GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BC_1F_6 POPULATION OF *Brassica napus* L.

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CERTIFICATE

*This is to certify that thesis entitled, "**GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BC_1F_6 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 (M.S.)** in **GENETICS AND PLANT BREEDING** , embodies the result of a piece of bona fide research work carried out by **FARHANA AFRIN**, Registration No: **11-04469** 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:
Place: Dhaka, Bangladesh

…… ….
(Dr. Firoz Mahmud)
Professor
Supervisor

DEDICATED

TO

MY BELOVED PARENTS

AND

MY SISTER

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By

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ABSTRACT

Thirty BC_1F_6 populations of *Brassicanapus* were evaluated to study the genetic variability, correlation, path analysis, genetic diversity and selection of population based on yield and yield component traits. The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka during November 2016 to February 2017. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Analysis of variance revealed significant variations were observed among the genotypes for all the traits studied. Considering genetic parameters, high GCV values were observed for number of secondary branches per plant and seed yield per plant. High heritability values coupled with high genetic advances in per cent mean were obtained for number of secondary branches per plant, number of siliqua per plant and seed yield per plant. Correlation studies revealed significant positive association of seed yield per plant with plant height, number of secondary branches per plant, siliquae per plant and 1000 seed weight at both genotypic and phenotypic levels. Path coefficient indicated positive direct contribution towards seed yield per plant through siliquae per plant, seeds per siliqua, 1000 seed weight, plant height and primary branches per plant.The genotypes were grouped into five clusters. The highest nine populations were included under the Cluster III and the cluster II contained the lowest with solitary. Cluster II and cluster V shown the highest distance indicating genotypes from these two clusters were diverse. While the lowest inter-cluster distance was observed between cluster III and IV. Considering group distance, seed yield per plant and other agronomic performance genotypes G6 (Nap108 X Nap2066 (Nap2066)), G8 (Nap108 X Nap9908(Nap9908)), G10 (Nap205 X Nap0130 (Nap0130)), G11 (Nap206 X Nap205 (Nap205)), G14 (Nap2066 X Nap0130 (Nap2066)), G20 (Nap9905 X Nap9908 (Nap9905)) and G29 (Nap9906 X Nap0130 (Nap9906)) might be used as open pollinated verities and need to further performance and stability test; and could be used as parents in future hybridization program.

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COMMONLY USED SOME ABREVIATIONS

Full word	Abbreviation
At the rate	@
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
By way of	via
Backcross in the sixth generation of a cross between two dissimilar homozygous parents	BC_1F_6
Cultivars	cv.
Centimeter	cm
Canonical Variate Analysis	CVA
Cluster Analysis	CA
Degrees of Freedom	Df
Days to 50% flowering	D50%F
Days After Sowing	DAS
Days to Maturity	DM
Duncan`s Multiple Range Test	DMRT
Etcetera	etc.
Environmental variance	σ^2_e
Food and Agricultural Organization	FAO
Genotypic variance	σ^2_g
Gram	g
Genotype	G

Genetic Advance	GA
Genotypic coefficient of variation	GCV
Heritability in broad sense	h^2_b
International Center for Agricultural Research in Dry Areas	ICARDA
Indian Agricultural Research Institute	IARI
Journal	J.
Kilogram	Kg
Meter	M
Mean sum of square	MS
Murate of Potash	MP
Ministry of Agriculture	MOA
Number	No.
Namely	Viz.
Principal Component Analyais	PCA
Principal Coordinate Analysis	PCO
Phenotypic coefficient of variantion	PCV
Percent	%
Phenotypic variance	σ^2_p
Percentage of Coefficient of Variation	CV%
Plant height	PH
Primary branches per plant	PBP
Residual Effect	R
Randomized Complete Block Design	RCBD
Science	sci.
Standard Error	SE
Siliqua length	LS
Secondary branches per plant	SBP
Seeds per siliqua	SPS

Seed yield per plant	SYP
Square meter	m^2
Sher-e-BanaglaAgicultural University	SAU
Triple Super Phosphate	TSP
Thousand seed weight	TSW
The third generation of a cross between two dissimilar homozygous parents	F_3
University	Uni.
Variety	var.

