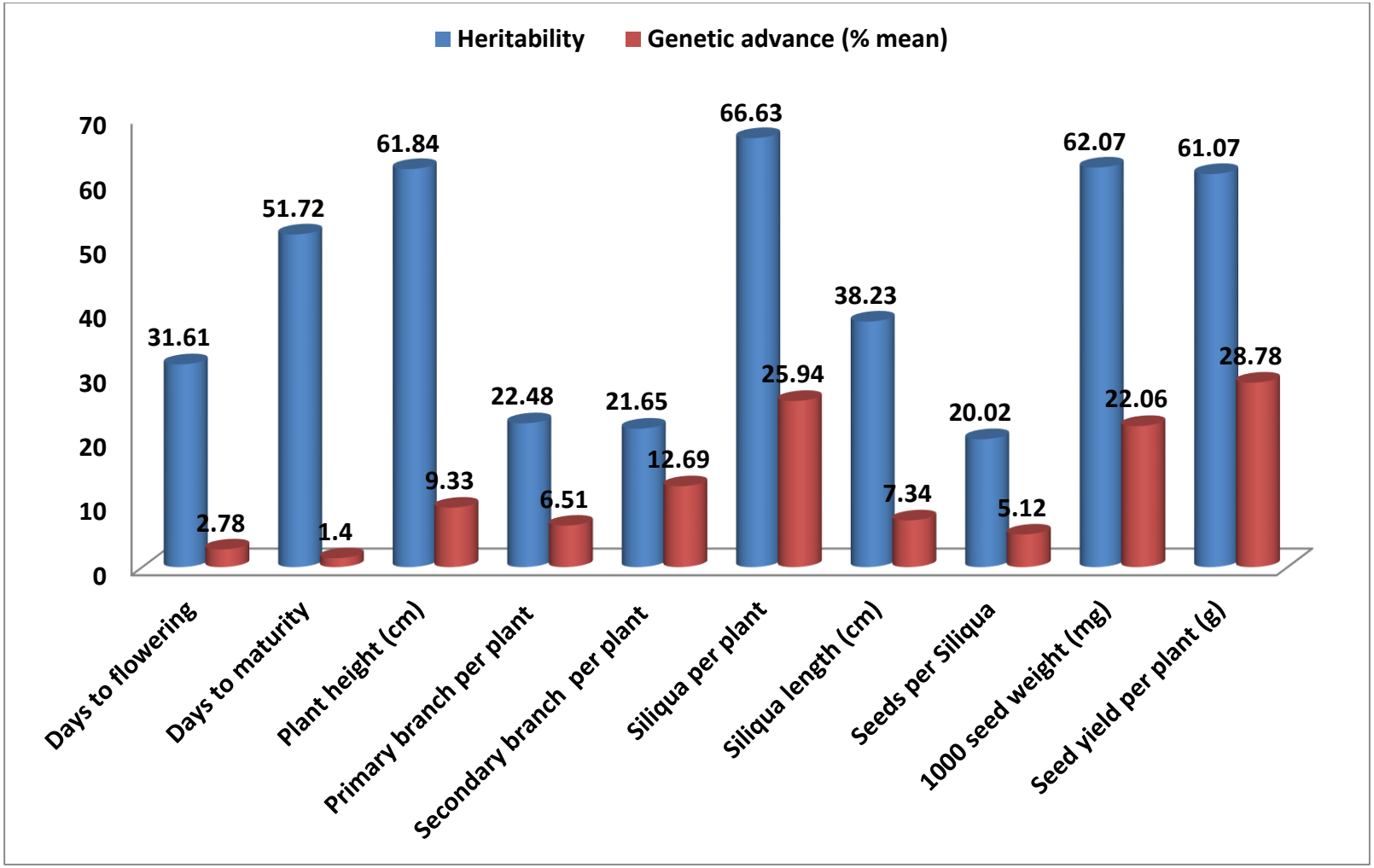


Figure 2: Heritability and genetic advance over mean in *Brassica napus*

large influence of environment (Table 5). Chowdhury *et al.* (1987) also found significant differences for number of primary branches per plant

4.1.1.5 Number of secondary branches per plant

Among the 26 BC_1F_7 populations the highest number of secondary branches/plant was observed in G2 (2.95) whereas the minimum number of secondary branches/plant was observed in G25 (1.20) (plate 11). Higher estimate of PCV (28.46%) and GCV (13.24%) values indicated presence of considerable variability among the genotypes for this trait (Table 5). Lekh *et al.* (1998) found highest genotypic coefficient of variation for number of secondary branches while working on 24 genotypes of *Brassica napus.* Chowdhury *et al.* (1987) found significant differences for number of secondary branches per plant. Genotypic and phenotypic variability in mustard are shown in Figure 1.

4.1.1.6 Number of siliqua per plant

The number of siliqua per plant was observed the highest in G1 (144.28) and the lowest in G15 (66.21) (Plate 12). Number of siliqua per plant showed the highest phenotypic variance (326.58) and genotypic variance (217.61) with large environmental influence and the difference between the PCV (18.90%) and GCV (15.43%) indicated existence of adequate variation among the genotype (Table 5). High genetic variation was also found by Kudla (1993).

4.1.1.7 Length of siliqua (cm)

Length of siliqua was observed the highest in G24 (9.21cm) and the minimum length of pod was observed in G9 (6.63) (Table 3) (Plate 13). Length of siliqua showed phenotypic variance (0.54) and genotypic variance (0.21) with little difference between them indicating that they were less responsive to environmental factors for their phenotypic expression an relatively medium PCV (9.32%) and GCV (5.76%) indicating that the genotype has moderate variation for

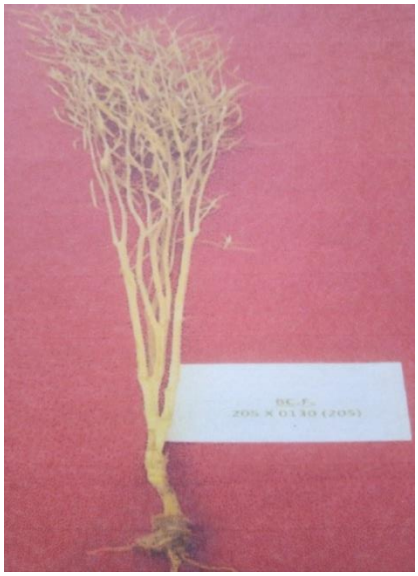
this trait (Table 5). High co-efficient of variation for this trait for both genotypic and phenotypic variability was recorded by Masood *et al.* (1999). High genetic variability for this trait was also found by Olson (1990).

