GENETIC ANALYSIS IN YIELD AND ITS CONTRIBUTING CHARACTERS IN F_5 POPULATION OF *Brassica napus* L.

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BY

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CERTIFICATE

This is to certify that thesis entitled, **"GENETIC ANALYSIS IN YIELD AND ITS CONTRIBUTING CHARACTERS IN F_5 POPULATION 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* ***FARZANA ALAM BHUIYAN****, Registration No.* ***12-05099*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2018
Place: Dhaka, Bangladesh

Dr. Firoz Mahmud
Professor
Supervisor

DEDICATED

TO

MY BELOVED PARENTS

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ABSTRACT

Thirty two F_5 population of *Brassica napus* L. were evaluated. The experiment was laid to study the variability, correlation, path analysis and genetic diversity. The genotypes were found significantly variable for most of the characters. Phenotypic variances were higher than the genotypic variances for most of the character studied. The high GCV value was observed for number of secondary branches per plant (43.11). Number of secondary branches (98.67) exhibited the highest value of heritability followed by seed yield per plant (98. 43) while days to maturity (88.23) exhibited the lowest value of heritability. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering (0.034) and days to maturity (-0.095). Path co-efficient analysis revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 80% maturity, plant height, number of primary branch and siliqua length had the negative direct effect on yield per plant. On the basis of cluster analysis, all the genotypes were classified in five clusters.The highest inter cluster distance was observed between cluster I and IV(10.311). The lowest inter-cluster distance (3.513) was observed between the cluster III and IV (3.521). Considering group distance and other agronomic performance genotypes Nap-248 X Nap-159, Nap-2037 X Nap-2057, Np-9908 X Np-2022, Nap-2012 X Nap-2022, Bs-13 X Nap-2022 and Bs-7 X Nap-206 might be suggested for future breeding program.

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SOME COMMONLY USED ABBREVIATIONS

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

CHAPTER I

INTRODUCTION

Brassica napus (commonly referred to as rapeseed/oilseed rape/canola) belongs to the Brassicaceae (formerly cruciferae) family. The Brasscicaceae family consists of approximately 330 genera and 3700 species of plants (154 accessions available). 344 oil-producing *Brassica* species are mentioned among which mustard and rapeseed are the most important edible oil crops of the subcontinent (Razzak, M. A. and Hossain, M. G. 2007). Rapeseed was originally cultivated in Europe and used for its oil, and its industrial use has persisted throughout time (Shahidi, 1990). In recent history, rapeseed oil was limited to applications in cosmetics, lubrication, plastics and inks, but 20thcentury improvements in seed oil chemistry have broadened the uses for rapeseed to include human consumption and animal feed.

The oil from *Brassica* is the third most important sources of edible vegetable oils in the world. It has economic and commercial value that beggars description and play a major role in fulfilling the consumers' nutritional demand.

It is thought that *B. napus* was formed on the coast of northern Europe where both *B. oleracea* and *B. rapa* grow wild; other researchers believe that *B. napus* originated in the Mediterranean region or in western or in northern Europe (Tsunoda, 1980). It is thought to have originated from a cross where the maternal donor was closely related to two diploid species, *B.oleracea* and *B.rapa*.

Annual edible oil requirement in Bangladesh is about 5 lac MT and rapeseed contain 40-45% oil and 20-25% protein (Mondal and Wahhab, 2001). Using local ghani average 33% oil may be extracted. Oil cake is a nutritious food item for cattle and fish. Oil cake is also used as a good organic fertilizer. Dry mustard plants may be used as fuel. *B. rapa* accounts for 59.4% of total oilseed production in this country and occupied 0.532 million ha of land and the production was 0.596 MT with the yield of 1.12 MT/ha in 2013-14 (AIS, 2015). Total *Brassica napus* production in Bangladesh accounts for 603 MT worth 2878 tk/quintal (BBS, 2015). Bangladesh has been facing acute shortage of edible oil for the last several decades. Our internal production can meet only about 21% of our consumption. The rest 79 % is met from the import (Begum, F, Hossain, F. & Mondal, M.R.I. 2010).

Being a principal oilseed crop, which plays a vital role in the national economy of Bangladesh, the yield production/unit area of rapeseed is very low compared to other rapeseed growing countries in the world due to the lack of advanced high yielding varieties. So, high yield potential genotypes can be fully exploited with its proper environment.

Due to high cost and long growing period, farmers are not interested to mustard seed production. So we need to spend high amount of money to import large quantities of edible oil. Evauation of F_5 population which is generated by crossing among ten parents of mustard varieties to be short durational, high yielding and brown seeded. By comparison among them, it would be possible to select the lines for mitigating the demand of edible oil for future.

OBJECTIVES

- To estimate the yield and its contributing characters among the thirty two F_5 population of *Brassica napus*
- To compare the genotypes in respect of the genetic variability and heritability of different morphological characters
- To analyze genetic diversity among the genotypes for the selection of the best promising lines

CHAPTER II

REVIEW OF LITERATURE

There are six *Brassica* species which have the highest agricultural importance and are referred to as 'crop *Brassicas'* (Gómez-Campo 1999). The triangle of U (U, 1935) shows the relationship between these 'crop *Brassicas'*. Initially three ancestral diploid species: *B. rapa* (AA, n=10), *B. nigra* (black mustard) (BB, n=8) and *B. oleracea* (CC, n=9) existed. Through spontaneous hybridization followed by chromosome doubling, three amphidiploid species emerged: *B. napus* (AACC, n=19), *B. carinata* (BBCC, n=17) and *B. juncea* (AABB, n=18). Artificial resynthesis of *B. napus* from *B. rapa* and *B. oleracea* showed the same agreement with the triangle of U (Olsson, 1960), which has been confirmed by molecular analysis (Warwick and Black, 1991). As long as the high nutritious value and the demand of the consumers are concerned, necessary steps are to be taken for the improvement of production and quality the local cultivars in our country. With that view, a number of techniques and practices are applied for the enrichment of quality and yield of different rapeseed varieties and cultivars to obtain better yield. By application of various strategies in breeding process, tremendous progress has been seen in both quality and quantity of rapessed oil. Quite a number of literatures are found under the following criteria which are attempted to be summarized afterwards:

- 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

Sources of genetic variability is an important way for the breeder to the path of improvement in crops. Higher genetic variability and correlation of yield with yield components are major prerequisites for the breeders who are willing enhance quality and yield of *Brassica*. Genetic variability is a measure of the tendency of individual genotypes in a population to differ with one another. On the other hand, Variability is the amount of variation observed in a particular population. Quite a few literatures explaining the variability in the *Brassica spp*. are out there. These literatures are tried to be compiled here.

Khan *et al*. (2014) worked with four contrasting genotypes of *Brassica napus*. The study was carried out during 2011-2012 at The University of Agriculture, Peshawar to estimate the pattern of inheritance and heritability for important traits. The genotypes were crossed in a diallel manner and in the following season (2011-2012) all the F1 hybrids along with parents were evaluated under field condition in a randomized complete block design. Highly significant ($P \leq 0.01$) differences were observed for plant height, primary branches plant-1, seeds pod-1, pods plant-1, weight of1000 seed, seed weight plant-1. Additive-dominance model was fully adequate for plant height, primary branches plant-1, pods plant-1, seeds pod-1, whereas for the rest of the traits it was partially adequate. Genetic parameters estimation showed significant and higher magnitude of dominancecomponent for all the studied traits. Graphical analysis showed overdominance for all of the parameters. The value of average degree of dominance for plant height (1.858), primary branches plant-1(4.355), pods plant-1 (3.704), seeds pod-1(2.417), 1000

seed weight (3.995) and seed weight plant-1(1.852) also indicated the presence of overdominance gene action controlling these yield attributes, as it was greater than one. Low narrow (0.16-0.31) and broad (0.81-0.96) sense heritabilities were estimated for all the studied parameters, suggesting the low value of additive gene actionand genetic potential for the improvement of such traitsthrough selection in later generations.

Heiliger, A. (2012) worked with quantitative trait locus mapping of yield and yield components of *B. napus*. Two DH canola mapping populations were grown in side-by-side irrigated and rainfed treatments near Fort Collins, Colorado: population SE1in 2010 (n=183) and population DHYB (n=150) in 2011. DTF, seed yield, and yield-related traits were measured in order to understandrelationships among these traits under different water regimes, to studytrait heritabilities, and to better understand genotype, treatment, and treatment by genotype interactioneffects. QTL mapping was conducted separatelyfor each treatment in each population using R-QTL software to detect additive and epistatic effects. Yield components that were studied included siliques per main inflorescence (SMI), seeds per silique (SS), and thousand seed weight (TSW). Seed coat color was also classified for the DHYB population. Analysis of variance revealed an influence of genotype ($P<0.0001$) on all traits in both populations, treatment effects on seed yield, SMI, and SS ($P<0.05$) in the SE1 population, and treatment effects on seed yield, SMI, TSW, and DTF in the DHYB population. Genotype by treatment interactions were significant ($P<0.01$) for all traits in the SE1 population and for seed yield and TSW ($P<0.05$) in the DHYB population.

Bilal *et al*. (2015); worked with 23 genotypes of *B. napus*. The study was carried out to evaluate some indigenous genotypes of rapeseed for adaptability and yield traits in different agro-climatic zone of Mansehra. These genotypes were evaluated in randomized complete block design with three replications. Broad sense heritability was moderate to high in magnitude for all traits. 1000-seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions. Greater variability among the accessions for 1000-seed weight was observed.

21 genotypes of *B. napus* which were chosen based on diversity of agronomic traits. The genotypes were evaluated based on RCBD with three replications. Rameeh (2015) observed that Broad sense heritability estimates differed from 0.18 to 0.98 for pods length and days to end of flowering after. High broad sense heritability was observed for phenological traits, plant height and seed yield demonstrating selection gain for improving these traits will be high. Pods on main axis and pods per plant had high value of genetic coefficient of variation.

Razi *et al*. (2016); conducted an experiment to estimate genetic variability, heritability and genetic advance for important attributes in *Brassica napus* using 10 parental lines and their 21 F4 populations. Significant differences were observed among genotypes, parents, F4 populations and parents versus F4 populations for days to 50% flowering, days to maturity, plant height, primary branches plant-1 and main raceme length. Plant height and main raceme length displayed moderate to high broad sense heritability and maximum genetic advance for most of the F4 populations.

Ali *et al*. (2015); studied combining ability and broad sense heritability in F populations of diallel crosses of Brassica napus L. Data were recorded on various yield and yield related traits i.e. primary branches plant, pods main raceme, pods plant, seeds pod, 1000-seed weight and seed yield plant. Breeding material comprised four parental genotypes along with their 12 F populations. Analysis of variance exhibited significant ($P \leq 0.01$) differences among the genotypes for all the studied traits. On the basis of meanperformance, parental genotype G6 was good general combiner for pods main raceme, primary branches1 plant, pods plant, seeds pod and 1000-seed weight, while G9 had the highest GCA for seed yield plant. The cross G2 × G4 was the best specific combiner for primary branches plant, seeds pod and seed yield plant, while population G4 × G6 showed maximum SCA for pods main racemeand pods plant. Broad sense heritability estimates for studied traits were high for pods plant (0.63), primary branches plant(0.68), 1000-seed weight (0.74), seed yield plant (0.80) and seeds pod (0.96) while moderate for pods main raceme (0.44), suggesting the effectiveness of selection of these traits in different generations. Most of the crosses with positive SCA effects for yield components had at least one of parents with positive GCA effects.

With regards to the importance of estimation of general combining ability (GCA), specific combining ability (SCA), additive and dominance genetic variances, gene action, heterosis and heritability, Jamshid *et al*. (2011); conducted an experiment in a 9×9 diallel design. Nine parents with 36 crosses were studied in a randomized complete block design (RCBD) with three replications. Diallel analysis showed both additive and dominant type of gene action in the inheritance of the studied traits. Graphical analysis of the characters, displayed over

dominance for seed yield, thousand kernel weight, plant height, sub-branches and chlorophyll content, while partial dominance was observed for other traits. Calculation of the average degree of dominance for all traits except days to maturity, days to flowering and pod length also indicated dominant effect for control of these traits, thereby to increase and improve these traits by the phenomenon of heterosis.

Shaukat *et al*. (2015); evaluated eight *Brassica napus* genotypes to find out genetic variability and heritability. It was reported that analysis of variance showed highly significant differences ($P \leq 0.01$) among *Brassica napus* genotypes for primary branches per plant. The coefficient of variation for primary branches was 13.04 %. High broad sense heritability estimates were observed for primary branches per plant (0.83), plant height (0.78), pods per main raceme (0.65), seeds per pod (0.61), 1000-seed weight (0.61), while moderate heritability values were recorded for pod length (0.57), pods per plant (0.55), and seed yield per plant (0.50).

A research was carried out by Helal *et al*. (2014) to experiment genetic variability, correlation of yield and yield contributing characters and coefficient of variance in oilseed rape. The results showed that production was the highest in the varieties and 15% variation at genotypic and phenotypic level. 28 rapeseed (*B. napus* L.) genotypes were selected based on different phonological characters. Broad sense heritability result ranged from 0.12 to 0.98 for plant height and 50% flowering day, respectively. Genetic coefficient of variation, that indicates genetic diversity among the genotypes, varied from 18.7 to 26.8 for days to maturity and seed yield, respectively. (Rameeh, 2014).