CHAPTER I

INTRODUCTION

Brassicaceae family comprises of 338 genera and 3709 species (Khaleque, M.A., 1985). The genus *Brassica* holds the most economically valuable position in the tribe Brassiceae, which is a part of family Brassicaceae. This genus consists of a versatile batch of species that includes major oilseed crops and vegetables. There are different species in *Brassica* family i.e., turnip, cauliflower, broccoli, brusssels sprouts, cabbage, weeds and various mustards which are so much important due to their presence in different food, feed and edible oil etc.

The genus is remarkable for containing more important agricultural and horticultural crops than any other genus. Most are annual or biennial, but some are small shrubs. Due to their agricultural importance, Brassica plants have been the subject of much scientific interest (Bilal *et al*., 2015). Six economically valuable species are comprises in this genus with huge genetic and morphological variation and is cultivated in all over the world. Among these, three species are diploid (*Brassica oleracea*, 2n = 18; *Brassica rapa*, 2n = 20; *Brassica nigra*, 2n = 16), and three are amphidiploid (*Brassica napus*, 2n = 38; *Brassica juncea*, 2n = 36; *Brassica carinata*, 2n = 34). Rapeseed-mustard (*Brassica napus, Brassicacampestris and Brassica juncea*) are grown all over the world as an important source of edible oil as described by the Triangle of U theory (Abideen*et al*., 2013).

Brassica napus L. also known as rapeseed, oilseed rape and canola, is the best one with respect of oil production. Rape seed originated in either the Mediterranean area or Northern Europe. Oilseed rape (*Brassica napus L.)* is the second most important oilseed crop in the international oilseed market following soybean (Sharafi*et al*., 2015). The seeds of modern varieties typically contain 40% to 45% oil.

Despite of oil, it also holds 18 to 22 percent proteins which consist of different protein units like cysteine, methionine and lysine. In cereal the amount of these amino acids is too much low so *Brassica napus* L. is the alternate source to get these proteins (Khan, 2014).

Rapeseed (mustards) is the second largest oilseed crop in the world providing 13% of the world's edible oil after soybean. During 2014, rapeseed/ mustard were globally grown on area of 36.5 million hectare with the total production of 72.7 million metric tons having average yield of 1991.0 kg ha^{-1} (FAO Statistics, 2014).

It is the most important oilseed crop in Bangladesh and it occupies the 1^{st} position in respect of area and production among the oil crops grown in Bangladesh. In Bangladesh, 252238.13 ha of land was under rapeseed cultivation during 2014-15 which produced about 246494 tons of seed and average yield was 0.977 ton per ha (BBS, 2011). 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 meet from the import (BBS, 2011). The major reasons for such poor yield in Bangladesh may be attributed due to pressure of other crops, lack of improved varieties and poor management practices.

In spite of the large benefits and as a good source of vegetable oil it is used in minute amounts because it contains very high amount of erucic acid and glucosinolates which cause harm to the cardiac muscle and make the animal feed weaker and innutritious. For improving seeds yield and adaptability of rapeseed and other *Brassica* species, important breeding strategies are; understand and utilization of genetic, physiological and morphological basis of yield linked traits in different environmental conditions.

Significantly, it provides both the essential fatty acids such as linolenic acid and linoleic acid to the human body which is lack most of the edible oil. But in Bangladesh, there is a limited scope to increase acreage due to pressure of other

crops in the Rabi season and due to high cost and long growing period, farmers are not interested to mustard seed production. So, development of improved varieties of *Brassicanapus* with short durational, better quality, higher yield are the most important issues with high priority. For replacing the long durational low yielding variety of *brassicanapus*, this research carried out with BC_1F_6 populations which are generated by crossing among the parents of mustard varieties which would be expected to be short durational and high yielding. By comparison among them, it would possible to select for mitigating the demand of edible oil for future. Seed yield is a complex character that can be determined by several components reflective positive or negative effects upon this trait, whereas it is important to examine the contribution of each of the various components in order to give more attention to those having the greatest influence on seed.