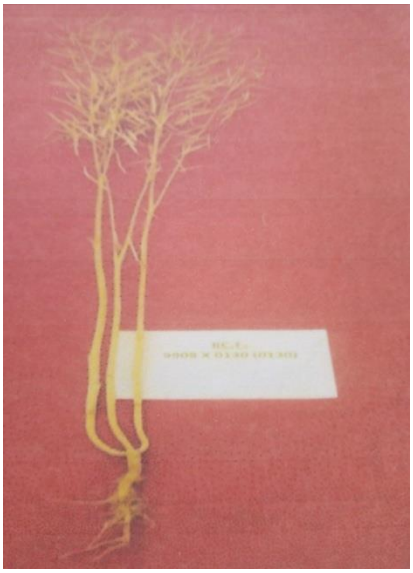
4.1.1.8 Number of seeds per siliqua

The number of seeds per siliqua was observed the highest G21 (25.92). The minimum number of seeds per siliqua was observed G14 (18.57) (Table 3). The phenotypic and genotypic variances for this trait were 7.76 and 1.55 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 12.41% and 5.55% respectively for number of seeds per siliqua which indicating that medium variation exists among different genotypes (Table 5). Similar variability was also recorded by Kumar and Singh (1994).

4.1.1.9 Thousand seed weight (g)

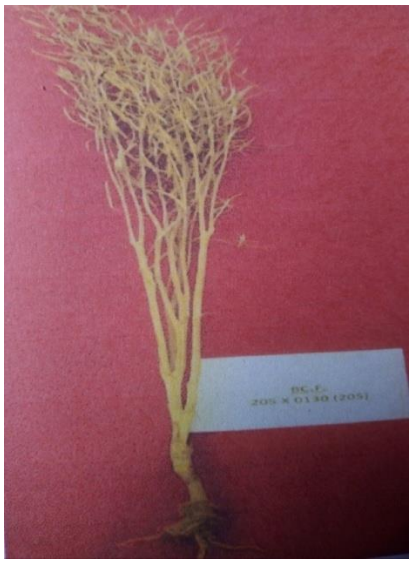
Thousand seed weight was found the maximum in G13 (6.59g) whereas the minimum thousand seed weight was found in G10 (3.77 g) (Table 3) (plate 14). Thousand seed weight showed very low genotypic (0.76) and phenotypic (0.47) variance with high differences indicating that they were high responsive to environmental factors. The phenotypic coefficient of variation (17.25%) and genotypic coefficient of variation (13.59%) were not close to each other (Table 5). The difference between phenotypic and genotypic co-efficient of variation indicating major environmental influence on this character. Significant variability for this trait was also found by Kumar and Singh (1994). Masood *et al.* (1999) found high coefficient of variation for thousand seed weight while working with seven genotypes of *Brassica napus* to study genetic variability.

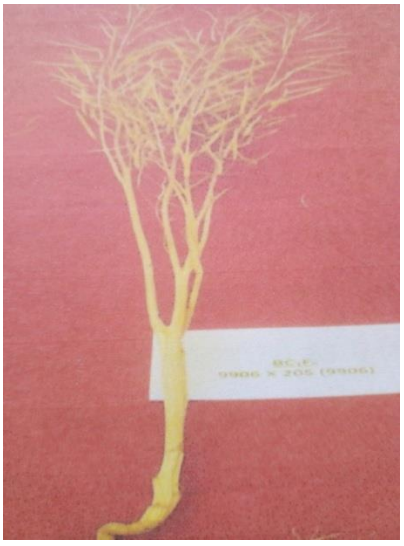




E. G2 **F. G25**

Plate 11: Photograph of selected genotype showing the maximum (E) and the minimum (F) no. of secondary branches of plant





G. G1 **H. G15**

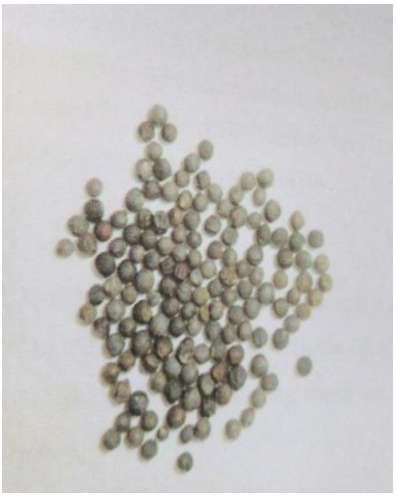
Plate 12: Photograph of selected genotype showing the maximum (G) and the minimum (H) no. of siliqua per plant

I. G24

J. G9

Plate 13: Photograph of selected genotype showing maximum (I) and minimum (J) length of siliqua

K .G13



L.G10

Plate 14: Photograph showing the genotypes of the highest (K) and the lowest (L) genotypes of 1000 seed weight

4.1.1.10 Yield per plant (g):

Yield per plant was found the maximum in G15 (5.86 g) when it was the minimum yield per plant was found in G7 (2.53g) (Table 3) (Plate 15). The phenotypic variances and genotypic variances for this trait were 0.93 and 0.57 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The values of PCV and GCV were 22.87% and 17.88% indicating that the genotype has considerable variation for this trait (Table 5). Similar variability was also found by Khera and Singh (1988).

Plate 15: photograph showing the maximum seed yield per plant (G15).

4.1.2 Genetic variability, heritability and genetic advance

The success of crop improvement program depends on the amount of genetic variability presented in the population. The extent of genetic variability can determine the speed and quantum of genetic improvement through selection or hybridization followed by selection. Phenotypic variance measures the magnitude of variability arising out of differences in phenotypic values while the genotypic variance measures the magnitude of variation due to difference within the genotypic values.

The heritability estimates separate the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. Its aim in determining the relative amount of heritable portion of variation. As such the heritability in broad sense is the proportion of genotypic variability to the total variability, its importance has been emphasized by Lush (1949) in animals and Johnson *et al.* (1995) in plants.

4.1.2.1 Days to 50% flowering:

Table 5 shows the days to 50% flowering exhibited low heritability (31.61%) with low genetic advance (1.05) and genetic advance in percentage of mean (2.78%) indicated that this trait was controlled by non-additive gene. This results support the reports of Malik *et al.* (1995).

4.1.2.2 Days to maturity:

Days to maturity shows low heritability (51.72%) with low genetic advance (1.63) and genetic advance in percentage of mean (1.40%) indicated in table 5 that this trait was controlled by non-additive gene and medium possibility of selecting genotypes that would mature earlier. In some of the crosses the frequency of the segregating plants showing reduced maturity was comparatively higher than the

other crosses. Low heritability coupled with low genetic advance for this trait was also observed by Sharma (1988).