An experiment was conducted by Muhammad *et al*. (2014); that consisted F_2 populations of *Brassica napus* L. to determine combining ability and heritability for important traits. Both GCA and SCA effects were highly significant ($P \leq 0.01$). Analysis of variance revealed significant ($P \leq 0.01$) differences for plant height, main raceme length, pod length, while significant ($P \leq 0.05$) differences were observed for days to 50% flowering, main raceme length. Broad sense heritability recorded was 0.26, 0.52, 0.65 and 0.73 for days to 50% flowering, main raceme length, plant height and pod length respectively.

Abideen *et al*. (2013); worked with eight *Brassica napus* L. genotypes to figure out the variability and association in these different genotypes. For plant height of these genotypes the differences found were highly significant ($P<0.01$). The differences found among the genotypes for primary branches per plant and pod per plant were non-significant ($P> 0.05$), while for pod per siliqua, pod length, seed yield per plant, 1000-seed weight and seeds per pod highly significant differences were found.

Nasim *et al*. (2013); evaluated 10 *Brassica napus* L. cultivars through agro-morphological parameters to study the genetic differences, inter relationships and the rate of heritability in these genotypes. For morphological parameters of 1000-seed weight, days to half flowering, days to full flowering, siliqua width, siliqua length, seed per siliqua and plant height they found highly significant differences while for main raceme length, siliquae on main raceme and primary branches per plant, they found non-significant differences. Similarly for flower initiation, fifty percent flowering, complete flowering, plant height, seeds per siliqua and 1000-seed weight they found high heritability and high heritable advances. High heritability (92.48%) with moderate genetic advance (18.87%) was also found by Saifullah (2010).

Rameeh (2013), characterized two genotypes and twenty two advanced line of *Brassica napus* L. in RCBD (randomized complete block design) with 3 replications. He observed that the range of heritability in broad sense for the parameters of siliquae per plant and days to flowering were in the range of 21 percent to 94 percent, correspondingly.

Rameeh (2011), evaluated 36 *Brassica napus* L. cultivars to determine the associations for yield components in these genotypes. The broad sense heritability was in the range of 0.42 and 0.81 percent which were the heritability values respectively for 1000-seed weight and pods per plant. Similarly morphological parameters of pods main per raceme, seed per pod and pods per plant were highly heritable with heritability values of seventy percent, seventy seven percent and eighty one percent, correspondingly.

Afrin *et al*. (2011); reported that the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seeds per siliqua, number of siliqua per plant, 1000-seed weight and seed yield per plant showed moderate broad base heritability while plant height exhibited the highest heritability.

Three rapeseed varieties (Foseto, Option500 and Goliath) including the offspring of their F_2 and F_3 generations were planted for two years at complete randomized block design with three replications at experimental field of Rice and Citrus Research Institute, University of Agricultural Science and Natural Resources of Sari, Iran. The results indicated that all traits except date of maturity and number of seed per pod were significant at 1% probability. Also the estimation of coefficient of genotypic variation (GCV) showed less than the estimate of coefficient phenotypic variation (PCV). GCV values for number of pod per plant

(16.93 and 23.57 in F_2 and F_3 generations, respectively) and seed yield (21.69 and 26.60 in F_2 and F_3 generations, respectively) was high, but for some traits were negligible. (Sadat *et al*., 2010).

An experiment was conducted by Aytac and Kinaci (2009) with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for 2 years. They observed maximum broad sense heritability, get genetic advance for seed yield.

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

Basalma (2008), evaluated 25 winter rapeseed genotypes for correlation and path analysis. Positively high correlation were found ($P<0.01$) among the parameters of branches per plant, siliquae per main raceme and for plant height in both years. The correlation of plant height was negative with seed yield, 1000-seed weight and for the trait of oil ratio in the first year of his study. He found from the judgment of seed and oil yield on other various yield constituent that oil contents are affected directly by seed yield.

140 F1 hybrids of winter oil seed rape (*Brassica napus* L.) was studied by Lefort (1982) and found that for seed yield average hybrids vigour was 23.5% on the basis of the mid parent. In a few cross combinations the value reached up to 50% in relation to the best parent value. This emphasizes the interest of hybrids varieties for improving yield.

Ahmad (1993) worked with parents and F1 hybrids from crosses between resynthesized lines and improved 00 varieties. F1 were earlier maturing than resynthesized lines and heterosis was observed for spring regrowth and plant height. In trails, the best resyn. line H128 could only produce 87% of the mean yield of the improved varieties.

Gupta *et al.* (1993) studied 56 hybrids from a half diallel set of crosses involving eight genetic stocks with 28 hybrids being derived from crosses of the initial S0 population and the rest from crosses of S1 families from each of the parents. The use of S1 families generally gave hybrids with a higher degree of commercial heterosis (over the best open pollinated commercial variety) than hybrids using S0 materials, though the S0 × S0 crosses gave high commercial heterosis for yield in many cases.

Kumar and Singh (1994), reported that 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.

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 self pollinated crops. Selection for bold seed size from F2 to F5 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.

2.2 Correlation among different characters

Analysis of correlation coefficient is a crucial factor in determining the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association. But measure of correlation does not consider dependence of one variable over the other. Correlation analysis among different traits is important in breeding program. Significant number of literatures on

correlation among characters of *Brassica sp.* are available. Some of these literatures are reviewed here:

Bilal *et al*. (2015); evaluated 23 genotypes of rapeseed to study the correlation between the yield and yield contributing characters. Positive significant correlation was observed between days to maturity and yield per plant (r = 0.279) as well as with 1000-seed weight (r = 0.057). Negative significant correlation was observed between plant height and pods per plant and 1000-seed weight. Number of pods per plant revealed positive significant correlation with 1000-seed weight and positive correlation with pod length, number of seeds per pod, yield per plant.

Rameeh (2015), studied 36 rapeseed (*Brassica napus* L.) genotypes including four checks and 32 advanced lines and found that pods per plant, seeds per plant and 1000- seed weight traits were positively correlated with seed yield.

Halder *et al*. (2014); conducted an experiment with 14 genotypes including 11 advanced lines and 3 check varieties to study the correlation and observed that days to first flowering showed positive non-significant relationship with yield but high positive significant correlation with the days to 50% and 80% flowering. Highly significant negative correlation was found with number of secondary branches per plant and siliqua length.

Nasim *et al*. (2013); studied ten *Brassica napus* L. genotypes to determine correlation between various traits and observed that pod length was positive highly significantly ($p \leq 0.01$) and significantly ($p \leq 0.05$) correlated with 100-seed weight (0.59**) and pod width (0.37*) respectively. Pod width was revealed to have negative significant

correlation with days to flowering inititaion (-0.40*) whereas positive significant correlations with100-seed weight (0.37*).

Rameeh (2012), studied 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 for these traits. The 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.

Rameeh (2011), evaluated 36 *Brassica napus* L. cultivars to determine the associations for yield components in these genotypes in RCBD experimental design which consisted of three replications. Siliquae per plant was significantly and highly correlated with seed yield with correlation value of 0.80.

10 rapeseed cultivars were evaluated by Aytaç and Kınacı (2009) and they observed that plant height had positive genotypic and phenotypic correlations with pods per main stem, pod length, oil yield and protein yield. Number of pods per plant has positive genotypic and phenotypic correlation with oil yield, protein yield, pod length, plant height and branches per plant.

Basalma (2008), conducted an experiment with 25 winter oil seed rape cultivars to study the correlation. They observed 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.

An experiment was conducted with 40 oleiferous *Brassica* species by Rashid (2007) to estimate correlation and observed that highly significant positive association of yield per plant with number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

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

Eight quantitative characters of *Brassica* species were evaluated by Mahak *et al.* (2004) to study the correlation among them. Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard. Afroz *et al.* (2004) also studied correlation and found seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliquae per plant.

Ali *et al*. (2003); carried out an experiment with 25 winter rapeseed and observed that positive flowering duration was significantly correlated (0.238) with seed yield. Seed yield per plant was negatively and non-significantly correlated with days to maturity and branches per plant. The seed weight of these genotypes was positively and significantly correlated with harvest index, flower duration and seed yield

Correlation analysis of yield related traits of *Brassica napus* was studied by Malik *et al*. (2000) and reported that days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. They also reported that number of branches per plant and number of siliquae per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight.

Eighty one genotypes of Indian mustard were evaluated by Shalini *et al.* (2000) for the magnitude of association between their quantitative characters of secondary branches, plant height, number of siliquae and seeds per siliquae were highly associated with seed yield.

According to Tyagi *et al.* (1996) plant height, siliqua per plant, siliqua length, seed weight, and seeds per siliqua had positive and significant effects on seed yield per plant while working with six yield components in three cultivars of mustard.

Singh *et al.* (1987); mentioned that number of primary branches per plant negatively correlated with siliqua length and 1000 seed weight, but positively correlated with number of siliqua per plant while working with *Brassica* species.

Shivahare *et al.,* (1975) also observed days to flowering were positively correlated with primary branches per plant and plant height.

Katiyar and Singh (1974), reported that 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.

2.3 Path co-efficient analysis.

In correlation study, if several characters are involved it is hard to determine the yield contributing traits. The most effective way to determine the direct and indirect contribution of these traits is path analysis.

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

Emrani *et al*., (2012); evaluated two rapeseed cultivars and reported that negative indirect effect of plant height via number of seeds per fruits and 1000 seed weight could mask the positive direct effect of plant height on seed yield per plant and positive correlation between number of fruits per plant and seed yield despite the indirect effects of number of fruits per plant via number of seeds per fruit and 1000 seed weight.

Khayat *et al*. (2012); reported that the number of pods per plant had the highest direct effect on grain yield. In addition, total dry matter, 1000-grain weight, and flowering and days to maturity also had a high direct effect on grain yield.

Afrin *et al*. (2011); studied 22 advanced lines of *Brassica napus* and observed that days to 50% flowering had negative direct effect on seed yield per plant. The highest indirect positive effect was found via plant height followed by number of siliqua per plant. Plant height had direct positive effect on seed yield per plant. It had positive indirect effect on seed yield via days to maturity, number of seeds per siliqua, number of siliquae per plant and 1000-seed weight per plant.

Basalma (2008), reported that the direct effects of plant height, branches per plant, and number of seeds per pod and oil ratio were all negative and the effects of others characters were positive on seed yield.

An experiment was conducted by Rashid (2007) 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.

Ali *et al*. (2003); carried out an experiment with 25 winter rapeseed and observed that the direct effect of seeds per pod on plant yield was less but positive. Negative direct effects on plant yield were exhibited by days to maturity and branches per plant with values of -0.015 and -0.164, harvest index and seed weight were the only characteristics that exhibited the highest direct effect on yield per plant.

Shalini *et al.* (2000); conducted an experiment with Indian mustard germplasm to study the path analysis 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.

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

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. But many scientists like 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.

Siliqua length had the highest positive direct effect and number of primary branches per plant had the highest negative direct effect on seed

yield were observed by Chowdhury *et al.* (1987) while working with 42 strains of mustard.

2.4 Genetic Diversity analysis

The foundation of improvement is said to be diversity, naturally if there is no diversity in nature then no improvement would possibly take place. But during continuous selection process for better quality and productivity, the gene pool of the selected final varieties has been made narrow down due to eliminating of genes for undesirable traits for example, declining amount of erucic acid in oil and glucosinolates in seeds. Due to which the differences at genetic level in *Brassica napus* L. has been made very limited which were so much important for many other promising characters

Twenty one rapeseed genotypes were evaluated based on randomized complete block design with three replications. On the basis of cluster analysis, the genotypes were classified in three groups and the group with high seed yield had high mean values of plant height, days to maturity and pods per plant. All the genotypes were classified in three groups with different mean values of the traits. The high seed yield genotypes with high mean value of pods on main axis and pods per plant were classified in group1 (C1). Group 1 (C1) and group 2(C2) had 1545.56 and 2160.55 kg per ha of seed yield (Rameeh, 2015).

Iqbal *et al.* (2014); studied different genotypes to determine the genetic variability and diversity among different mustard genotypes and reported that all the characters demonstrated high heritability (>80%) irrespective of any genotypes. The genotypes were grouped into four clusters by using Euclidean distance following Ward's method. The cluster III had higher intra cluster distance and the maximum inter cluster distance was

observed between genotypes of clusters I and IV followed by clusters III and IV.

Khan (2014), studied 211 genotypes of *Brassica napus* to evaluate the genetic diversity. The recorded data were analyzed through two complementary methods, i.e., cluster analysis and principal component analysis. Through cluster analysis all the genotypes were divided into five main groups. It was found that 7 out of 21 principal components with an eigenvalue of ≥ 1.0 accounted for 69.99% of the overall differences found among 211 genotypes of *Brassica napus* L. The contribution of first three PCs in overall PCs was 26.96%, 10.00% and 8.9%, respectively.