Success of any crop improvement depends upon the presence of substantial amount of genetic variability, heritability, as well as genetic gain in selection. The potential of a crop to favorably respond to breeding/selection and bioengineering programs depends upon nature and magnitude of genetic variability (Shaukat*et al*., 2015).

Generally, correlation coefficients show relationships among independent characteristics and the degree of linear relation between these characteristics. For plant breeders it is thus essential to learn the relationships among pairs of characters in order to make a decision on the proper selection criteria for a breeding program. Information about genetic variability gives a dependable tool to the breeder for improvement in crops. Higher genetic variability and correlation of yield with yield components are important requirements of breeders who wish to improve production and quality of *Brassica* (Abbas *et al.*,2013).

Therefore, the path coefficient analysis has been used by many researchers for a more and complete determination of impact of independent variable on

dependent one. The path coefficient analysis helps the breeder(s) to explain direct and indirect effects and hence has extensively been used in breeding work in different crop species by various researchers (Ali *et al*., 2013).

Rapeseed is an important oilseed crop. Considering the importance of edible oil in country, an experiment was carried out with following objectives:

Objectives:

1. To study the variability in BC_1F_6populations generated through inter-genotypic crosses,

2. To find out the relationship among the different traits and their contribution to the yield, assess genetic diversity among the genotypes and

3. To select promising genotypes considering early maturity and high yielding population.

CHAPTER II

REVIEW OF LITERATURE

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

2.1 Variability, heritability and genetic advance

2.2 Correlation among different characters

2.3 Path co-efficient analysis

2.4 Genetic diversity

2.1. Variability, heritability and genetic advance

Katiyar*et al.*,(1974) studied in *Brassica rapa*L. var. sarson grain on ten characters in 54 plants from each of 40 varieties; seed yield per plant showed a high genotypic coefficient of variation. Heritability in the broad sense was associated with high genetic advance for number of siliqua on the main shoot and for seed yield per plant.

While working with 65 strains of *B. rapa*byNanda *et al.*,(1995)reported that days to first flowering varied both by genotypes and date of sowing.

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

An experiment was conducted by Shalini*et al.,* (2000) to study variability in *Brassicajuncea* L. Different genetic parameters was estimated to assess the magnitude of genetic variation in 81 diverse Indian mustard genotypes. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all 10 characters studied. Genotypic coefficient of variation, estimates of variability, heritability values and genetic gain were moderate to high for 1000 seed weight, number of siliqua per plant and number of secondary branches per plant, indicating that the response to selection would be very high for these yield components. For the other characters, low coefficient of variation, medium to low heritability and low genetic gain were observed.

An experiment was conducted by Khulbe*et al.*,(2000) to estimate variability, heritability and genetic advance for yield and its components in Indian mustard revealed maximum variability for seed yield. All the characters except oil content exhibited high heritability with high or moderate genetic advance, suggesting the role of additive gene action in conditioning the traits. Non-additive gene action appeared to influence the expression of days to maturity, while environment had a major influence on oil content. The use of pedigree selection or bi-parental mating in advanced generations was advocated to achieve substantial gains.

Tyagi*et al.*,(2001) evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components.The highest variation for plant height of parents and their hybrids was reported. The seed yield per plant exhibited the highest coefficient of variation (41.1%).

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

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

Ghosh and Gulati, (2001) studied genetic variability and association of yield components in Indian mustard among 12 yield components for 36 genotypes selected from different geographical regions. The genotypic and phenotypic coefficients of variability (GCV and PCV, respectively) were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied, coupled with high heritability except plant height, indicating the usefulness of phenotypic selection in improving these traits. High heritability, coupled with high genetic advance was observed for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua. This result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection.

Shen et *al.,* (2002)tested 66 F_1 hybrids of *Brassica rapa*and significant differences were found between F_1s and their parents for yield per plant and seed oil content.