4.1.2.3 Plant height (cm):

Plant height of BC_1F_7 showed high heritability (61.84%) with moderately high genetic advance of (9.09) and genetic advance in percentage of mean of (9.33%)(Table 5), revealed the possibility of predominance of additive gene action in the inheritance of this trait and indicating that this trait could be improved through selection process. High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *et al.* (1986). Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *Brassica rapa*. Heritability and genetic advance in percentage of mean are shown in Figure 2.

4.1.2.4 Number of primary branches per plant:

Number of primary branches per plant exhibited low heritability 22.48% with low genetic advance of 0.25 and genetic advance in percentage of mean of 6.51%, (table 5) which revealed that this trait was controlled by non-additive gene. As a whole, the low heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by Singh et al. (1987). Yadava *et al.* (1985) found high heritability and genetic advance for number of primary branches per plant.

4.1.2.5 Number of secondary branches per plant:

Number of secondary branches per plant exhibited low heritability (21.65%) with low genetic advance 0.26 and genetic advance in percentage of mean (12.69%) (table 5), such results revealed that this trait was controlled by non-additive gene.

As a whole, the low heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes. Moderately low heritability coupled with low genetic advance was also found by Singh *et al.* (1987). Sheikh *et al.* (1999) found high heritability coupled with high genetic advance for number of secondary branches per plant while working with 24 genotypes of toria.

4.1.2.6 Number of siliqua per plant:

Number of siliqua per plant exhibited moderatly high heritability 66.63% with high genetic advance 24.81 and genetic advance in percentage of mean 25.94% (Table 5).These results revealed the possibility of predominance of additive gene action in the inheritance of this trait. This trait possessed high variation; it is high potential for effective selection for further genetic improvement of this character. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). Mahmood *et al*. (2003) reported that the number of siliqua per plant were highly heritable coupled with high genetic advance. Akbar *et al.* (2007) also found higher GCV, higher heritability and genetic advance for this trait.

4.1.2.7 Siliqua length:

Siliqua length showed low heritability (38.23%) with low genetic advance (0.58) and low genetic advance in percentage of mean 7.34% in Table 5 indicated that this trait was controlled by non-additive gene. High heritability for this trait was observed by Chaudhury *et al*. (1987).

4.1.2.8 Number of seeds per siliqua:

Number of seeds per siliqua showed low heritability 20.02% coupled with high genetic advance 1.15 and high genetic advance in percentage of mean 5.12% in Table 5 indicated that this trait was controlled by additive gene and selection for

this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Singh (1986).

4.1.2.9 Thousand seed weight:

Thousand seed weight exhibited high heritability 62.07% with low genetic advance 1.11 and high genetic advance in percentage of mean 22.06% (Table 5) revealed that this trait was controlled by non-additive gene. Walker (2001) reported that moderate values of heritability and the genetic advance may be due to non-additive gene action which includes dominance and epistasis. Johnson *et al*. (1955) reported that heritability estimates along with genetic group were more useful in prediction selection of the best individual. High heritability for this trait was also observed by Yadava *et al.* (1993).Singh *et al.* (2002) reported the high heritability and genetic advance for thousand seed weight.

4.1.2.10 Seed yield per plant:

Seed yield per plant showed high heritability 61.07% with low genetic advance 1.21 and moderately high genetic advance in percentage of mean 28.78% in Table 5 indicated this trait was controlled by additive gene and selection for this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). High heritability and genetic advance for seed yield per plant was reported by Singh (1986) while working with 22 genotypes of *Brassica napus.*

Significant variability was found in almost all the BC_1F_7 materials *Brassica napus* for most of the characters studied.

4.2 Correlation coefficient

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much

essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for BC_1F_7 materials of *B. napus* are shown in (Table 6).

4.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity (G = 0.194, P = 0.114) indicated that if days to 50% flowering increased then days to maturity also increased. It also exhibited insignificant and positive interaction with number of seed per siliqua (G = 0.030, P = 0.079), siliqua length (G = 0.138, P = 0.135). However it has significant difference with yield per plant (G = 0.319, P = 0.070) and number of siliqua per plant (G = 0.375, P = 0.186) (Table 6). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Parveen (2007) also revealed that days to 50% flowering had insignificant and positive interaction with yield per plant.

4.2.2 Days to maturity

Days to maturity showed significant and negetive correlation with number of seeds per siliqua (G= -0.230, P= -0.038) and siliqua length (G = 0.151, P = -0.029). It had insignificant and negetive correlation with yield per plant (G = -0.119, P = -0.073) with thousand seed weight (G = -0.241, P = -0.042) (Table 6). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Parveen (2007) also revealed that days to maturity had insignificant and positive interaction with yield per plant.

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

Traits		DF	DM	PH (cm)	PBP	SBP	SPP	SL (cm)	SPS	TSW (mg)
DM	G	0.194								
	P	0.114								
PH (cm)	G	0.161	-0.388**							
	P	0.122	-0.216							
PBP	G	0.727**	0.006	0.593**						
	P	0.270*	-0.054	0.272*						
SBP	G	0.447**	-0.995**	0.468**	0.816**					
	P	0.089	-0.296**	0.337**	0.567**					
SPP	G	0.375**	-0.220	0.564**	0.717**	0.382**				
	P	0.186	-0.170	0.536**	0.389**	0.361**				
SL (cm)	G	0.138	0.151	0.031	0.360**	0.269*	-0.084			
	P	0.135	-0.029	0.048	0.273*	0.064	-0.036			
SPS	G	0.030	-0.230*	0.748**	0.440**	0.677**	-0.204	1.000**		
	P	0.079	-0.038	0.206	0.266*	0.193	-0.067	0.336**		
TSW (mg)	G	0.103	-0.241*	-0.031	0.151	0.263*	-0.071	0.539**	0.182	
	P	0.084	-0.042	-0.064	-0.048	-0.044	-0.133	0.314**	-0.017	
SYP (g)	G	0.319**	-0.119	-0.338**	-0.071	-0.178	-0.173	0.068	-0.094	0.170
	P	0.070	-0.073	-0.140	0.001	-0.114	-0.102	0.015	-0.088	0.126

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

DF : Days to flowering
DM : Days to maturity
PH (cm) : Plant height (cm)
PBP : Primary branch per plant
SBP : Secondary branch per plant
SPP : Siliqua per plant
SL (cm) : Siliqua length (cm)
SPS : Seeds per Siliqua
TSW (mg) : 1000 seed weight (mg)
SYP (g) : Seed yield per plant (g)

possitive associations between plant height and other characters indicate that the traits were governed by same gene and simultaneous improvement would be effective. However, it had significant and negative interaction with thousand seed weight (G = -0.228, P = 0.198) and seed yield per plant (G = -0.338, P = -0,140) (Table 6). Significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showed resemblance to the reports of Parveen (2007). Shalini *et al.* (2000) also observed that plant height was highly associated with seed yield. Similar result was reported by Srivastava *et al.* (1983). Significant positive correlation between plant height and seed yield was found by Khan and Khan (2003). Chaudhary *et al.* (1990) found positive correlation of plant height with number of seed per siliqua, number of siliqua per plant. Basalma (2008) reported opposite result for this trait.