Twenty four rapeseed genotypes including 2 cultivars and 22 advanced lines were evaluated by Rameeh (2013). The results of factor analysis exhibited four factors including sink factor (pod per plant, pods length and seed yield), fixed capital factor (phenological traits), secondary fixed capital factor (duration of flowering), and metric factor (plant height). On the basis of cluster analysis, the genotypes were classified in four groups, and the group with high seed yield had high mean value of pods per plant.

Zare and Sharafzadeh (2012), studied 8 genotypes of rapeseed to determine the genetic divergence. The genotypes were grouped into four clusters. Based on the results, Modena and Sarigol, which had the highest grain yield, were located in a major cluster and Okapi, which had the lowest grain yield, was located in a single cluster else. SLM046, RGS003 and Hyola308 cultivars, which had lower grain yield, were placed in the third cluster that was partitioned into two small clusters. The fourth cluster included Licord and Zarfam cultivars also had high grain yield.

A field experiment was conducted comprising eighteen advanced lines of mustard in a randomized block design with three replications for estimation of divergence among advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (6) and the cluster III contained the lowest (3). The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant (Zaman *et al*., 2010).

Different multivariate analysis techniques were used by Afrin (2009) to classify 22 *Brassica napus* genotypes. The genotypes were grouped into four clusters. The highest inter-cluster distance was observed between clusters II and IV whereas the maximum intra-cluster distance was found in cluster II. Therefore, the genotypes belonging to cluster I and cluster II, cluster II and cluster III and cluster III and cluster IV have been selected for future hybridization program. The PCA gives eigen values of principal component axes of coordination of genotypes with the first three axes accounted for 68.927% of total variation whereas the first principal components accounted for 28.695%.

Hossain *et al.* (2008); studied 40 genotypes of rapeseed to determine genetic divergence. They used D^2 statistic in 40 genotypes. The genotypes differed significantly for 10 yield and yield contributing characters and they grouped then into nine clusters. They observed that

there was no close correspondence between geographical distribution and genetic divergence. A number of siliqua on the main raceme, seeds per siliqua and harvest index were the major contribution to genetic divergence and cluster IV and these genotypes were suggested for use in heterosis breeding.

Mahmud *et al.* (2008); studied 22 advanced lines of rapeseed to determine genetic diversity 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.

genotypes each and similarly, cluster IV and VIII included one genotype each.

An experiment was conducted by Nath *et al.* (2003) with varieties, inter-variety and interspecies hybrids of *Brassica* oil crop to determine genetic divergence. The diversity study indicated that parent, inter-variety and inter-species hybrids almost clearly form five groups indicating that they are divergent. Based on the study on genetic divergence of the *Brassica*, the varieties having the achievement and located in the distant clusters

could be utilized for hybridization program to develop desired high yielding varieties.

Choudhary and Joshi (2001), studied different *Brassica* species to determine the genetic distances among them 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 similar 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.

Islam and Islam (2000), evaluated 42 genotypes of rapeseed and mustard using D^2 analysis to study the genetic divergence among them. They found 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 per plant.

Singh and Gupta (1984), used D^2 analysis to study genetic diversity based on 12 characters. 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 III

MATERIALS AND METHODS

3.1 Experimental site

The research was conducted in the experimental fields of Sher-e-Bangla Agricultural University, Dhaka–1207 during Rabi season (Mid November 2017 to February 2018). The location of the experimental site was situated at 23^0 77' N latitude and 90^0 37' E longitudes with an elevation of 8.5 meter from the sea level. Photograph showing experimental sites (Appendix I).

3.2 Soil and Climate

The research area was situated in the sub-tropical zone. The soil of the experimental site represents the Agro ecological Zone 28 which is popularly known as "Madhupur Tract". The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.48 to 5.70 and organic carbon content was 0.81% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

Thirty two healthy parents of F_5 generation of *Brassica napus* L. were used as experimental materials which were collected from the Germplasm under the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University. The materials used in that experiment is shown in Table 1.

3.4 Methods

Methods that are precisely used to conduct this research are briefed here:

3.4.1 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by removal of weeds and stubbles. Laddering, harrowing and fertilizing was done followed by incorporating with tractor and power tiller to bring about good tilth.

Table 1. Materials used for the experiment

Genotype	F_s Population	Source
G1	Nap- 9908 × Bs- 13	SAU
G2	Nap- 179 × Nap- 2001	SAU
G3	Nap- 248 × Nap- 159	SAU
G4	Nap- 2037 × Nap- 2057	SAU
G5	Nap- 94006 × Bs- 7	SAU
G6	Nap- 2012 × Nap- 2013	SAU
G7	Nap- 94006 × Nap- 2013	SAU
G8	Nap- 248 × Nap- 206	SAU
G9	Nap- 206 × Nap- 2012	SAU
G10	Nap- 2037 × Nap- 2022	SAU
G11	Nap- 9908 × Nap- 94006	SAU
G12	Nap- 9908 × Nap- 2037	SAU
G13	Nap- 2037 × Nap- 248	SAU
G14	Nap- 206 × Nap- 2013	SAU
G15	Bs- 7 × Nap- 206	SAU
G16	Nap- 2001 × Nap- 2022	SAU
G17	Nap- 94006 × Bs- 13	SAU
G18	Nap- 2037 × Nap- 2012	SAU
G19	Nap- 2037 × Nap- 206	SAU
G20	Nap- 9908 × Nap- 2022	SAU
G21	Bs- 13 × Nap- 2022	SAU
G22	Nap- 179 × Nap- 206	SAU
G23	Nap- 9908 × Nap- 206	SAU

G24	Nap- 9908 × Nap- 248	SAU
G25	Nap- 2012 × Nap- 2022	SAU
G26	Nap- 248 × Nap- 2022	SAU
G27	Bs- 13 × Nap- 2013	SAU
G28	Nap- 9908 × Nap- 2001	SAU
G29	Nap- 2037 × Bs- 13	SAU
G30	Bs- 13× Nap- 206	SAU
G31	Nap- 9908 × Nap- 2013	SAU
G32	Nap- 248 × Nap- 2013	SAU

3.4.2 Application of manure and fertilizer

The field was fertilized at the rate of 7 tons of Cowdung, The fertilizers like urea, TSP, MoP and boric acid were applied in quantities of 280, 172, 98 and 5 kg/ha, respectively, along with 7 ton/ha of cow dung. The half amount of urea, total amount of Cowdung, TSP, MP and Boron was applied during final land preparation. The remaining half of urea was applied after 25 days of sowing as top dressing.

3.4.3 Experimental design and layout

Layout of the plot was done after final land preparation. The experiment was carried out in Randomized Complete Block Design (RCBD) with three replications. The total area of the plot was 58m × 15m = 870m^2. Each replication size was 58m × 4m, and the distance between replication to replication was 1m. The spacing between lines to line was 35cm. Seeds were line-sown in the experimental plots on 16 November, 2017. The seeds were placed at about 2 cm depth in the soil. The seeds were covered with soil carefully to prevent overlapping with clods.

3.4.4 Intercultural operations

Weeding, thinning, irrigation, pest management, etc. were practices in an identical manner in all the plots. After the seed sowing, irrigation was provided with a pipe to balance the wetness of the soil for allowing the seeds to germinate uniformly. A good drainage system was maintained in case excessive rain occurred during the growing period. The first weeding was done after 16 days of sowing followed by 1st thinning. Seven days after the 1st thinning, 2nd to maintain a distance of 10 cm from plant to plant in rows of 30 cm apart. The critical weed free period for *Brassica* is 15 to 30 days after sowing. Second weeding was done after 31 days of sowing. During the siliqua development stage, Aphid attack was observed while Malathion-57 EC @ 2ml/liter of water was applied on 20 December, 2017 afternoon to control this pest.

3.4.5 Crop harvesting

Harvesting was taken place on approximately 90 DAS depending on the maturity level of the siliqua. After assessing straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, 80% of the crop was assessed to reach maturity. Fifteen plants were chosen at random F_4 progenies in each replication. The plants were harvested on February 14, 2018 by uprooting and were tagged in accord afterwards. Data on different parameters was recorded. A pictorial view of experimental field at flowering and harvesting stage is presented in Plate 1 & 2.

3.4.6 Data collection

Ten characters were taken into consideration to study different genetic parameters and inter-relationships. The data were recorded on fifteen

selected plants for each cross and ten selected plants for each parent on the following traits-

i. Days to 50% flowering
ii. Days to 80% maturity
iii. Plant height (cm)
iv. Number of primary branches per plant
v. Number of secondary branches per plant
vi. Number of siliquae per plant
vii. Siliquae length (cm)
viii. Number of seeds per siliqua
ix. 1000-seed weight (g)
x. Seed yield per plant (g)

3.5 Statistical analysis

Different components were taken into consideration for data collection. The formula by Johnson *et al.* (1955) was used to estimate phenotypic and genotypic variance. The formula given by Singh and Chaudhury (1985) and Allard (1960) was used to estimate heritability and genetic advance. The formula of Burton (1952) was used to calculate genotypic and phenotypic co-efficient. Simple correlation coefficient was estimated using the formula given by Clarke (1973)., Singh and Chaudhury (1985) and finally the path coefficient was analysed following the method suggested 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 was analysed in accordance with the steps employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient is splited into direct and indirect independent variables on the dependent variable.

For estimating 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 refer to simple correlation co-efficient and P's refer to path co-efficient (Unknown). P's in the followed formulas can be conveniently resolved through 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)

It is of the multivariate techniques that is used to determine the interrelationship among several characters and may be done from the summation of squares and product matrix for the characters. Therefore, principal component were calculated 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)

It is equivalent to principal component analysis but used to compute inter-unit distances. Using of all dimensions of P it gives the maximum distances between each couple of the n point using similarity matrix (Digby *et al.*, 1989).

c. Canonical Vector Analysis (CVA)

The canonical vector analysis is used to find a linear combination of original variability that enhance 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

It is calculated for each cluster through taking possible D^2 values within the member of a cluster found from the 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 shows the distances (D) within cluster.

e. Clustering

Clustering were done using non-hierarchical classification for dividing the genotypes into some number of mutually exclusive groups. Begining from

some initial sorting of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another,, the algorithm swaps into another stage which determine the effect of switching two genotypes of different classes and so on.

CHAPTER IV

RESULTS AND DISCUSSION

The study allowed to evaluate thirty two F_5 population of *Brassica napus* L. genotypes to find out the variability amongst these genotypes and to find the correlation, path co-efficient for seed yield and different yield contributing characters and genetic diversity as well. All these accessions were grown in 2017-2018 in experimental plot of Sher-e-Bangla Agricultural University. As mentioned before, the data were recorded on different characters such as plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, days to 50% flowering, no. of siliqua per plant, days to maturity, no. of seeds per siliqua, siliqua length (cm), 1000 seed weight (g) and seed yield per plant (g). After analyzing the data statistically, obtained results are explained below under the following heads:

- Variability study in *Brassica napus* L.
- Correlation coefficient of characters
- Path coefficient analysis
- Genetic diversity analysis

4.1. Variability study in *Brassica napus*

4.1.1 Variability among the thirty two F_5 materials for *Brassica napus*

Results of analysis of variance of the obtained data on various yield components of thirty two F_5 materials of *Brassica napus* genotypes, values of mean, range, CV%, phenotypic variances, genotypic variances are summarized in Table 2a and Table 2b showing the values of genetic advance, heritability for various characters that determine yield. Of all the genotypes, about every character showed highly significant variation leaving a greater chance of selection, which provides a good scope for improving traits of interest in breeding programs.

4.1.1.1 Plant height (cm)

Ultimately plant height shows the growth nature of a plant. Several factors i.e. genetic and environmental play a vital role in determining the plant height. Analysis of variance showed highly significant differences ($P \leq 0.01$) of all the genotypes for plant height (198.83) (Table 2a) that means presence of genotypic difference between the genotypes. Data ranged from 88cm to 119.83 cm with the mean value of 103.02 cm where minimum plant height (88cm) were recorded for genotype G19(Nap-2037 × Nap-206) (Plate 4). Maximum data in this case was obtained in G4 (Nap-2037 × Nap-2057) (119.83) (Plate 3) (Table 2a). Ali *et al.* (2002) and Khan *et al.* (2008) found notable difference among mustard.

Table 2a. Estimation of genetic parameters in ten characters of 32 genotypes in *Brassica napus* L.

Parameters	Min	Max	Mean	MS	CV(%)	o^2g	o^2e	o^2P
50F	28.00	45.030	37.26	54.13**	3.91	18.25	1.88	18.79
DM	76.00	92.00	82.70	59.28**	1.86	18.08	2.56	22.25
PH	88	119.83	103.02	198.83**	1.89	66.12	3.60	69.07
NPB	1.31	4.60	2.63	1.16**	3.8	0.48	0.01	0.38
NSB	0.93	5.75	2.04	2.18**	4.61	0.72	0.01	0.78
NSP	48.85	141.01	89.53	1501.11**	7.23	481.23	29.79	513.03
SL	7.32	10.70	8.61	1.38**	3.27	0.44	0.06	0.57
NSS	14.89	39.83	24.93	18.073**	2.86	4.93	0.37	5.53
TSW	2.92	4.13	3.42	0.222**	1.41	0.081	0..002	0.076
SYP	3.15	10.66	5.87	9.042**	4.2	2.98	0.05	3.02

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

50F = Days to 50% flowering, DM = Days to 80% maturity,PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondary branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length,TSW= Thousand Seed Weight (g), SYP=Seed yield per plant, MS = mean sum of square,CV (%) = Coefficient of Variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmentalvariance

Table 2b. Estimation of genetic parameters in ten characters of 32 genotypes in *Brassica napus* L.