Choudhary*et al.*,(2003) studied variability in Indian mustard for 10 characters during rabi season in India. A wide range of variability was observed for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua and thousand seed weight. Genotypic and phenotypic coefficient of variability was recorded high for secondary branches per plant, seed yield per plant and number of siliqua per plant. High heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action.

Afroz*et al.*,(2004) studied genetic variability of 14 genotypes of mustard and rape. The highest genetic advance was observed in percent of pollen sterility.

Mahak*et al.,* (2004) conducted an experiment on genetic variability, heritability, genetic advance and correlation for eight quantitative characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters. High heritability coupled with high genetic advance in percentage of mean was observed for days to flowering, followed by thousand seed weight, days to maturity and plant height.

Niraj and Srivastava, (2004) studied on variability and character association in Indian mustard of 21 genotypes of *Brassicajuncea*. RH-9704 and IGM-21 recorded the highest seed yield. Phenotypic coefficient of variation was high for oil yield per plant, seed yield per plant and seed weight. Heritability was high for test weight, days to flowering, days to maturity and plant height.

Akbar *et al.*,(2007) evaluated eight advanced lines of *Brassicajunea* in Pakistan and studied variability, heritability and genetic advance of different yield components that were under experiment. The highest GCV was found in seed yield per plant followed by plant height, siliqua per plant and thousand grain weights while the lowest GCV was in number of primary branches per plant. The highest heritability was found yield per plant followed by plant height, thousand grain weight, siliqua per plant and number of primary branches per plant. The maximum genetic advance was found in seed yield per plant followed by siliqua per plant, plant height, thousand grain weight and minimum in primary branches per plant.

Rashid, (2007) studied variability of forty oleiferous*Brassica* species. Result revealed that genotypes showed wider variation for morphological characteristics and thus were categorized under three cultivated species - *B. rapa, B. napus and B. juncea* considering genetic parameters. High GCV (Genotypic Co-efficient of Variation) value was observed for days to 50% flowering, days to maturity, plant height and number of siliqua per plant.

Parveen, (2007) studied variability in F_2 progenies of the inter-varietal crosses of 17 *Brassicarapa* genotypes. The result revealed that there were significant variations among the different genotypes used in the experiment. Number of primary branches/plant and secondary branches/plant showed high heritability

coupled with high genetic advance and very high genetic advance in percentage.

A study was conducted by Hosen, (2008) using five parental genotypes of *Brassicarapa* and their ten F_3 progenies including reciprocals. The result revealed that there were large variations present among all the genotypes used in the experiment. Number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, length of siliqua, number of seeds per siliqua, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was considerable variation among the all characters except days to maturity. The plant height, days to 50% flowering and number of siliqua per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

A field experiment was conducted by Jahan, (2008) to study on inter-genotypic variability and genetic diversity in 10 F_4 lines obtained through inter-varietal crosses along with 8 released varieties of *Brassicarapa*L. Significant variation was observed among all genotypes for all the characters studied. Considering genetic parameters high genotypic coefficient of variation (GCV) was observed for number of secondary branches/plant, siliqua/plant, yield/plant whereas days to maturity showed very low GCV. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective.

An experiment was carried out by Mahmud, (2008) with 58 genotypes of *Brassicarapa* L. to study inter-genotypic variability. Significant variation was observed among all the genotypes for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in

percentage of mean were obtained for days to 50% flowering, number of secondary branches per plant, seeds per siliqua, and siliqua length.

Singh, (2010) studied sixty two F_1 and twenty four parental lines of *Brassica juncea* and observed that higher genotypic variation, high heritability and high genetic advance in seed per plant, secondary branches per plant, primary branches per plant, thousand seed weight and seed per siliqua.

Alam, (2010) conducted an experiment by using twenty six F_4 populations of some inter-varietal crosses of *Brassicarapa* L. to study the variation among them. Higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant.