4.2.4 Number of primary branches per plant

Number of primary branches per plant showed positive and significant interaction with number of secondary branch (G = 0.816, P = 0.567), number of siliqua per plant (G = 0.717, P = 0.389), siliqua length (G = 0.360, P = 0.273) and seeds per siliqua (G = 0.440, P = 0.266) (Table 6). These suggesting if number of primary branches increases then yield per plant also increases. Malik *et al.* (2000) reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. However, it had insignificant and negative interaction was found in seed yield per plant (G = -0.071, P = 0.001), thousand seed weight (G = 0.151, P = -0.048) (Table 6). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Similar results were obtained by Rashid (2007).

4.2.5 Number of secondary branches per plant

Number of secondary branch showed highly significant and positive interaction with number of siliqua per plant (G = 0.382, P = 0.361), seeds per siliqua (G = 0.677, P = 0.193) and siliqua length (G = 0.269, P = 0.064) indicated in Table 6 that the traits were governed by same gene and simultaneous improvement would be effective and branching was an important contributor to yield , independent of its association with plant size. However, it had insignificant and negative interaction with thousand seed weight (G = 0.263, P = -0.044), seed yield per plant (G = -0.178, P = -0.114) (Table 6). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showing similar to the reports of Chowdhary *et al.* (1987).

4.2.6 Number of siliqua per plant

Siliqua per plant showed significant and negative correlation with days to maturity (G = -0.220, P = -0.170), yield per plant (G = -0.173, P = -0.102) and seeds per siliqua (G = -0.084, P = -0.036) showed in Table 6. Malik *et al.* (2000) reported negetive correlation between siliqua per plant and seed yield. Whereas the insignificant and negetive interaction was found in number of seed per siliqua (G = -0.204, P = -0.067), thousand seed weight (G = -0.071, P = -0.133) (Table 6). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Tyagi *et al.* (1996) reported that no. of seed per siliqua had positive and insignificant effect on seed yield per plant.

4.2.7 Siliqua length (cm)

Siliqua length showed insignificant and positive correlation with seed yield per plant (G=0.068, P=0.015) indicated that the traits were governed by same gene and simultaneous improvement would be effective. It also showed highly

significant and positive correlation with thousand seed weight (G=0.539, P=0.314) (Table 6) indicated that if siliqua length increased then thousand seed weight decreased. 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 length (G = 1.00, P = 0.336) (table 6). Highly significant positive associations between number of seeds per siliqua and seed length indicated that the traits were governed by same gene and simultaneous improvement would be effective. It had insignificant and negative interaction with thousand seed weight (G = 0.182, P = -0.017). However, it had insignificant and negative interaction with yield per plant (G = -0.094, P = -0.088) (Table 6). Insignificant association of these traits indicated that the association between these traits largely influenced by environmental factors. Nasim *et al.* (1994) reported that no. of seeds per siliqua had negative and significant effects on seed yield per plant. Ahmed (1993) also found similar results for this trait.

4.2.9 Thousand seed weight

Thousand seed weight showed insignificant and positive interaction with yield per plant (G=0.170, P=0.126) (Table 6). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Saini and Kumar (1995), Kakroo and Kumar (1991) and Olsson (1990) found positive associations which support the results. Tuncturk and Ciftci (2007) reported positive correlation between seed yield with 1000-seed weight which does not support the present findings.

4.2.10 Seed yield per plant (g)

Seed yield per plant had highest significant negative correlation with number of secondary branches per plant (G = -0.178, P = -0.114) and plant height (G = -0.338, P = -0.140) (Table 6) at both phenotypic and genotypic level suggesting, if the number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant increase then seed yield per plant also increase. Yield per plant had also significant positive correlation with days to 50% flowering (G = 0.319, P = 0.070). This trait had also negative insignificant correlation with days to maturity (G = -0.119, P = -0.073), primary branches per plant (G = -0.071, P =0.001) (Table 6). Kumar *et al.* (1999) reported that seed yield had positive correlation with plant height, number of siliqua per plant and thousand seed weight. Jeromel *et al.* (2007) found complete positive correlation between plant height and yield. Siddikee (2006) revealed that yield per plant had highest significant positive correlation with number of siliqua per plant. Srivastava and Singh (2002) revealed that number of primary branches per plant and number of secondary branches per plant were positively associated with seed yield.

4.3. Estimation of path co-efficient

As such from existing agro climatic situation based performed using correlation coefficient to determine direct and indirect influence considering ten characters. Seed yield being the complex outcome of different characters was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters are shown in Table 7. Among the characters that have positive direct effect on seed yield per plant, days to 50% flowering (1.180), plant height (0.009), secondary branches per plant (0.210), number of siliqua per plant (0.493), siliqua length(0.498), number of seeds per siliqua (0.005) had positive direct effects on seed yield per plant. The genotypic correlation of days to maturity, plant height, primary branches per plant, number of siliqua per plant, number of seeds per siliqua and 1000 Seeds weight with seed yield was high. Such high correlation with seed yield per plant was

mainly due to the high positive direct effect of these characters. Both correlation and path co-efficient studies revealed for days to maturity, primary branches per plant, number of siliqua per plant and 1000 seeds weight were the most important components for getting higher yield. Recent breeding research also emphasized on giving importance of these characters. Therefore, the present study suggested that days to maturity, primary branches per plant, number of siliqua per plant and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher seed yield in *Brassica napus.*

4.4 Genetic diversity

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. Genetic diversity serves as a way for populations to adapt to changing environments. The genetic diversity of 26 BC_1F_7 materials of *Brassica napus* genotypes are presented in Table 8 to 14.

4.1 Principal Component Analysis (PCA)

The computed Eigen values for the 10 variables subjected to principal component analysis together with the corresponding proportion and cumulative explained variance are given in Table 8. Following the proportion of variance criterion, two principal components were retained and these are the principal components whose cumulative explained variances were equal to or more than 99%. The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes (29.70).These three principal components account for 61.00% of the total variation (Table 8). Zaman *et al.* (2010) reported that first three axes accounted for 94.00% of the total variation whereas the first principal components accounted for 81.94%. Khan (2014) reported that the contribution of first three PCs in overall PCs was 26.96%.