Parameters	GCV	ECV	PCV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
50F	12.32	3.78	12.13	89.89	8.18	22.49
DM	5.31	1.93	5.64	88.23	8.27	10.28
PH	7.81	1.9	8.02	96.05	14.91	15.36
NPB	23.06	3.8	23.33	97.83	1.35	46.92
NSB	43.11	4.81	42.68	98.67	1.87	86.31
NSP	24.91	6.18	25.24	94.96	43.49	51.17
SL	7.56	2.29	7.89	91.98	1.17	15.08
NSS	11.25	2.88	11.73	94.92	4.78	22.49
TSW	7.85	1.32	7.82	97.06	0.63	15.64
SYP	29.20	4.6	29.44	98.34	3.50	58.87

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondary branches per plant,NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, GCV = Genotypic Coefficient ofVariation, PCV = Phenotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation.

genotypes for plant height as well. Genotypic variances for plant height were 66.12, whereas phenotypic variance appeared to higher than the genotypic variance (69.07) which suggested that besides genotypes, environmental factors also put impact on the gene expression. The estimates of PCV (8.02%) and GCV (7.81%) also showed variability among the genotypes for this trait (Table 2b). Tyagi *et al*.(2001) observed the highest variation in plant height among parents and their hybrid.

4.1.1.2 Number of primary branches per plant

Significant variance among the genotypes (1.16) at the level of 1% probability. Ranging from 1.31 to 4.60 for number of primary branches per plant with the mean value of 2.63 (Table 2a), the minimum number of primary branches per plant was observed in G23 (Nap 9908× Nap 206) (1.31) followed by G32 (Nap 248× Nap 2013) (Plate 4) whereas the maximum number of primary branches/plant was observed in G3 (Nap 248× Nap 159) (4.60) (Plate 5). Phenotypic variance and genotypic variance were observed as 0.38 and 0.48 respectively (Table 2a) which indicates that there was little influence of environment on the gene expression. The PCV and GCV was 23.06 and 23.039 respectively which reflects that inherent variability existed among the population (Table 2b). Significant differences for number of primary branches per plant was also found by the research of Chowdhury *et al*.(1987).

G4 **G19**

Plate4. Photograph showing variation between the highest G4 (Nap 2037× Nap2057) and the lowest plant height G19 (Nap 2037 × Nap206) of *Brassica napus*L.genotypes

G3 **G32**

Plate 5. Photograph showing variation between the highest G3 (Nap 248× Nap 159) and the lowest G32 (Nap 248× Nap 2013) primary branches of *Brassica napus*L.genotypes

4.1.1.3 Number of secondary branches per plant

Secondary branches per plant showed significant variance (2.18) at 1% level of significance. With the mean being of 2.04, the range from minimum to maximum was 0.93-5.75cm. G3 (Nap 248 × Nap 159)(Plate 5) showed maximum and G26 (Nap 248 × Nap 2057) (Plate 6 and Table 2a) showed minimum number of secondary branches. Phenotypic variance and genotypic variance were observed as 0.78 and 0.72, respectively that means the environmental effect on gene expression was less. The PCV and GCV was 42.68 and 43.11, respectively which showed that considerable variability existed among the genotypes for this trait (Table 2b). Significant differences for number of secondary branches per plant was found by Hosen *et al*.(2008). An illustration of genotypic, phenotypic and environmental coefficient of variation in *Brassica napus* L. are given in Figure 1.

4.1.1.4 Days to 50% flowering

The mean value for 50% flowering was 37.26 where minimum days was found in G25 (Nap 2012 × Nap 2022) (28 days) and highest (45 days) was observed in G28 (Nap-9908 × Nap-2001) (Table 2a). Phenotypic and genotypic variation was noticed as 18.79% and 18.25% respectively(Table 2b). The value of GCV(12.32) is higher than PCV(12.13) which indicated that variation was mostly driven by genotype. High genotypic and phenotypic co-efficient of variation was reported by Lekh*et al.* (1998). Significant genetic variability in case of 50% flowering day of *B. napus* was also noticed by Hosen (2008).

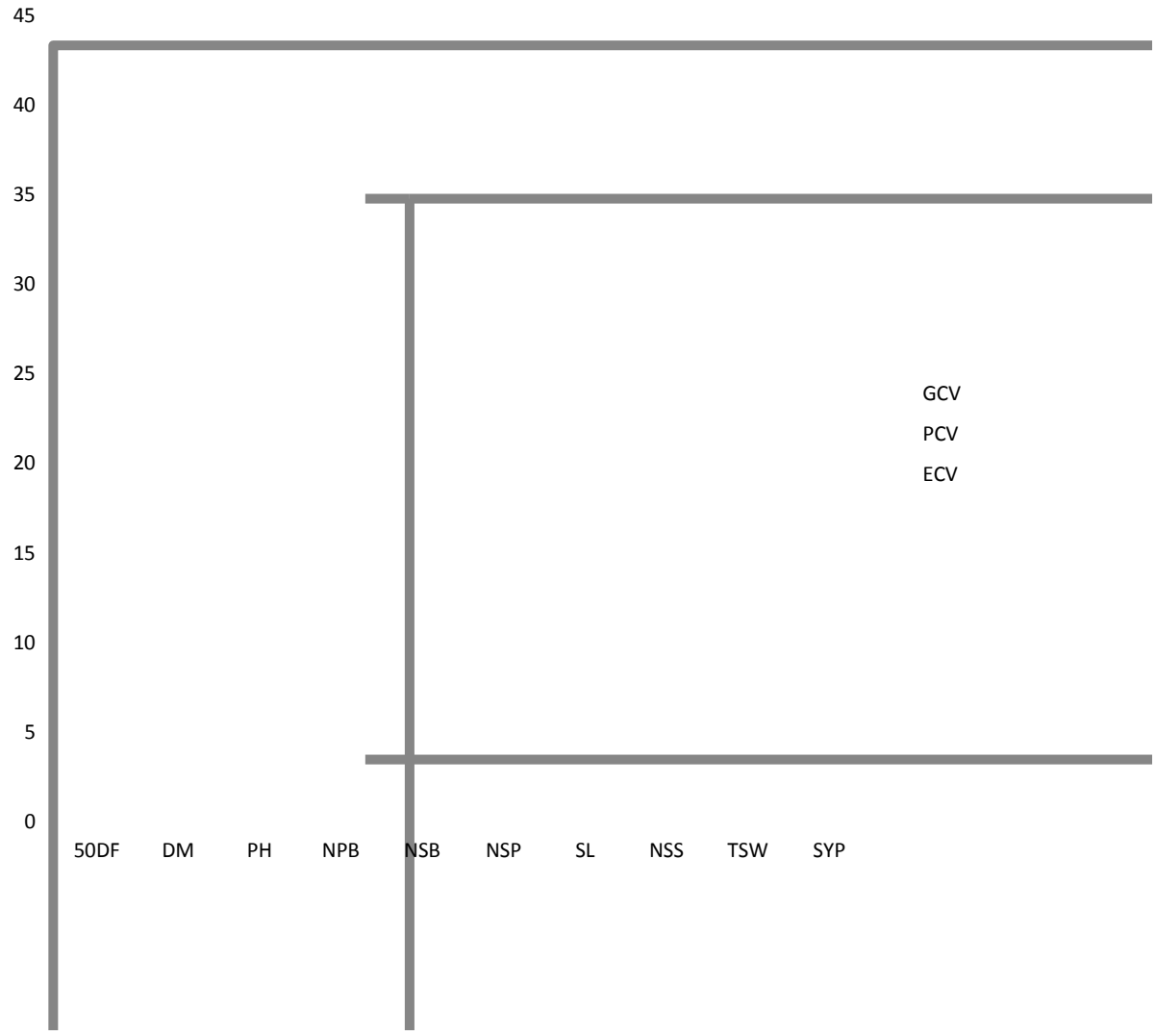

Figure 1. Genotypic, phenotypic and environmental coefficient of variation in *Brassica napus*L. genotypes

G3 **G26**

Plate 6. Photograph showing variation between the highest G3 (Nap 248×Nap 159) and the lowest G26 (Nap 248 × Nap 2057) secondary branches of *Brassica napus* L. genotypes

4.1.1.5 Days to maturity

Results showed significant differences (59.28) at 1%level of significance in case of days to mturity. The limit was 76-92 days with the mean being 82.70. Days to maturity varied significantly among the studied genotypes. The highest days to maturity was observed in G14 (Nap 206 × Nap 2013) (91 days) and the least days to maturity was observed in G24 (Nap 9908 × Nap 248 (75 days) (Table 2a). Genotypic variance of days to 50% maturity was found 18.08 whereas phenotypic variance was 22.25 which indicates environmental impact on their phenotypic expression.. The phenotypic coefficient of variation (5.64%) was moderately higher than the genotypic coefficient of variation (5.31%) (Table 2b), which denotes the effect of environment on the gene expression. Higher genotypic variation allows greater transmissibility of a character from parent to progeny. Identical result was found in this case by Rameeh (2014) and Katiyar *et al*.(1974).

4.1.1.6 Number of siliqua per plant

Results denoted significant differences amongst the accessions (1501.11) at 1% level of significance. The mean value was 89.53 with the range being 48.85-141.01(Table 2a). Maximum siliqua per plant was remarked for G4 (Nap 2037 × Nap 2057) (141.01), whereas, minimum was recorded for G23 (Nap 9908 × Nap 206) (48.85) (Plate 6). The highest phenotypic variance (513.03) and genotypic variance (481.23) that denotes the heavy influence of environmental factors over genotypes. The PCV (25.24) was higher than GCV (24.91) also shows that adequate variance among the genotype exists (Table 2b and Plate 7). Similar result of. high genetic variance was also observed by Zare and Sharafzadeh, (2012).

4.1.1.7 Length of siliqua (cm)

The data recorded for siliqua length exhibited significant *(P≤0.01)* differences (1.38). The mean value was 8.61 ranging from (7.32) G15 (Bs -7 × Nap 206) to (8.61) cm G3 (Nap 248 × Nap 159) (Table 2a & Plate 8).The genotypic (0.44) and phenotypic variances (0.57) denoted noticable environmental influence on genotypes. Genotypic expression and genotypic (GCV) and phenotypic coefficients of variation (PCV) values for siliqua length were 7.56% and 7.89%, respectively (Table 2b).High co-efficient for both genotypic and phenotypic variability was reported by Masood *et al.* (1999). Similar statemement was given by Zare and Sharafzadeh, (2012).

4.1.1.9 Thousand seed weight (g)

The data collected pertaining to 1000-seed weight exhibited significant (p≤0.01) differences confronting the existance of genetic variance between the studied accessions (0.222). G4 (Nap 2037 × Nap 2057) showed maximum weight of 4.13g, where G13 (Nap 2037× Nap 248) was found to be with minimum weight of 2.92g, (Table 2a and Plate 9). Low genotypic (0.081) and phenotypic (0.076) variance was noted with less differences denoting that they were minimal responsive to the environment. The PCV and GCV were 7.82% and 7.85% respectively (Table 2b), which is less difference. Significant variability for this particular trait was also reported by Aytac & Kinaci, 2009).

G4 **G23**

Plate 7. Photograph showing variation between the highest G4 (Nap 2037 × Nap 2057) and the lowest G23 (Nap 9908 × Nap 206) siliqua per plant of *Brassica napus*L.genotypes

G3 **G15**

Plate 8. Photograph showing variation between the highest G3 (Nap248×Nap 159) and the lowest G15 (Bs 7 × Nap 206)siliqua length of *Brassica napus*L.genotypes

2.91 g **4.12 g**

Plate 8. Photograph showing variation between the lowest G32 (Nap 248×Nap 2013) and the lowest G4 (Nap 2037 × Nap 2057)genotypes of thousand seedweight of *Brassica napus*L. genotypes

4.1.1.10 Seed Yield per plant (g)

Recorded data showed high significance of variations (9.042) between the accessions at 1% level of probability. Yield per plant was remarked maximum in G4 (Nap 2037 × Nap 2057) (10.66 g) and minimum for G19 (Nap 2037 × Nap 206) (3.15g) (Table 2a). The values of GCV was 29.20% and PCV was 29.44%. that is slightly higher than GCV denoting that the genotype had moderate variation (Table 2b). Identical variability was also refered by Rameeh (2014).

4.1.2 Heritability, genetic advance and selection

Heritability is the measure of value of selection of a particular character and an index of transmissibility of genes controlling the character. In calculating the selection effects, heritability accompanied with genetic advance is more effective than just heritability. These are also determinants of the type of gene action taking place in character expression.

4.1.2.1 Plant height (cm)

Plant height of F_5 exhibited high heritability 96.05% with moderately high genetic advance of 14.91 and genetic advance in percentage of mean of 15.36% (Table 2b) denoted that environmental effects were minimal and the possibility of predominance of additive gene action in the inheritance of this trait thus showing that this trait can be improved by selection. High heritability (93.48%) with moderate genetic advance (18.89%) was reported by Saifullah (2010).