Afrin *et al.,* (2011) conducted an experiment in *Brassicanapus* and studied heritability. The plant height showed the highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliqua, number of siliqua per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

Ali *et al.,* (2013) conducted an experiment with the thirty lines of *Brassicacarinata* and reported that PCV and GCV ranged from 4.92-48.24% and 3.2-38.1%, respectively. The highest heritability values were recorded for pod length (0.83) followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield per plant and pods on main raceme.

Khan *et al.,* (2013) evaluated thirty F_7 segregating lines and two parents of *Brassicarapa* to study variability, heritability and genetic advance. The result revealed thatsignificant variation was presented among all the genotypes for all the charactersexcept thousand seed weight. The highest genotypic, phenotypic and environmental variances were observed in plant height while the lowest one was in length of siliqua followed by thousand grain weight. Thousand seed

weight, number of secondary branches per plant, seeds per siliqua, and siliqua length showed high heritability along with low genetic advance in percent of mean. Considering important performances, the genotypes G-15, G-19, G-1, G-3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program.

Abideen*et al.,* (2013) studied with eight genotypes of *Brassicanapus* and observed that there were highly significant variations among the genotypes for most of the traits studied. Non-significant differences were in primary branches per plant and pods per plant among the genotypes.

Walle*et al.,* (2014) carried out a study with thirty six genotypes of Ethiopian mustard (*Brassicacarinata*) and result revealed that there were significant difference in days to 50% flowering, plant height and primary branches per plant. GCV was lower than the PCV for all yield related characters studied. High heritability with high genetic advance was observed in plant height, number of secondary branches per plant and days to 80% maturity.

Mekonnen*et al.,* (2014) evaluated thirty six genotypes of Ethiopian mustard, *Brassicacarinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were observed for number of pods per plant, primary and secondary braches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in primary branches per plant. Higher GCV and PCV for seed yield, number of pods per plant, primary and secondary branches which indicated that, it might provide better scope for improvement through selection. Besides these, higher heritability along with higher genetic advance was observed in days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, seed yield/plot and hectare and thelowest one was in primary branches per plant.

Muhammad *et al.,* (2014) studied with four parental genotype along with twelve F_2generation of Brassica napus and reported that days to 50% flowering were significantly different at 5 % level of significance. Plant height and pod

length showed high heritability and days to 50% flowering showed moderate heritability.

Ejaz-Ul-Hasan*et al.,* (2014) studied on heritability of *Brassicanapus* and the result stated that plant height, yield per plant and days to 50% flowering showed high heritability.

2.2 Correlation among different characters

Analysis of correlation among different traits is important in breeding program. A good number of literatures are available on correlation among characters of *Brassica* spp. Some of these literatures are reviewed here:

Days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. The number of branches per plant and number of siliqua per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight was reported by Malek*et al.,* (2000)while studied correlation analysis.

Badsra and Chaudhary, (2001) studied correlation on 14 traits of 16 Indian mustard genotypes. Seed yield was positively correlated with stem diameter, number of siliqua per plant and oil content, while oil content was positively correlated with harvest index only. Among the characters only three characters positively correlated with seed yield.

Association of yield components in Indian mustard among 12 yield components were studied in 36 genotypes selected from different geographical regions by Ghosh and Gulati, (2001) Seed yield exhibited significant positive association with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliquae on main shoot and oil content.

Pankaj*et al.*,(2002) studied four parental cultivars and the 174 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of the characters. The number of siliqua per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliquae and test weight at

both levels. The number seeds per siliquae were positively associated with siliqua length and yield per plant at both levels.

Afroz*et al.*, (2004) studied correlation and found seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliqua per plant. Path coefficient revealed maximum direct positive effects on plant height followed by number of siliqua per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant.

Mahak*et al.*, (2004) conducted an experiment and studied correlation for eight quantitative characters. 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.

An experiment conducted by Niraj and Srivastava, (2004) on character association studies in Indian mustard of 21 genotypes of *Brassicajuncea*. Seed and oil yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

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

Tusar*et al.*,(2006) studied phenotypic correlation and observed that seed yield per plant was positively and significantly associated with plant height, total dry matter production. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield.