Table 7. Partitioning of genotypic correlations into direct (bold) and indirect effects of important characters by path analysis of *Brassica napus*

	DF	DM	PH (cm)	PBP	SBP	SPP	SL (cm)	SPS	TSW (mg)	Genotypic correlation with yield
DF	**1.180**	-0.019	0.001	-1.190	0.094	0.185	0.068	0.000	-0.002	0.319**
DM	0.229	**-0.096**	-0.003	-0.009	-0.209	-0.109	0.075	-0.001	0.004	-0.119
PH (cm)	0.190	0.037	**0.009**	-0.970	0.098	0.278	0.015	0.004	0.001	-0.338**
PBP	0.858	-0.001	0.005	**-1.637**	0.171	0.353	0.179	0.002	-0.002	-0.071
SBP	0.527	0.096	0.004	-1.336	**0.210**	0.188	0.134	0.003	-0.004	-0.178
SPP	0.442	0.021	0.005	-1.173	0.080	**0.493**	-0.042	-0.001	0.001	-0.173
SL (cm)	0.162	-0.015	0.000	-0.589	0.056	-0.041	**0.498**	0.005	-0.009	0.068
SPS	0.035	0.022	0.006	-0.720	0.142	-0.101	0.519	**0.005**	-0.003	-0.094
TSW (mg)	0.121	0.023	0.000	-0.247	0.055	-0.035	0.268	0.001	**-0.016**	0.170

Residual effect: **0.490**

** = Significant at 1%.

DF : Days to flowering
DM : Days to maturity
PH (cm) : Plant height (cm)
PBP : Primary branch per plant
SBP : Secondary branch per plant
SPP : Siliqua per plant
SL (cm) : Siliqua length (cm)
SPS : Seeds per Siliqua
TSW (mg) : 1000 seed weight (mg)
SYP (g) : Seed yield per plant (g)

Table 8. Eigen values and yield percent contribution of 10 characters of 26 genotypes

Principle component axis	Eigen values	Percent variation	Cumulative % of Percent variation
I	2.970	29.70	29.70
II	1.754	17.54	47.24
III	1.376	13.76	61.00
IV	1.264	12.64	73.64
V	0.836	8.36	82.00
VI	0.690	6.90	88.90
VII	0.534	5.34	94.24
VIII	0.349	3.49	97.73
VIX	0.130	1.30	99.03
X	0.097	0.97	100.00

4.4.2 Non-Hierarchical Clustering

Twenty six genotypes were grouped into five clusters through non-hierarchical clustering (Table 9). Most of the genotypes (11) were grouped into cluster II .They are G2, G4, G5, G6, G7, G8, G12, G13, G16, G24, G25 followed by cluster I (5) G3, G11, G14, G22, G26 and cluster V (5) G10, G18, G20, G21, G23 . Four genotypes were grouped into cluster IV (G9, G15, G17, G19). G1 alone is in cluster III. Rameeh (2015) reported three clusters, Iqbal *et al.* (2014) reported four clusters and Begum *et al.* (2007) reported five clusters in linseed.

4.4.3 Cluster mean

The genotypes from cluster IV earned the lowest cluster mean value for days to 50% flowering (37.25) and highest cluster mean value for Days to maturity (116.40), number Of seeds per siliqua (23.97) (Table 10).Thus indicates that genotype of this cluster could be used for parent in future hybridization program for early flowering and high seeds per siliqua.

On the other hand Cluster III produced the highest mean for plant height (107.24), primary branches per plant (4.12), secondary branches per plant (2.33), siliqua per plant (144.28) indicated the genotype of this cluster could be used for future hybridization program for higher siliqua per plant and higher branches per plant. The genotypes included in cluster III were lowest mean value for days to maturity (144.00). It indicated the genotype of this cluster could be used for future hybridization program for early maturity plant type. On the other hand, cluster V showed the late 50% flowering (38.80) (Table 10). It indicated the genotype of this cluster could be used for future hybridization program for late maturity plant type. Zaman *et al*. (2010) reported that the highest cluster means for primary branches per plant and maximum seeds per siliqua with minimum seed yield per plant were obtained from the cluster II.

Table 9. Distribution of 26 genotypes of *Brassica napus* in different clusters

Cluster no.	Accession No.	No. of populations
I	G3, G11, G14, G22, G26	5
II	G2, G4, G5, G6, G7, G8, G12, G13, G16, G24, G25	11
III	G1	1
IV	G9, G15, G17, G19	4
V	G10, G18, G20, G21, G23	5
Total		26

Table 10. Cluster mean values of 10 different characters of 26 genotypes

Characters	**I**	**II**	**III**	**IV**	**V**
Days to flowering	38.47	37.67	38.00	37.25(L)	38.80(H)
Days to maturity	116.33	115.91	114.00(L)	116.17	116.40(H)
Plant height (cm)	95.89	95.98	107.24(H)	90.76(L)	105.35
Primary branch per plant	3.92	3.77	4.12(H)	3.32(L)	3.90
Secondary branch per plant	2.19	2.09	2.33(H)	1.71(L)	2.06
Siliqua per plant	109.29	91.92	144.28(H)	71.35(L)	99.72
Siliqua length (cm)	7.77	8.02(H)	7.10(L)	7.52	8.01
Seeds per Siliqua	20.84(L)	22.74	21.22	21.99	23.97(H)
1000 seed weight (mg)	4.67(L)	5.37(H)	5.02	4.82	4.88
Seed yield per plant (g)	4.47	4.06	4.45	4.95(H)	3.62(L)

4.4.4 Cluster distance

The average intra and inter cluster D^2 values are given in Table 11 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 12. It was observed that inter cluster distance were always higher than those of intra cluster distance. The maximum inter cluster distance was observed between genotypes of cluster III and IV (16.453) followed by clusters II and III (11.693) and III and V (11.015). Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding program. The zero distance observed in cluster III (0.00) (Table 11) indicated there is only one genotype only in this cluster. Pandey *et al.* (2013) found maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. Zaman *et al.* (2010) reported that the genotypes from cluster I and III could be utilized in the hybridization program for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration. It appears that the crosses between genotypes from cluster III with cluster IV might produce high level of segregating population.