4.1.2.2 Number of primary branches per plant

It showed high heritability 97.83 with low genetic advance 1.35 and high genetic advance in percentage of mean of 46.92%, which refers that this character was controlled by non-additive gene but high genetic advance in percentage of mean indicates that possibility of predominance of additive gene leaving huge scope to make improved variety. This result was governed by the influence of environmental factors instead of genotypes. The possibility of selection of genotypes for this trait is lower due to the low genetic advance. Low heritability with high genetic advance in percentage of mean was reported by Afrin *et al*.(2011).

4.1.2.3 Number of secondary branches per plant

It showed high heritability (98.67) along with low genetic advance (1.87) that denotes less possibility of selection. The high genetic advance in percentage of mean(86.31) shows moderate effect of environmental factors and presence of non-additive gene in the expression of this trait. Khan *et al*.(2013) remarked high heritability paied with high genetic advance for number of secondary branches per plant.

4.1.2.4 Days to 50% flowering

Days to 50% flowering exhibited high heritability (89.89%) with low genetic advance (8.18) and moderately high genetic advance in percentage of mean (22.49%) indicated that expression of the gene was governed by non-additive gene. Belete *et al*.(2012) observed heritability along with high genetic advance in percentage of mean for days to flowering.

4.1.2.5 Days to maturity

It exhibited high heritability (88.23%) with low genetic advance (8.27) and genetic advance in percentage of mean (10.28%) pertains that the character was mostly controlled by non-additive genes and greater influence of environment in the physical expression genes. That also tones down the scope for selection. Heritability and genetic advance in percentage of mean are shown in Figure 2.

4.1.2.6 Number of siliqua per plant

Calculated heritability was considerably high (94.96%) with significantly higher genetic advance 43.49 and genetic advance in percentage of mean 51.17%. It means that probably heritability occurred because of additive gene effects. Crop quality improvement through direct selection is possible in this case .Sadat *et al.* (2010) found some similar reports in *Brassica spp*.

4.1.2.7 Siliqua length

High heritability (91.98%) with low genetic advance (1.17) and medium genetic advance in percentage of mean 15.08% which refers that this trait was controlled by non-additive gene. Selection based research would not be that effective. Sharafzadeh (2012) reported low broad sense heritability for pod length in rapeseed.

4.1.2.8 Number of seeds per siliqua

High heritability (94.92%) in combination with low genetic advance 4.78 indicates that this trait was governed by non-additive gene. Selection on this trait would not give a good result but with medium high genetic advance in percentage of mean 22.49% shows a way of opportunity to

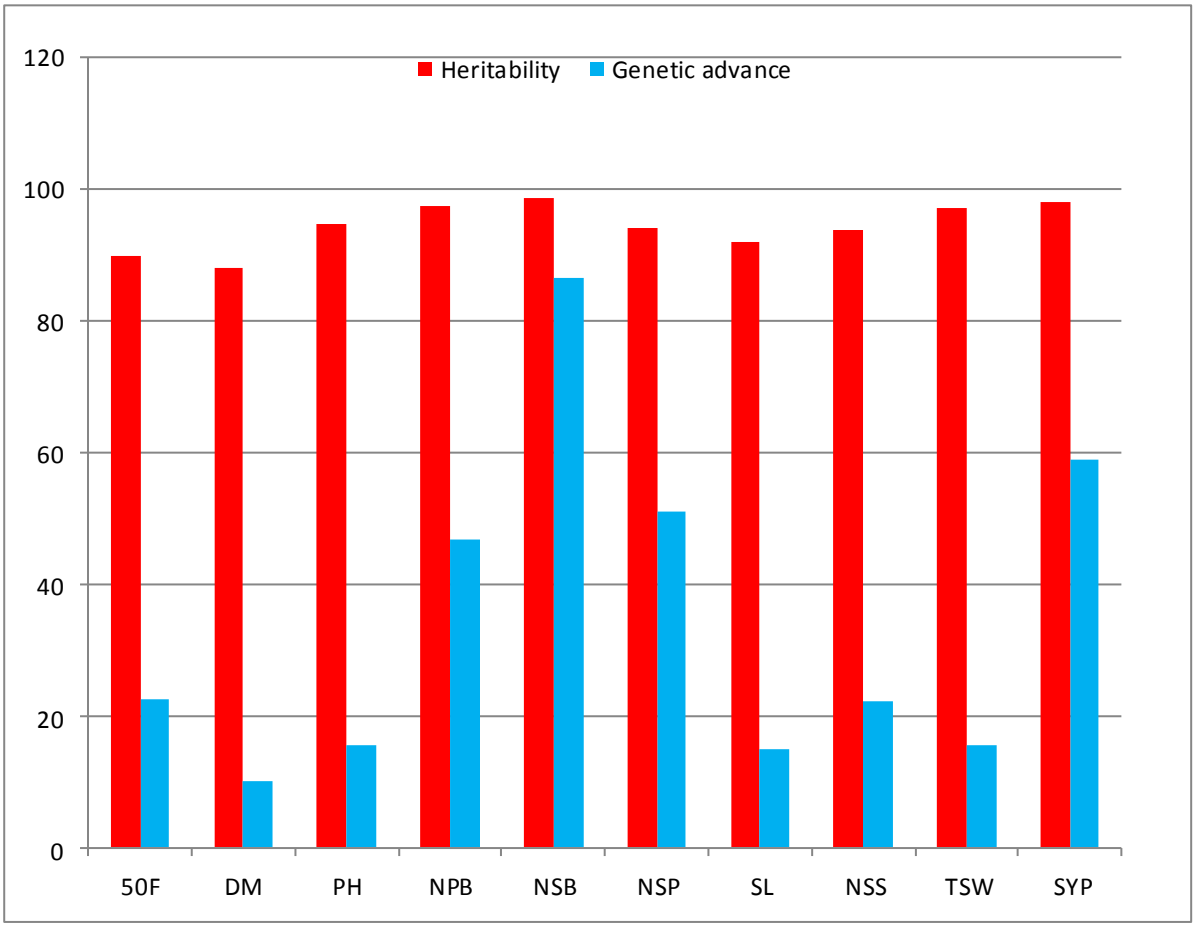

Figure 2. Heritability and genetic advance over mean in *Brassica napus* L. genotypes

select high valued genotype for breeding program. Mahmud (2008) found seeds per siliqua showed high heritability with low genetic advance.

4.1.2.9 Thousand seed weight

High heritability (97.06%) with low genetic advance 0.63 and moderate genetic advance in percentage of mean 15.64%, showed that this trait was governed by non-additive gene but there is possibility of predominance of

additive gene actions. Keeping up with our result, low genetic advance was observed by Saifullah (2010) for the traits in *Brassica sp.*. Paired effect of high heritability and considerable genetic advance in percentage of mean was reported by Afrin *et al.*(2011).

4.1.2.10 Seed yield per plant

This trait showed high heritability 98.34% with low genetic advance (3.50) and high genetic advance in percentage of mean 58.87% indicates that this character was governed by additive gene and selection can be an effective method for future breeding program. Rameeh (2014) also observed coupled effect of high heritability with high genetic advance for seed yield in *B. napus*.

4.2 Correlation coefficient

Polygene controls yield and environment has a considerable influence in it. So depending on only yield for selection can be ineffective. Correlation co-efficient helps to select the yield contributing characters. Significant improvement of different traits including yield can be carried out by correlation co-efficient.

4.2.1 Days to 50% flowering

It was correlated with days to maturity and was positively and highly significant (r_g=0.722**, r_p= 0.723**) at 1% probability level, but positive and significantly correlated with plant height (r_g= 0.131*,r_p= 0.112*). It denotes that it will be useful for breeders in constant improvement of each trait. It also showed insignificant and positive correlation with number of primary branches (r_g= 0.015, r_p= 0.014), number of siliqua per plant (r_g= 0.103, r_p= 0.092), number of seed per siliqua (r_g= 0.019, r_p=

0.011) and yield per plant (r_g=0.034, r_p= 0.033) that reflects the independent nature of two characters. However, it had insignificant and negative interaction with siliqua length (r_g= - 0.139, r_p= - 0.131), number of secondary branches (r_g=- 0.012, r_p= - 0.014) and thousand seed weight (r_g = -0.077, r_g= - 0.067) (Table 3) which showed that association between these traits was highly influenced by the environment. Similar result was also observed by Rameeh (2012).

4.2.2 Days to maturity

It exhibited insignificant positive correlation with number of primary branches (r_g= 0.066, r_p= 0.068), number of secondary branches (r_g= 0.076, r_p= 0.078), number of siliqua per plant (r_g= 0.119, r_p= 0.116). However, it had insignificant and negative interaction with siliqua length (r_g= -0.151, r_p= - 0.137), number of seed per siliqua (r_g= -0.095, r_p= -0.086), thousand seed weight (r_g= -0.046, r_p= - 0.037) and seed yield per plant (r_g= -0.094, r_p= - 0.094) (table 3). Non-significant association of these characters refers that association among each trait was highly influenced by the environmentas. However it showed positive significant correlation with plant height (r_g= 0.146, r_p= 0.137) ($p \leq 0.05$) (Table 3) that means if days to maturity rises then plant height increases. Similar correlation was reported by Bilal *et al.* (2015).

4.2.3 Plant height (cm)

Highly significant and positive interaction was observed with plant height and number of primary branches (r_g= 0.303**, r_p= 0.302**) and number of secondary branches (r_g= 0.427**, r_p= 0.418**), number of siliqua per

Table 3. Genotypic and phenotypic correlation coefficients between different pairs of yield and yield contributing characters for different genotype of *Brassica napus* L.

		DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
50F	r_g	0.722**	0.131*	0.015	-0.012	0.103	-0.139	0.019	-0.077	0.034
	r_p	0.723**	0.112*	0.014	-0.014	0.092	-0.131	0.011	-0.067	0.033
DM	r_g		0.146*	0.066	0.076	0.119	-0.151	-0.095	-0.046	-0.094
	r_p		0.137*	0.068	0.078	0.116	-0.137	-0.086	-0.037	-0.094
PH	r_g			0.303**	0.427**	0.429**	0.295*	0.138*	0.110	0.365**
	r_p			0.302**	0.418**	0.421**	0.289*	0.136*	0.100	0.358**
NPB	r_g				0.811**	0.420**	-0.320**	-0.093	0.193*	0.492**
	r_p				0.801**	0.411**	-0.317**	-0.087	0.184*	0.467**
NSB	r_g					0.232	-0.249*	-0.119	0.104	0.376**
	r_p					0.229	-0.238*	-0.117	0.093	0.371**
NSP	r_g						0.159	0.118	0.037	0.686**
	r_p						0.153	0.115	0.035	0.698**
SL	r_g							0.553**	0.040	0.328**
	r_p							0.539**	0.037	0.309**
NSS	r_g								-0.147	0.441**
	r_p								-0.136	0.415**
TSW	r_g									0.229**
	r_p									0.219**

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

50F= Days to 50% flowering, DM= Days to 80% maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, NSP=Number of siliqua per plant, NSS=Number of seed per siliqua,SL=Siliqua length, TGW= Thousand seedweight(g), SYP= Seed yield per plant, r_g= Genotypic correlation coefficient, r_p= Phenotypic correlation coefficient

plant (r_g= 0.429**, r_p= 0.421**) seed yield per plant (r_g= 0.365**, r_p= 0.358**). It showed positive significant correlation with siliqua length (r_g= 0.295*, r_p= 0.289*) and number of seed per siliqua (r_g= 0.138*, r_p= 0.136*) (Table 3). It refers that if plant height goes up then number of primary branches, secondary branches, siliqua length, number of seed per siliqua and yield also increase. It also implies that highly significant positive correlation between plant height and other characters shows that the traits were controlled by a common gene and constant improvement may be possible. These observations resembles to the reports of Alam (2010), Parveen (2007) and Abideen *et al*. (2013).

4.2.4 Number of primary branches per plant

It had highly significant positive correlation with number of secondary branches per plant (r_g= 0.811**, r_p= 0.801**), number of siliqua per plant (.r_g= 0.420**, r_p= 0.411**) and seed yield per plant (r_g= 0.492**, r_p= 0.467**). Significant and positive correlation was observed with thousand seed weight (r_g= 0.193*, r_p= 0.184*). Given findings suggestthat if number of primary branches and yield per plant increase proportionally. Similar result was remarked by Malik *et al.* (2000). Again, it had highly significant but negative correlation with siliqua length (r_g= -0.320**, r_p= -0.3197**) that denotes these two would act disproportionately.

4.2.5 Number of secondary branches per plant

It had ignificant and positive correlation with seed yield (r_g= 0.376**, r_p= 0.3671**) ($p \leq 0.01$) which means they would change proportionally. But significant and neagtive correlation was noticed with siliqua length (r_g= -0.232*, r_p= -0.229*) ($p \leq 0.05$) that means they would act

disproportionally. The observation indicates that secondary branching was an important attribute to yield, independent of its correlation with thousand seed weight. These observations were identical to the findings of Afrin *et al*.(2011).