Zahan, (2006) studied correlation and reported that yield/plant had highly significant positive association with plant height, length of siliqua, siliqua/plant and seed/siliqua but insignificant negative association with days to 50% flowering, days to maturity.

Akbar *et al.,* (2007) evaluated eight advanced lines and two check variety of *Brassicajunea* in Pakistan and reported that siliqua per plant had strong positive correlation with the seed yield followed by plant height while non-significantly negative correlation with thousand grain weight. But significantly negative correlation was present in siliqua per plant and primary branches per plant.

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

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

A study was conducted by Hosen, (2008) using five parental genotypes of *Brassicarapa* and their ten F_3 progenies including reciprocals. He found yield per plant showed the highest significant and positive correlation with days to maturity followed by number of seeds per siliqua, number of secondary branches per plant, length of siliqua and number of siliqua per plant.

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

Singh *et al.,*(2010) studied sixty two F_1 and twenty four parental lines of *Brassicajuncea* and observed that positive correlation was present in plant height, primary branches per plant, secondary branches per plant, seed per siliqua, thousand grain weight with seed yield.

Afrin *et al.,* (2011) studied on *Brassicanapus* and found positive correlation with seed yield per plant in plant height, number of primary branches per plant

and number of siliqua per plant. Highest significant positive correlation was found between days to 50% flowering and plant height.

Maurya*et al.,* (2012) carried out an experiment with one hundred genotypes of *Brassicajuncea* and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50% flowering.

Uddin*et al.,* (2013) conducted an experiment with seven parental and twenty one F_2 progenies of *Brassicarapa* to study correlation among different yield component and found that yield per plant had high significant positive correlation with number of primary branches per plant, number of secondary branches per plant and siliqua per plant at both phenotypically and genotypically and significant positive correlation at genotypically in days to flowering and days to maturity.

Ali *et al.,* (2013) conducted an experiment with thirty lines of Brassica cwinaiø and observed that highly positive phenotypic correlation for seed yield per plant with plant height and primary branches per plant which was the indication that the traits were the most important contributors to seed yield per plant.

Abideen*et al.,* (2013) studied with eight genotypes of *Brassica napus* and the resulted that positive phenotypically correlation was observed in plant height, pod length and seed yield. Significant positive correlation was also found in seed yield per plant and pods per plant.

Ejaz-Ul-Hasan*et al.,* (2014) studied correlation between different traits of *Brassicanapus* and found high and positively significant phenotypic correlation between plant height and seeds per plant.

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

2.3 Path co-efficient analysis

The path analysis helps to determine the direct and indirect contribution of traits towards the yield. Direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfills this study. It was first developed and described by Wright (1921), as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components. The association between the various characters in a rapeseed and mustard and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

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

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

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

Afroz*et al.,*(2004) studied path analysis of 14 genotypes of mustard and observed that maximum direct positive effects on plant height followed by number of siliqua per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant.

By path analysisZahan, (2006) reported that siliqua/plant had positive direct effect on yield/plant. And days to 50% flowering had negative direct effect on yield/plant.

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

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

Rashid, (2007) carried out an experiment with 40 oleiferous*Brassica* species to estimate path analysis and observed that yield per plant had the highest direct

effect on days to maturity, number of seeds per siliqua, number of siliquae per plant and number of primary and secondary branches per plant.

Parveen, (2007) conducted an experiment with F_2 population of *Brassicarapa* to study the path analysis and observed that number of seeds per siliqua showed thehighest direct effect on yield per plant.

The path co-efficient analysis by Hosen, (2008)exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassicarapa* and their ten F_3 progenies including reciprocals.

An experiment was carried out by Mahmud, (2008) with 58 genotypes of *Brassicarapa*. Path analysis showed that yield per plant had the highest direct effect on number of primary branches per plant, number of siliqua per plant, number of secondary branches per plant and number of seeds per siliqua.