The intra cluster D^2 values were given in Table 11. The intra cluster distance was higher in cluster V (2.44) and lowest in cluster III (0.00) (Table 11). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

Table 11. Intra (Bold) and inter cluster distances (D^2) for 26 genotypes

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**1.65**	4.908	8.483	9.214	6.243
II		**0.94**	11.693	5.414	4.560
III			**0.00**	16.453	11.015
IV				**1.21**	8.832
V					**2.44**

Table 12. The nearest and farthest cluster distances from each cluster between D^2 values of *Brassica napus*

Cluster	Nearest cluster distance	Farthest cluster distance
I	II (4.908)	IV (9.214)
II	V (4.560)	III (11.693)
III	I (8.483)	IV (16.453)
IV	II (5.414)	III (16.453)
V	II (4.560)	III (11.015)

4.4.5 Contribution of traits towards divergence of the genotypes

The latent vectors (Z1 and Z2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z1) were days to 50% flowering (0.1732), days to maturity (0.1123), plant height (0.0589), primary branches per plant (0.6117), secondary branches per plant (0.1352), siliqua per plant (0.1997), siliqua length (0.2991), 1000 seed weight (0.0346) and lastly in vector II days to maturity (0.2959), secondary branches per plant (3.1059), siliqua per plant (0.08340) and seed yield per plant (1.3740) (Table 13). The characters contributing the most to the divergence are given greater importance when deciding on the cluster for the purpose of further selection and choice of parents for hybridization. The role of days to maturity, secondary branches per plant and siliqua per plant in both the vectors were important components for genetic divergence in these materials. Islam and Islam (2000) reported days to 50% flowering, plant height, primary branches per plant and number of siliqua per plant contribute maximum in divergence in rapeseed and mustard. Begum *et al.* (2007) reported that branches per plant and number of number of seeds siliqua contributed the maximum towards divergence in the existing linseed germplasm.

4.4.6 Cluster diagram

The position or the genotypes in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes (Figure 3)

Table 13. Relative contributions of the ten characters of 26 varieties to the total divergence

Characters	Principal Component	
	Vector-1 (Z1)	Vector-2 (Z2)
Days to flowering	0.1732	-0.7677
Days to maturity	0.1123	0.2959
Plant height (cm)	0.0589	-0.2764
Primary branch per plant	0.6117	-1.3236
Secondary branch per plant	0.1352	3.1051
Siliqua per plant	0.1997	0.0834
Siliqua length (cm)	0.2991	-0.1942
Seeds per Siliqua	-0.2053	-0.2165
1000 seed weight (mg)	0.0346	-0.1812
Seed yield per plant (g)	-0.2850	1.3740

4.4.7 Selection of genotypes

Considering the cluster analysis (Table 14) Cluster I genotypes exposed lower seed weight and less no. of seed and cluster II produced highest seed weight and long siliqua. Under cluster III genotypes possessed early maturity, highest plant height, more primary and secondary branches per plant, more siliqua per plant and short siliqua. Early flowering, short siliqua , less branches and less siliqua were observed under genotypes of cluster IV. The genotype of cluster V exposed late flowering, late maturity and less yield. On the basis of diversity pattern and agronomic performance genotypes **G2** (Nap 2066 X Nap 205) X Nap 2066, **G13**(Nap 9908 X Nap0130) X Nap9908, **G24**(Nap 9901 X Nap 203) X Nap 9901 are selected from cluster II.. The genotype **G1** (Nap 205 X Nap 0130) X Nap 205 is selected from cluster III. The genotype selected from cluster IV are **G15** (Nap 9908 X Nap 0130) X Nap 0130, **G19**(Nap 9905 X Nap 108) X Nap 108 and genotypes **G18**(Nap 9906 X Nap 2066) X Nap 9906 and **G21**(Nap 9905 X Nap 108) X Nap 9905 are selected from cluster V. It will produce more diverse line for future early variety release. Among these cultivars, the superior genotypes may be used in future breeding program to develop short duration cultivar of mustard. This variability may be used for the selection of superior and short duration genotypes for commercial cultivation at farmer's level.

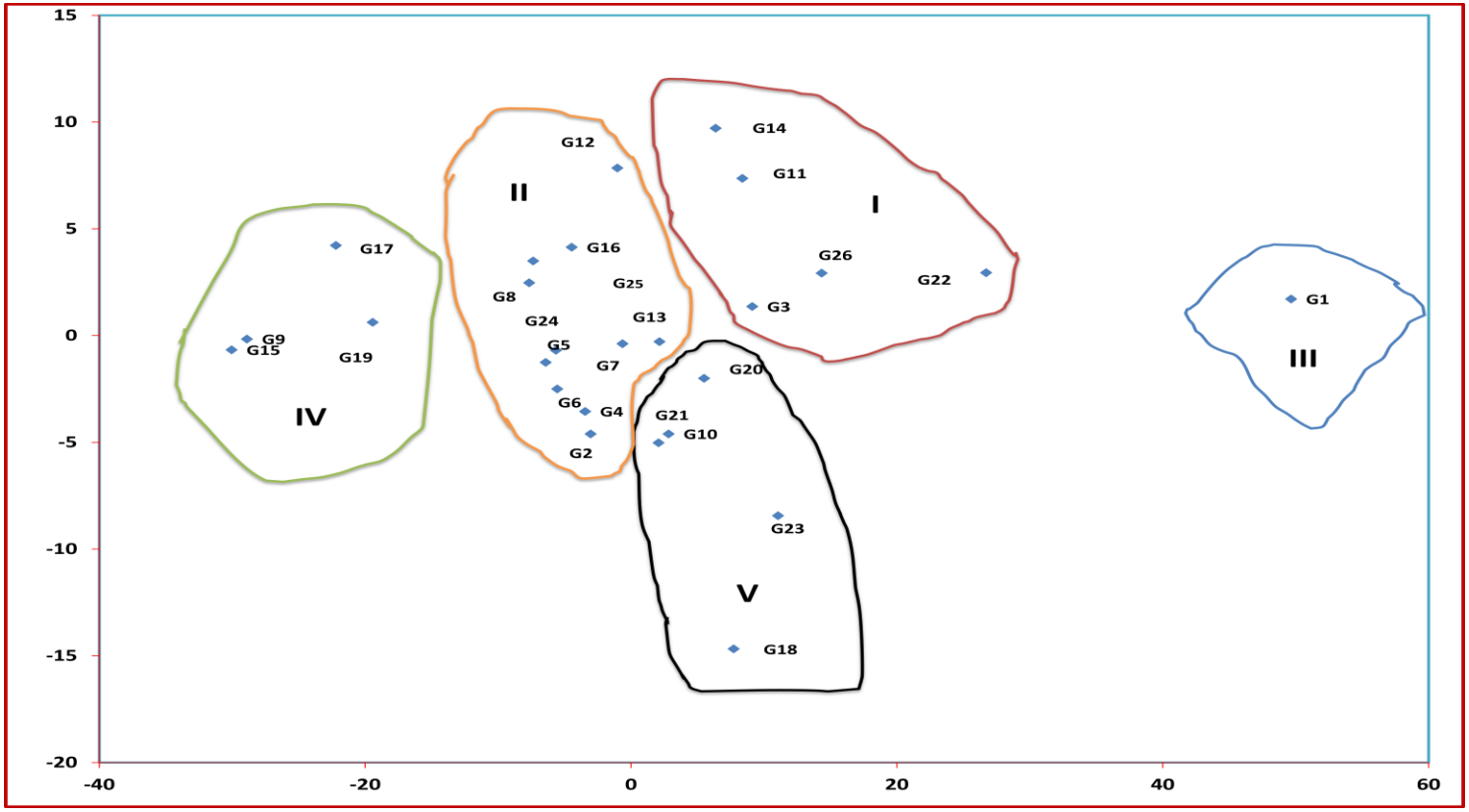


Figure 3. Cluster diagram of *Brassica napus* genotypes of based on their principal component scores