4.2.6 Number of siliqua per plant

NSP had positive correlation with pod per plant and seed yield per plant (r_g= 0.686**, r_p= 0.678**). Jeromela *et al*. (2007) also found positive association between siliqua per plant and seed yield. This refers that primary branches and yield per plant increases proportionally that allows to make constant improvement of both the traits. On the other hand insignificant and positive interaction was found in siliqua length (r_g= 0.159, r_p= 0.153), number of siliqua per seed (r_g= 0.118. r_p= 0.115) and thousand seed weight (r_g= 0.037, r_p= 0.035) (Table 3). This insignificant association indicates that these traits is highly influenced by the environment. Bilal *et al*. (2015) and Rameeh *et al*. 2011) also showed positive significant correlation between siliqua per plant and seed yield.

4.2.7 Siliqua length (cm)

It had highly significant and positive interaction with number of seed per siliqua (r_g= 0.553**, r_p= 0.539**) and seed yield per plant (r_g= 0.328**, r_p= 0.309**) indicating their proportional change. Identical findings were found from Alam (2010). It also had insignificant and positive correlation with thousand seed weight (r_g= 0.040, r_p= 0.037) (Table 3).

4.2.8 Number of seeds per siliqua

Highly significant positive correlation between NSP and yield per plant (r_g= 0.441**, r_p= 0.415**). It refers that the traits were controlled by a

common gene and they change proportionally and the traits can be improved simultaneously. It showed insignificant and negative correlation with thousand seed weight (r_g= - 0.147, r_p= - 0.136) (Table 3). Rameeh (2015) noticed that number of seeds per siliqua had positive correlation with seed yield per plant.

4.2.9 Thousand seed weight

1000-seed weight was highly significant positively correlated with seed yield per plant (r_g= 0.229**, r_p= 0.219**) (Table 3). Jeromela *et al*. (2007) found positive associations which is similar to this results.

These observations regarding correlation analysis implied that all characters were positively correlated with seed yield except days to maturity. By comparing correlation coefficient values of ten variables on seed yield, significant variations were noticed. In the cases where genetic correlation coefficient was higher than phenotypic correlation coefficient, association of two characters was because of common genes, but the phenotypic estimate was decreased by the significant interaction of environmental factors.

4.3 Path Co-efficient analysis

Ultimately seed yield is the desired trait of all yield contributing characters. Path analysis is done to define he direct and indirect effects of yield contributing characters on seed yield. In this particular study, seed yield per plant was considered as effect (dependent variable) and days to 50% flowering, days to 80% maturity, plant height, siliqua length, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, number of siliqua per plant and 1000-seed weight were defined independent variables. Calculation of direct and

indirect effect of path co-efficient analysis for *rapeseed* is illustrated in Table 4.

4.3.1. Days to 50% flowering

By analyzing path co-efficient it was found that days to 50% flowering had positive direct effect (0.169) on yield per plant. But it imposed indirect positive effect on yield per plant through number of primary branches (0.005), number of siliqua per plant (0.069), siliqua length (0.045). Also, it had indirect negative effect on days to maturity (-0.056) followed by plant height (-0.019), number of secondary branches (-0.003), number of seed per siliqua (-0.089), thousand seed weight (-0.090). But positive correlation with seed yield (0.034) (Table 4) was observed. Chauhan and Singh (1995) showed that days to 50% flowering had positive direct effect on yield per plant.

4.3.2. Days to maturity

DM had insignificant and negative effect on seed yield per plant (-0.088). It also had indirect negative effect on yield via plant height (-0.0089), number of primary branches per plant (-0.011), number of secondary branches per plant (-0.004), number of seed per siliqua (-0.094) and thousand seed weight (-0.084). Also positive indirect effect was found via days to flowering (0.084), number of siliqua per plant (0.075) and siliqua length (0.024) (Table 4). It indicates the reason of indirect effects of the character through another component trait, indirect selection through such trait should be practiced to reduce the undesirable effect. Rashid (2007) noted that days to maturity had positive direct effect on seed yield of rapeseed.

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on yield of *Brassica napus* L.

Characters	Direct effect	Indirect effect									Genotypic correlation with yield
		50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	
50F	0.169	-	-0.056	-0.019	0.005	-0.003	0.069	0.045	-0.089	-0.090	0.034
DM	-0.088	0.083	-	-0.008	-0.011	-0.004	0.075	0.024	-0.094	-0.084	-0.095
PH	-0.127	0.079	-0.004	-	0.031	0.017	0.30	-0.004	0.077	0.008	0.367**
NPB	-0.07	-0.008	-0.007	0.115	-	0.13	0.391	-0.054	-0.058	0.03	0.474**
NSB	0.17	0.018	-0.017	-0.014	-0.007	-	0.29	-0.033	-0.017	-0.01	0.367**
NSP	0.683	0.014	-0.007	-0.013	-0.019	0.002	-	-0.042	0.071	0.016	0.688**
SL	-0.156	-0.024	0.021	-0.087	0.039	0.002	0.119	-	0.358	0.020	0.320**
NSS	0.544	-0.015	0.018	-0.016	0.028	0.015	0.073	-0.143	-	-0.0789	0.424**
TSW	0.10	-0.016	0.03	0.005	-0.02	0.002	0.13	-0.006	-0.058	-	0.238**

Residual effect: **0.217**

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

50F = Days to 50% flowering, DM = Days to 80% maturity,PH = Plant height (cm), NPB=Number of Primary branchesper plant, NSB=Number of secondary branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique,SL=Siliqua length, TGW = Thousand Grain Weight (g), SYP=Seed yeild per plant.

4.3.3. Plant height

Plant height and seed yield per plant was highly significantly correlated (0.367). On another context, it had low and negative effect indeed (-0.127). Indirectly realizing through 50% flowering (0.079), number of primary branches (0.031), number of secondary branches (0.017), number of siliqua per plant (0.30), number of seed per siliqua (0.077) and thousand seed weight (0.008) positively, but the indirect effect of days to maturity (-0.004) and siliqua length (-0.004) were negative (Table 4). Varshney (1986) studied several strains of *Brassica sp* and found that plant height had the negative direct effect on yield.

4.3.4. Number of primary branches per plant

It had negative direct effect on yield per plant (-0.07) and positive indirect effect on plant height (0.115), number of secondary branch (0.13), number of siliqua per plant (0.391) and thousand seed weight (0.03). On another context, negative indirect effect was observed on days to 50% flowering (-0.008), days to maturity (-0.007) and siliqua length (-0.054) (Table 4). It finally made positive highly significant correlation with seed yield (0.474). It refered that indirect effects of the character through another component trait caused correlation, so indirect selection by other such trait will be effective in improvement of yield. Basalma (2008) and Rashid (2007) reported that primary branching had the direct negative effect on seed yield.

4.3.5. Number of secondary branches per plant

It had positive direct effect (0.17) on seed yield per plant and positive indirect effect on 50% flowering (0.018) and number of siliqua per plant (0.29) on seed yield per plant. Negative indirect effect on yield per plant was found via days to maturity (-0.017), plant height (-0.014), number of primary branches(-0.007), siliqua length (-0.042), number of seed per siliqua (-0.017) and thousand seed weight (-0.01) (Table 4). This indicates that correlation between yield and this character was due to both direct and indirect effect. Rashid (2007) found that number of secondary branches per plant had the highest direct effect on seed yield per plant.

4.3.6. Number of siliqua per plant

Analysis of path-coefficient implied that number of siliqua per plant showed positive direct effect (0.683) on seed yield along with positive indirect effect on days to 50% flowering (0.014), number of secondary branches (0.002), number of seed per siliqua (0.071) and thousand seed weight (0.016). Otherwise days to maturity (-0.007), plant height (-0.013), number of primary branches(-0.019) and siliqua length (-0.042) (Table 4) had negative indirect effect on yield. Highly significant positive genotypic correlation was observed (0.688). By the indirect positive and negative effects it can be said that direct effect of a character caused correlation. Sharafi *et al*. (2015) noticed via their study that the number of siliqua per plant had the highest direct effect on seed yield.

4.3.7. Siliqua length

Correlation coefficient with siliqua length and seed yield per plant had highly positive significance (0.320). It had direct effect on seed yield per plant was negative (-0.156). Days to maturity (0.021), number of primary branches (0.039), number of secondary branches (0.002), number of siliqua per plant (0.119) number of seed per siliqua (0.358) and thousand seed weight (0.020) had indirect positive effect. Besides, indirect negative effect was noticed via length of siliqua on 50% flowering (-0.024) and plant height (-0.087) (Table 4). Therefore selection can be aa effective method for mere improvement. Alam (2010) noticed positive direct effect of siliqua length on yield per plant.

4.3.8. Number of seeds per siliqua

The study showed direct positive effect (0.544) of number of seeds per siliqua on yield per plant. It also has indirect positive effect on days to maturity (0.018), number of primary branches (0.028), number of secondary branches (0.015) and number of siliqua per plant (0.073). Moreover, indirect negative effect was found on 50% flowering (-0.015), plant height (-0.016), siliqua length (-0.143) and thousand seed weight (-0.073). At last significant positive genotypic correlation (0.424) was noted with yield per plant (Table 4). Selection might be practiced for improvement. Positive effect via number of seeds per siliqua on yield per plant was reported by Sharafi *et al*.(2015).

4.3.9 Thousand seed weight

Highly significantly positive correlation was observed(0.238). It had positive direct effect to seed yield per plant (0.10). Also positive indirect effect was found on days to maturity (0.03), plant height (0.005), number of secondary branches (0.002) and number of siliqua per plant (0.13) (Table 4). Moreover, days 50% flowering (-0.016), number of primary branches(-0.02), siliqua length (-0.006), and number of seed per siliqua (-0.058) (Table 4) had indirect negative effect. Sharafi *et al*.(2015) noted that thousand seed weight showed the highest positive direct effect on seed yield per plant. The value of residual effect was 0.217. It refered to some other attributes (approx. 21.6%) other than the character actually studied which contributed for yield.

4.4 Genetic Diversity Analysis

Genetic diversity refers to as the total number of genetic attributes in the genetic constitution of a species. It is totslly diferent from genetic variability, which is the tendency of genetic attributes to vary. It is a path for populations to adapt to whatever surroundings they are in. The genetic diversity of 32 F_5 materials of *Brassica napus* genotypes are presented in Table 5 to 10 and Figure 3 and 4.

4.4.1 Principal Component Analysis (PCA)

Significant differences was noticed amongst all the genotypes in the analysis of variance for all the 10 characters under research with the existance of notable genetic variance between the genotypes. PCA was staged with 32 genotypes of rapeseed. The calculated Eigen values for the 10 variables lead to PCA along with the related proportion and cumulative variation that are shown in Table 5. This analysis gives Eigen

values of principal component axes of coordination of genotypes with the first axes totally responsible for the variance between the genotypes (40.45). These three major elements account for 77.6% of the total variation (Table 5). Zaman *et al.* (2010) noted that first 3 PC's accounted for 95.00% of the total variation whereas the first principal components accounted for 81.93%. Khan (2014) noted that the contribution of first three axes in overall PCs was 26.86%. According to the main axes I and II, a (Z1 – Z2) chart which is a two dimensional chart of the genotypes using component score 1 as X axis and component score 2 as Y axis. The scatter illustration showed five relative clusters in which the genotypes were distantly placed from each other (Figure 3).The genotypes of cluster I were more diverse than those of cluster III(Fig. 4).

Table 5. Eigen values and yield percent contribution of 10 characters of 32 genotypes of *Brassica napus* L.

Principal component axes	**Eigen values**	**Percent variation**	**Cumulative % of Percent variation**
I	4.044	40.45	40.45
II	1.994	19.96	60.48
III	1.692	16.94	77.6
IV	0.836	8.33	99.53
V	0.622	6.20	99.67
VI	0.385	3.85	100
VII	0.192	1.92	100
VIII	0.135	1.32	97.78
IX	0.057	0.56	98.25
X	0.043	0.42	100

Z1-Z2 Graph

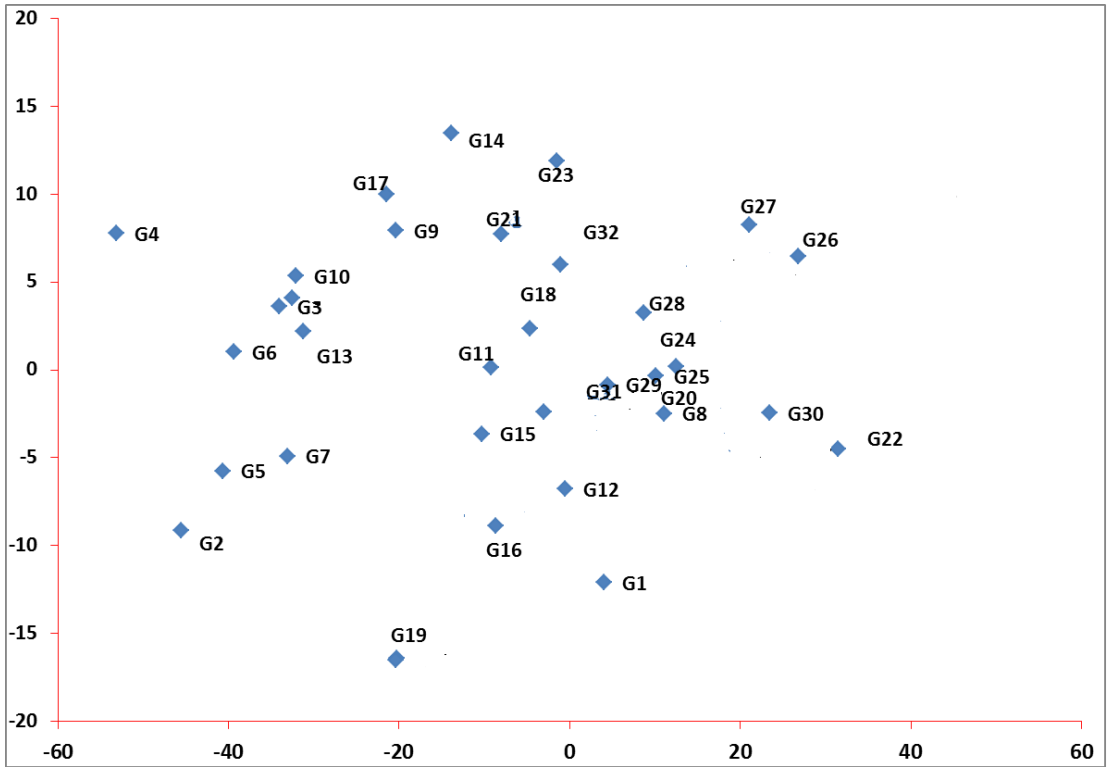

Figure 3. Scatter pattern of *Brassica napus* genotypes of based on their principal component score

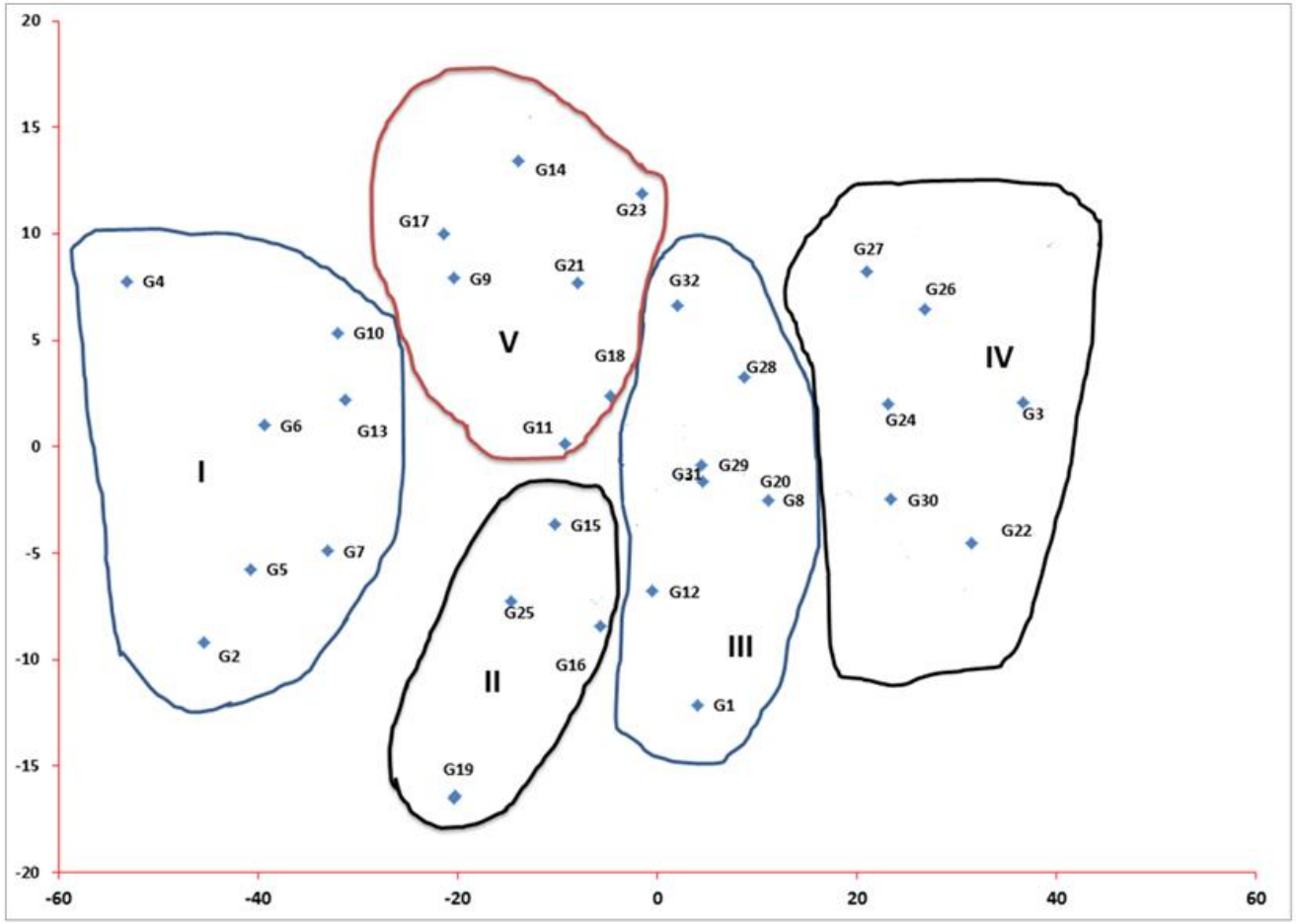

Figure 4. Scatter diagram of *Brassica napus* genotypes of based on their principal component scores.

4.4.2 Non-Hierarchical Clustering

Five clusters were formed with the 32 genotypes were via non-hierarchical clustering (Table 6). Most of the genotypes (8) were grouped into cluster IV, followed by 7 I and V, respectively. 6 and 4 genotypes were grouped into cluster IV and II (Table 6). Cluster I have G2, G4, G5, G6, G7, G10, G13 (Table 6). Cluster I genotypes obtained the highest cluster mean value for number of primary branch (3.33), number of secondary branch (3.231), number of siliqua per plant (123.55), thousand seed weight (3.55 g) and seed yield per plant (8.73) (Table 7) which denotes that genotypes under this cluster could be used as future parents regarding the mentioned traits. Cluster II produced the highest mean for seeds per siliqua (21.83) and 1000-seed weight (3.54 g) and lowest plant height (94.68), thus indicating that the genotype of this cluster might be used as future parents for greater seed quantity. The genotypes included in cluster III were highest mean value for siliqua length (7.76 cm) and lowest mean value for days to 50% flowering (35.39), days to maturity (80.88) and 1000 seed weight (3.24). So these genotypes can only be used as parents if early maturity is required. On the other hand, Cluster IV had lower cluster mean for number of primary branch (2.22), number of secondary branch (1.40), siliqua per plant (63.37), siliqua length (7.45), seeds per siliqua (19.62) and seed yield per plant (4.21). Cluster V includes the late 50% flowering (39.79), late maturity plant (84.795) and highest plant height (112.58) (Table 7). So the genotype can be used for late maturity plant in future breeding program.

Table 6. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G2, G4, G5, G6,G7, G10, G13	7	Nap 179 × Nap 2001, Nap 2037 × Nap 2057, Nap 2037 × Nap 248, Nap 94006 × Bs 7, Nap 2012 × Nap 2013, Nap 94006 × Nap 2013, Nap 2037 × Nap 2022
II	G15, G16, G19, G25	4	Bs 7× Nap 206, Nap 2001 × Nap 2022, Nap 2037 × Nap 206, Nap 2012 × Nap 2022
III	G1, G8, G12, G20, G28, G29, G31, G32	8	Nap- 9908 × BS- 13, Nap- 248 × Nap- 206, Nap- 9908×Nap- 2037, Nap- 9908×Nap- 2022, Nap- 9908 × Nap- 2001, Nap- 2037 × Bs - 13, Nap- 9908 × Nap- 2013, Nap- 248× Nap- 2013
IV	G3, G22, G24, G26, G27, G30	6	Nap 248 × Nap 159, Nap 179× Nap 206, Nap 9908 × Nap 238, Nap 248× Nap 2022, Bs 13× Nap 2013, Bs 13× Nap 206
V	G9, G11, G14, G17, G18, G21. G23	7	Nap 206 × Nap 2012, Nap 9908 × Nap 94006,Nap 206 × Nap 2013,Nap 94006 × Bs 13, Nap 2037 × Nap 2012,Bs 13 × Nap 2022,Nap 9908 × Nap 206
	Total	32	

Table 7. Cluster mean values of 10 different characters of 32 genotypes of *Brassica napus* L.

Characters	**I**	**II**	**III**	**IV**	**V**
Days to 50% flowering	35.89	36.20	35.39	35.61	39.79
Days to maturity	82.06	81.61	80.88	81.38	84.79
Plant height (cm)	113.00	94.68	101.37	98.23	112.8
Primary branches per plant	3.33	2.99	2.78	2.22	2.75
Secondary branches per plant	3.231	2.02	1.87	1.40	2.56
Siliqua per plant	123.55	101.78	83.25	63.37	96.54
Siliquae length (cm)	7.76	7.66	7.76	7.45	7.55
Seeds per siliqua	21.76	21.83	21.63	19.62	20.77
1000-seed weight (g)	3.55	3.54	3.24	3.42	3.49
Seed yield per plant (g)	8.73	6.93	5.73	4.21	6.33

4.4.3 Canonical Variate Analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 8 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 9. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Islam and Islam (2000) reported that the inter-cluster distances were larger than the intra-cluster distances.

Inter cluster distance

The highest inter-cluster distance was observed between clusters I and IV (10.309), followed by between cluster III and I (7.112), V and IV (6.390), II and IV (6.373). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and IV indicated the genotypes in these clusters were diversedthan those clusters. The greater the distance between two clusters the greater the divergence (Table 8). The minimum distance observed between clusters III and IV (3.513) (Table 9) indicated close relationship among the genotypes included and genotypes in these clusters were less diversed than others.

Intra cluster distance

The intra cluster D^2 values were given in Table 8. The intra cluster distance was observed in the clusters. The intra cluster distance was

higher in cluster IV (0.086) and lowest in cluster II (0.032) (Table 8). 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 8. Intra (Bold) and inter (Regular) cluster distances (D^2) for 62 genotypes of *Brassica napus*L.

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**0.061**	5.441	7.113	10.311	4.639
II		**0.031**	3.599	6.367	4.255
III			**0.077**	3.521	3.666
IV				**0.084**	6.389
V					**0.049**

Table 9. The nearest and farthest clusters from each cluster between D^2 values in *Brassica napus*L. genotypes

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**V (**4.639)	**IV (**10.311)
2	**II**	**III (**3.599)	**IV (**6.367)
3	**III**	**IV (**3.521)	**I (**7.113)
4	**IV**	**III (**3.521)	**I (**10.111)
5	**V**	**III (**3.666)	**IV (**6.389)

It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster I and IV (Table 9). 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 transgressivesegregants and high heterotic response due to getting maximum yield along with short duration. Keeping this in view, it appears that the crosses between genotypes from cluster I with cluster IV might produce high level of segregating

population. The crosses between the genotypes belonging cluster V with cluster IV, cluster III with cluster I, might produce high heterosis in respect of earliness and yield. So the genotypes belonging to these genotypes have been selected for future hybridization program.

4.4.4 Contribution of traits towards divergence of the genotypes

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were siliqua per plant (0.1487), siliqua length (0.1598) and seed yield per plant (0.1108). In vector II (Z_2), 50% flowering (0.1901), plant height (0.1659), number of secondary branch per plant (1.1125) (Table 10). 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 50% flowering, plant height and number of secondary branch 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 siliquae contributed the maximum towards divergence in the existing linseed germplasm.

Table 10. Relative contributions of the ten characters of 32 genotypes of *Brassica napus* L. to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days to 50% flowering	0.1256	0.1901
Days to maturity	-0.1310	-0.1407
Plant height (cm)	0.0643	0.1659
Primary branches per plant	-0.1931	-0.6343
Secondary branches per plant	0.1770	1.1125
Siliqua per plant	0.1487	-0.0443
Siliquae length (cm)	0.1598	-0.1166
Seeds per siliqua	-0.0725	-0.0539
1000-seed weight (g)	-0.1634	-0.6464
Seed yield per plant (g)	0.1108	-0.1884

4.4.5 Selection of parents for future hybridization

Selection of genetically diverse parents is the prime task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G12 (Nap 9906 × Nap 2066, P1), G14 (Nap 9906 × Nap 2066, P3), G15 (Nap 205× Nap 0130, P1), G16 (Nap 205× Nap 0130, P2), G22 (Nap 9908 × Nap 0130, P2), G24 (Nap 9908 × Nap 0130, P4) for short duration and early maturity and G17(Nap 205× Nap 0130, P3) for higher seed yield. Therefore, considering group distance and agronomic performance the inter-genotypic crosses between G3, G4, G20, G25, G21 and G15 might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The present experiment was undertaken to study the variability, character association and diversity in thirty two genotypes of *Brassica napus* L. based on ten characters. The salient findings of the present study have been summarized on the basis of the characters studied. Analysis of variance showed significant differences among the genotypes.