Table 14. Salient features of genotypes in five different clusters

Cluster	Salient feature
I	Minimum seed weight Minimum no. of seeds per siliqua
II	Highest 1000 seed weight High siliqua length
III	Highest Plant height Highest primary branches per plant Highest secondary branches per plant Highest siliqua per plant Intermediate days to 50% flowering Early matured
IV	High seed yield per plant
V	Late flowering late maturity Highest seeds per siliqua Less yield

Chapter 5

SUMMARY AND CONCLUSION

The present investigation was carried out in the experimental field of Sher E Bangla agricultural university to study genetic variability, character association, path analysis on seed yield and related traits in *Brassica napus* to identify the superior genotypes on yield and other desirable attributes. The experimental material consisting of 26 genotypes of *Brassica napus* were raised in RCBD Design with two replications at Experimental Farm, Department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka during Rabi season 2017-2018. The data was recorded on seed yield per plant and various other morphological traits viz. days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight and seed yield per plant. Analysis of variance showed significant differences for the genotypes.

From variability analysis of BC_1F_7 progenies, it was observed that significant variation exist among all the genotypes used for all the traits studied. The maximum days to 50% flowering was observed in genotype G20 (40.67) and the lowest found in the genotype G5 (36.00). The Maximum days to maturity was found in G25 and G26 (118.00) whereas the minimum from G23 (113.67). The maximum plant height was observed by the genotype G18 (113.63cm) and the minimum in G17 (87.90 cm). The Maximum primary branches per plant was found in G20 (4.42) whereas minimum from G19 (3.06). The genotype G2 (2.95) recorded the maximum secondary branches per plant while the minimum was observed by the genotype G25 (1.20). The maximum Siliqua per plant was found in the genotype G1 (144.28) while the minimum was observed in G15 (66.21). The Maximum siliqua length was observed in the genotype G24 (9.21cm) while

the minimum was observed in the genotype G9 (6.63 cm).The Maximum seeds per siliqua was found by the genotype G21 (25.92) and the minimum was observed from the genotype G14 (18.57). The maximum 1000 seed weight was observed in the genotype G13 (6.59g) and the minimum was observed in the genotype G22 (3.77 g). The maximum seed yield per plant was observed in G15 (5.86 g) while the minimum was observed in G7 (2.53 g).

Estimated phenotypic variance ranged from 0.28% for primary branches per plant to 326.58% for Siliqua per plant and genotypic variance ranged from 0.06% for Primary branches per plant to 217.61% for Siliqua per plant. The Highest environmental variance observed 108.97% was siliqua per plant. The Maximum genotypic and phenotypic variances were exhibited by Siliqua per plant (217.61% and 326.58%). The lowest environmental, genotypic and phenotypic variances were 0.22, 0.06 and 0.28, respectively for primary branches per plant.

PCV was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied. Higher estimates of PCV than GCV were observed for all the traits. PCV ranged from 1.32% for Days to maturity to 28.46% for Secondary branches per plant and GCV from 0.95% (Days to maturity) to 17.88% (seed yield per plant). The Maximum PCV and GCV were recorded for number of secondary branches per plant (28.46 and 13.24). Higher PCV and GCV were recorded for seed yield per plant (22.87% and 17.88%), seeds per siliqua (12.41% and 5.55%), 1000 seed weight (17.25% and 13.59%) siliqua per plant (18.90% and 15.43%).

High heritability was observed in days to flowering (31.61), days to maturity (51.72), plant height (61. 84), no. of primary branches per plant (22.48), no. of secondary branches per plant (21.65), siliqua per plant (66.63), siliqua length (38.23), seeds per siliqua (20.02), 1000 seed weight (62.07) and seed yield per plant (61.07). Genetic advance in percent was high for seed yield per plant (28.78), siliqua per plant (25.94), 1000 seed weight (22.06) and secondary

branches per plant (12.69). For days to flowering, days to maturity, plant height, primary branches per plant, siliqua length per plant, seeds per siliqua the genetic advance is 2.78, 1.40, 9.33, 7.34, 5.12 . High heritability with high genetic advance as percent of mean was noticed for seed yield per plant, 1000 seed wight, siliqua length, secondary branches per plant.

Seed yield per plant was significant and positive correlation with days to flowering (0.319 and 0.070), siliqua length (0.068 and 0.015) and 1000 seed weight (0.170 and 0.126). Plant height was significantly correlated with number of primary branches per plant (0.593 and 0.272), secondary branches per plant (0.468 and 0.337), siliqua per plant (0.564 and 0.536) and seed per siliqua (0.748 and 0.206) at both genotypic and phenotypic levels. Number of primary branches per plant was positively significant correlation with number of secondary branches per plant (0.816 and 0.567), number of siliqua per plant (0.717 and 0.389) and number of seeds per siliqua (0.677 and 0.193) at both genotypic and phenotypic levels. Siliqua length was positively significant correlated with number of seeds per siliqua (1.043 and 0.336), 1000 seed weight (0.539 and 0.314) and seed yield per plant (0.068 and 0.015) at both levels. Number of seeds per siliqua was negatively significant correlated with seed yield per plant (-0.094 and -0.088) at both levels.

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering ten characters. It was revealed that days to flowering, plant height, secondary branches per plant, siliqua per plant, siliqua length seeds per siliqua had the positive direct effect on yield per plant, whereas, primary branches per plant, days to maturity and 1000 seed weight had the negative direct effect on yield per plant. The path coefficient studies indicated that plant height, secondary branches per plant, siliqua per plant and seeds per siliqua were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

By genetic divergence analysis Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes (29.70) and three PCA account for 61.00% of the total variation. 26 genotypes were grouped into five clusters through non-hierarchical clustering and maximum genotypes (11) were included into cluster II.

By cluster distance it was observed that inter cluster distance was always higher than those of intra cluster distance. The cluster V had higher intra cluster distance (2.44) that indicates the highest amount of genetic divergence within the group. The maximum inter cluster distance was observed between genotypes of cluster III and IV (16.453) followed by clusters II and III (11.693). Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding program.