From variability analysis of F_5 progenies, it was observed that significant variation exist among all the genotypes used for most of the characters studied. Plant height exhibited highest in G4 an lowest in G19. The highest number of primary branches per plant was recorded in G3 and lowest number was recorded in G13 and G23. The highest number of secondary branches per plant was observed in in G3 and lowest in G23. The minimum days to 50% flowering was found in G25 and highest in G28. The lowest days to maturity was also observed in G24 and the highest in G14.

The number of siliqua per plant showed the highest in G4 and lowest in G23. The highest siliqua length was recorded in G3, G26 and the lowest in G15. The number of seeds per siliqua was found highest in G31 and the lowest in G21. The thousand seed weight was found highest in G4 and the lowest in G21. The seed yield per plant was the highest in G4 and the lowest observed in G23.

However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. Phenotypic

coefficients of variation were also close to genotypic coefficients of variation for most of the characters except Plant height, days to 50% flowering, days to maturity and number of siliqua per plant. On the other hand, number of primary branch, number of secondary branch, number of seeds per siliqua, siliqua length , 1000 seed weight and seed yield per plant showed least difference between phenotypic and genotypic variance suggesting least environmental influence and additive gene action for the expression of the characters.

Number of secondary branches per plant (98.70) exhibited the highest value of heritability while days to maturity (88.02) exhibited the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed for number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seed per siliqua and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.

High heritability with moderate genetic advance was observed for days to 50% flowering, plant height, siliqua length, number of seed per siliqua and thousand seed weight indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for days to maturity indicating that non-additive gene effects were involved for the expression of these characters.

Correlation coefficients among the characters were studied to determine the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and

suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering which was positive but non-significant and days to maturity (non-significant negative) with seed yield per plant.

Path co-efficient analysis revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 80% maturity, plant height, number of primary branch and siliqua length had the negative direct effect on yield per plant.

The genotypic correlation with seed yield per plant was positive and considerably higher in magnitude except days to 50% flowering which was non-significant but positive and days to maturity non-significant negative. It is mainly due to high positive direct effect and positive indirect effects via the other characters and selection would be effective for this trait. The path coefficient studies indicated that number of primary branch, number of secondary branch, siliqua per plant, number of seeds per siliquae and thousand seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis,

Canonical Variate Analysis (CVA) using GENSTAT computer program. The 62 genotypes fell into five distant clusters. The cluster IV comprised the maximum number (19) of genotypes followed by same in cluster cluster III (18). The cluster I and V comprised 10 and 9 genotypes respectively. The lowest number of genotypes was present in cluster II. The highest inter-cluster distance (10.309) was observed between the cluster I and IV, if involved in hybridization may produce a wide spectrum of segregating population. The lowest inter-cluster distance (3.513) was observed between the cluster III and IV.

The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire five clusters was more or less low indicating that the genotypes within the same cluster were closely related.

Based on the results of the study, the following conclusions and recommendations may be drawn:

1. The high heritability coupled with high genetic advance in percent of mean observed in number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seed per siliqua and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.
2. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering which was positive but non-significant and days to maturity (non-significant negative) with seed yield per plant. This results suggested that yield per plant can be increased by improving these characters.

3. The days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant. So yield improvement was associated with these characters.

4. Wide genetic diversity was observed in 32 genotypes of *Brassica napus* L., which were grouped into five clusters. The highest inter-cluster distance (10.309) was observed between the cluster I and IV. The genotypes of clusters I and V were more diversed from the genotypes of other cluster.

5. The role of days to 50% flowering, plant height and number of secondary branch in both the vectors were important components for genetic divergence in these materials.

Recommendations:

1. Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G4(Nap-2037 X Nap-2057) for higher seed yield per plant, plant height, number of siliqua per plant. G3(Nap-248 X Nap-159) for higher number of primary branches and secondary branches per plant, highest siliqua length and G11(Nap-9908 X Nap-94006) for seed per siliqua. G24(Nap-9908 X Nap-248) and G25(Nap-2012 X Nap-2022) for short duration and early maturity.

2. The genotypes of cluster I and IV could be used as parents for future breeding programme to developed *Brassica napus L*. variety.

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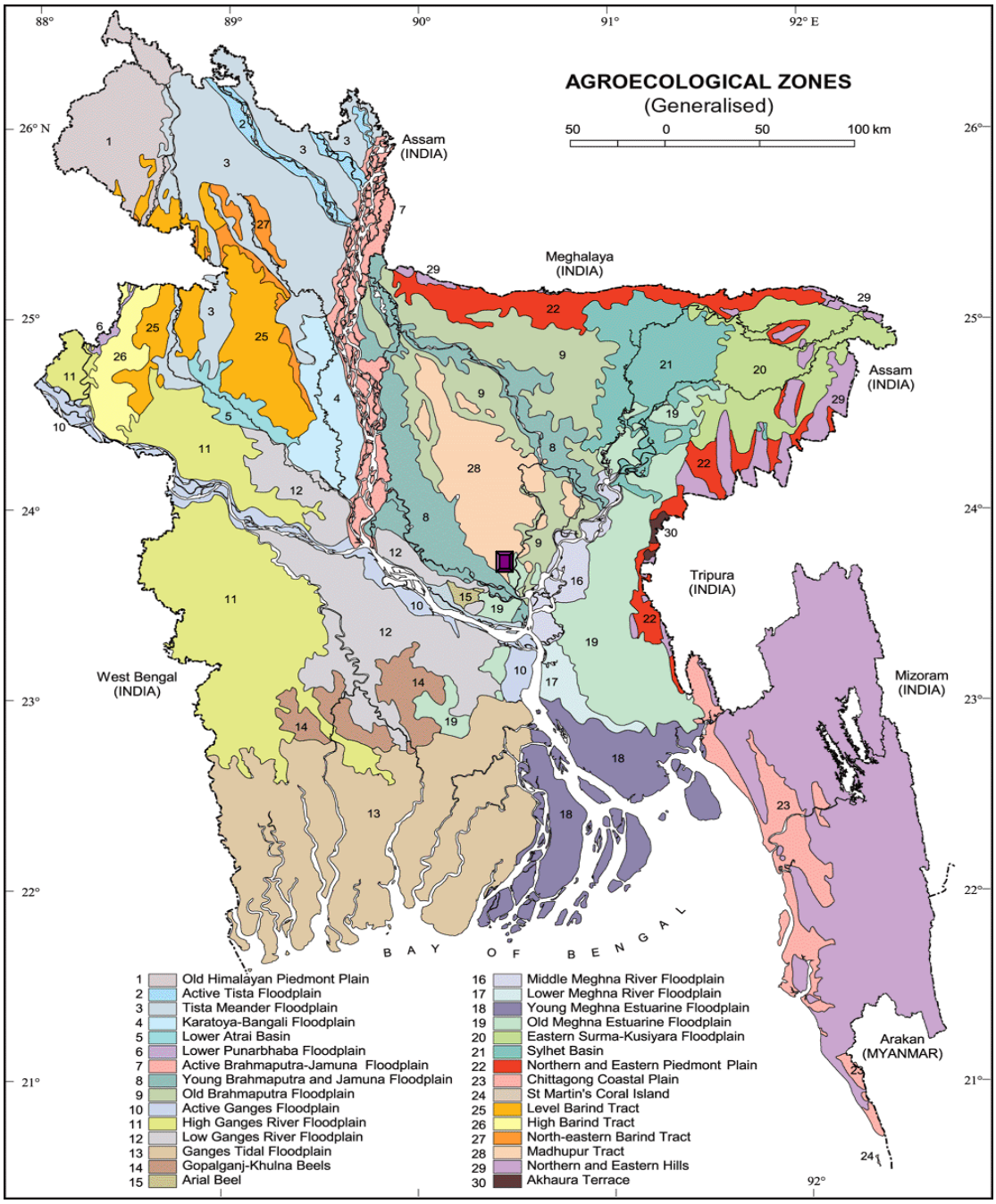
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

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

Month	Air temperature (°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	0	**3.9**
February, 2018	**28.1**	**11.1**	**72**	**1**	**5.7**

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

Appendix IV. Mean performance of various growth parameter and yield components

Genotype	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
G1	31.00	78.00	92.20	3.22	3.06	85.67	8.44	22.57	3.50	7.17
G2	33.00	79.00	105.77	3.99	3.80	133.30	7.94	22.64	3.62	9.83
G3	38.00	85.00	113.03	4.40	5.77	119.78	8.70	19.64	3.70	8.60
G4	41.00	86.00	120.53	3.11	3.27	137.67	7.10	19.45	4.12	10.47
G5	31.00	78.00	109.78	2.91	2.49	127.83	7.70	20.59	3.33	8.28
G6	30.33	77.00	117.83	3.51	3.33	124.57	7.17	22.39	3.45	8.86
G7	29.00	76.00	110.60	2.62	3.23	119.89	6.91	19.59	3.54	8.38
G8	31.00	77.67	101.63	2.68	2.26	76.47	8.38	23.33	3.73	6.24
G9	41.00	86.00	113.11	3.26	2.98	105.82	8.19	21.19	3.57	6.40
G10	37.00	84.00	115.40	3.35	2.55	117.53	7.91	20.65	3.43	6.70
G11	33.00	77.00	108.73	3.13	3.08	95.84	8.20	21.88	3.45	5.44
G12	32.00	79.00	98.46	3.08	3.19	88.93	8.00	21.99	3.25	7.31
G13	36.67	82.00	112.60	3.06	3.29	117.03	8.01	23.31	3.61	9.11
G14	43.00	91.00	115.02	2.74	2.60	98.57	7.65	21.73	3.48	7.01
G15	41.00	87.00	97.22	3.58	2.71	99.17	6.37	15.87	3.96	6.10
G16	34.00	78.00	97.37	2.46	2.12	94.66	7.72	21.00	3.50	5.45
G17	42.00	86.67	115.03	2.71	3.10	106.53	7.58	20.43	3.74	6.45
G18	39.00	82.00	105.63	3.66	2.73	91.53	7.38	19.33	3.94	6.68
G19	37.00	82.00	88.83	2.63	1.89	111.09	7.98	23.17	3.40	8.80
G20	32.00	77.00	103.03	2.47	1.31	78.92	7.22	19.27	3.49	4.80
G21	36.00	82.00	113.72	2.56	2.32	93.46	7.09	16.73	3.54	5.47
G22	37.00	81.00	90.71	1.63	1.06	57.90	8.20	22.29	3.56	4.35
G23	41.00	84.00	114.06	3.19	1.98	86.53	6.92	18.98	3.19	4.89
G24	32.00	75.00	104.97	2.65	1.58	74.37	8.19	23.67	2.94	5.07
G25	42.00	85.00	96.65	2.44	1.37	78.27	7.40	20.41	3.27	5.32
G26	37.00	84.00	103.03	1.93	1.41	59.93	8.70	21.43	3.41	4.49
G27	36.00	82.00	107.60	2.09	1.24	64.99	7.29	19.87	3.34	4.37
G28	44.00	89.00	98.60	2.60	1.33	79.09	8.35	21.43	3.14	5.17
G29	35.00	81.00	101.96	3.02	1.74	83.24	7.09	19.59	3.06	5.11
G30	32.00	76.00	99.02	2.92	1.89	64.59	7.25	19.34	3.67	4.87
G31	34.67	80.00	102.03	2.38	1.89	85.00	8.01	24.66	3.13	6.18
G32	33.00	79.00	112.72	2.49	1.72	83.27	7.23	25.63	2.91	6.25
Mean	36.25	81.89	103.08	2.67	2.06	87.41	7.61	20.93	3.41	5.95
Min.	27.00	75.00	88.83	1.42	0.90	47.85	6.37	14.20	2.91	3.11
Max.	44.00	91.00	120.53	4.40	5.77	137.67	8.70	27.93	4.12	10.47

50F = Day to 50% flowering, DM = Day to maturity, PH = Plant Height (cm), NPB = Number of Primary Branches per plant, NSB = Number of secondary branches per plant, NSP = Number of Siliqua per plant, SL = Siliqua length (cm), NSS = Number of seed per silique, TSW = Thousand seed weight (g), SYP = Seed yield per plant (g)

Appendix V. Principal component score 1 & 2.

Genotype	Z_1	Z_2
G1	4.03	-12.11
G2	-45.48	-9.16
G3	-34.01	3.6
G4	-53.11	7.77
G5	-40.69	-5.74
G6	-39.33	1.01
G7	-33.03	-4.9
G8	11.06	-2.49
G9	-20.33	7.92
G10	-32.05	5.35
G11	-9.24	0.14
G12	-0.5	-6.79
G13	-31.2	2.2
G14	-13.89	13.45
G15	-10.3	-3.64
G16	-5.65	-8.4
G17	-21.43	10.01
G18	-4.65	2.36
G19	-20.3	-16.4
G20	8.66	-1.59
G21	-7.96	7.72
G22	31.45	-4.52
G23	-1.49	11.9
G24	12.54	0.17
G25	10.14	-0.35
G26	26.79	6.45
G27	21.04	8.23
G28	8.75	3.25
G29	4.46	-0.85
G30	23.44	-2.47
G31	2.52	-1.69
G32	1.96	6.63