Cluster III performed the highest for plant height (107.24 cm), number of primary branch (4.12), number of secondary branch (2.33), number of siliqua per plant (144.28), cluster IV produced the highest value for seed yield per plant (4.95 g), early flowering but lower rate for plant height, primary branches, secondary branches, siliqua per plant, silqua length. Cluster I was the lowest value for seeds per siliqua and 1000 seed weight. Cluster II had higher cluster mean for siliqua length (8.02cm) and 1000 seed weight (5.37) and cluster V showed the late 50% flowering (38.80) and late maturity (116.40).

Cluster I genotypes exposed lower seed weight and less no. of seed and cluster II produced highest seed weight and long siliqua. Under cluster III genotypes possessed early maturity, highest plant height, more primary and secondary branches per plant, more siliqua per plant and short siliqua, early flowering, short siliqua , less branches and less siliqua were observed under genotypes of cluster IV. The genotype of cluster V exposed late flowering, late maturity, less yield.

CONCLUSION

On the basis of diversity pattern and agronomic performance genotypes **G2** (Nap 2066 X Nap 205) X Nap 2066, **G13(** Nap 99048 X Nap 0130) X Nap9908, **G24(** Nap 9901 X Nap 203) X Nap 9901 are selected from cluster II. The genotype **G1** (Nap 205 X Nap 0130) X Nap 205 is selected from cluster III; the genotype selected from cluster IV are **G15** (Nap 9908 X Nap 0130) X Nap 0130, **G19(** Nap 9905 X Nap 108) X Nap 108, and genotypes **G18(** Nap 9906 X Nap 2066) X Nap 9906 and **G21(** Nap 9905 X Nap 108) X Nap 9905 are selected from cluster V. It will produce more diverse line for future early variety release. Among these cultivars, the superior genotypes may be used in future breeding program to develop short duration cultivar of mustard. This variability may be used for the selection of superior and short duration genotypes for commercial cultivation at farmer's level.

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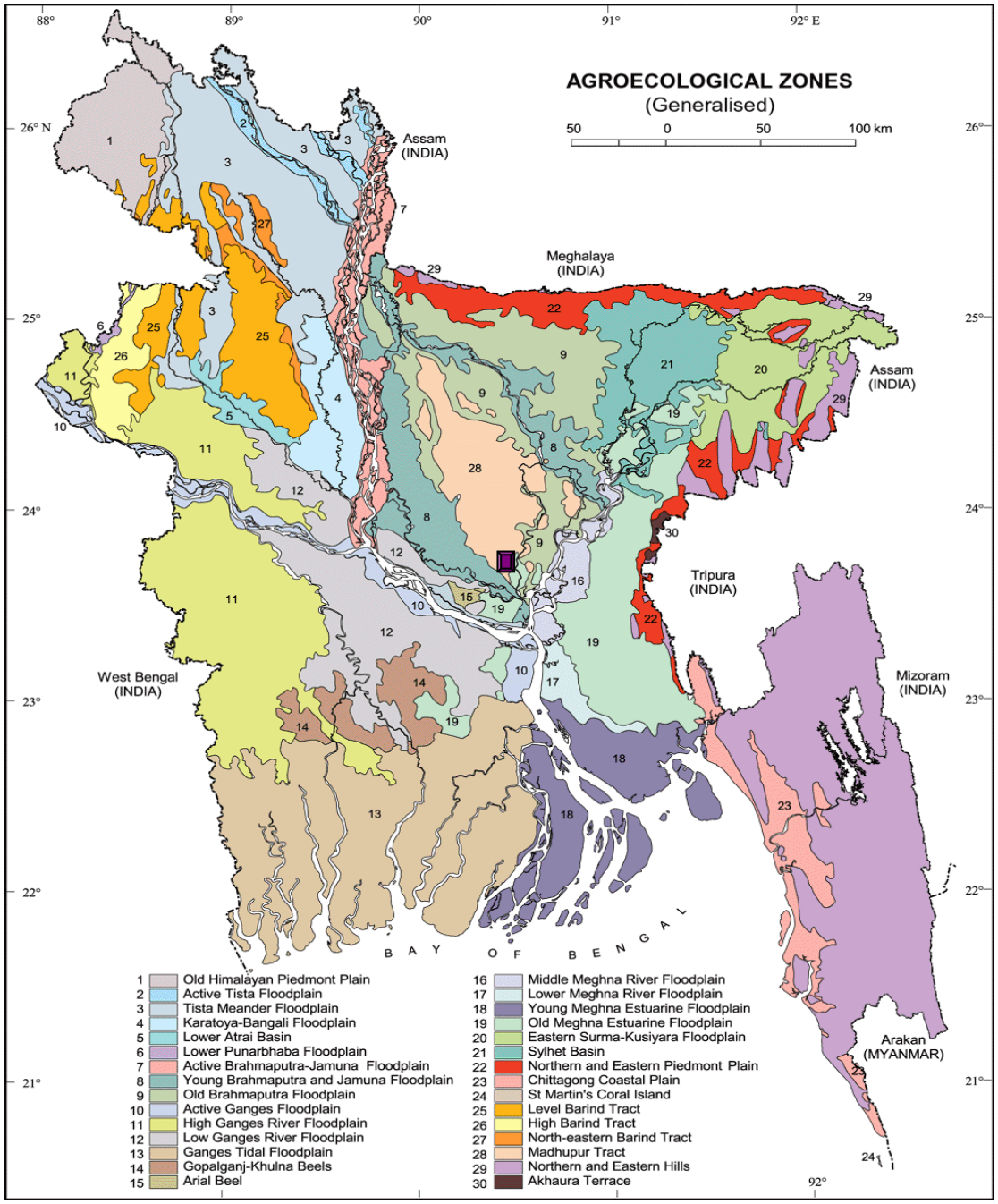
Appendix I. Map showing the experimental site under the study



Appendix II. Principal component score 1 & 2

	PCA 1	PCA 2
1	49.653	1.711
2	-3.034	-4.607
3	9.113	1.361
4	-3.457	-3.550
5	-6.417	-1.256
6	-5.557	-2.498
7	-0.644	-0.381
8	-7.660	2.475
9	-28.889	-0.161
10	2.821	-4.605
11	8.380	7.366
12	-1.022	7.852
13	2.137	-0.282
14	6.370	9.710
15	-30.055	-0.668
16	-4.466	4.137
17	-22.209	4.224
18	7.715	-14.672
19	-19.438	0.625
20	5.497	-1.999
21	2.068	-5.023
22	26.710	2.945
23	11.057	-8.437
24	-5.650	-0.686
25	-7.362	3.494
26	14.339	2.927

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

A. Physical composition of the soil

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

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 Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

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

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

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2017	34.7	18.0	77	227	5.8
December, 2017	32.4	16.3	69	0	7.9
January, 2018	29.1	13.0	79	1	3.9
February, 2018	28.1	11.1	72	1	5.7

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