Aytac*et al.*, (2008) evaluated on six genotypes of spring rape seed and studied path coefficient and the result stated that plant height, number of siliqua per plant, seeds per siliqua had highest and positive direct effect on yield per plant for all cultivars except cv. Star.

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

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

Uddin*et al.*,(2013) conducted an experiment with seven parental and twenty one F_2 progenies of *Brassicarapa* to study path coefficient and reported that days to 50% flowering, number of primary branches per plant, number of

secondary branches per plant, number of siliqua per plant, siliquae length, seed per siliqua and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association.

Mekonnen*et al.,* (2014) conducted an experiment to study path co-efficient in *Brassicacarinata* and found that days to maturity and secondary braches per plant had positive and direct genotypic correlation with seed yield.

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

2.4 Genetic divergence among mustard genotypes

Evaluation of germplasm through genetic divergence which quantifies variation among genotypes on the basis of a group of characters (yield and yield contributing) helps in identification of promising parental materials for crop improvement. Germplasm collections are also valuable gene pools providing diverse genetic material that may be applied for the improvement of cultivars and advanced agronomic productivity. An assessment of genetic diversity within these collections can be used to assign lines and populations to diverse groups. D^2 statistic developed by Mahalanobis (1936) provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence (Nair and Mukherjee, 1960). Mahalanobis D^2 statistic is more reliable in selection of potential parent for hybridization programme using these D^2 values cluster are formed. A summary of literature reviewed on mustard and other allied species are in presented below

Peter and Rai, (1995) studied genetic divergence using the D^2 statistics and canonical analysis among 25 genotypes of *Brassica napus*. They reported that genetic and geographical divergence was highly related with the genotypes. The genotypes were grouped into six clusters of which cluster I was the largest

accommodating among these genotypes. The cluster VI had large genetic distance from the remaining clusters.

Singh *et al.,* (1997) studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and their inter and intra cluster distances. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for use in breeding programme.

Khulbe and Pan, (1999) reported that siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight were positively associated with grain yield. Analysis of variance revealed that siliqua per plant, siliqua length, 1000 seed weight and seeds per siliqua were the major characters influencing grain yield.

Jagadev*et al*., (1999) studied on some 19 genotypes of rapeseed (*B. napus*). They studied yield and yield contributing characters grouped the genotypes into 5 clusters with clusters I comprising these genotypes, clusters II and 1112 each and clusters IV and V one each.

Aunwinithul*et al.,* (2004) studied 33 genetically diverse genotypes of Indian mustard for diversity. The genotypes were grouped into eight different clusters. The cluster III was the biggest with 11 genotypes followed by cluster-I with 9 genotypes, cluster V and VI consisted of 4 and 3 genotypes respectively. The cluster II and VII both had two genotypes each and similarly, cluster IV and VIII included one genotype each.

Yadava*et al.,* (2004)studied 50 lines of *B. napus* and reported that the lines were grouped into twelve clusters with maximum inter cluster distances between the clusters XII and IX (35.51), II and III (33.03) and XI and IX (31.21). The characters contributing to the maximum divergence were in descending order, oil content days to flowering, plant height, siliqua length and siliqua number on the main raceme.

Goswami*et al.,*(2005) conducted experiment on variability studies for number of secondary branches per plant, siliqua on main shoot, seed per siliqua, 1000-seed weight and seed-yield per plant. Results showed that the coefficient of variation of pods per plant.

Kardam and Singh,(2005)noted that the nature and magnitude of variability for 10 characters in 200 progenies of Indian mustard *(B. juncea)* obtained from six crosses were studied during Rabi 2002-03 in Jobner, Rajasthan, India. Phenotypic coefficients of variation were higher in magnitude compared to genotypic coefficients of variation for most of the characters. Seed yield per plant was significantly associated with plant height, primary branches per plant, and number of siliqua per plant, number of seeds per siliqua and 1000-seed weight. The number of siliqua per plant had the highest direct contribution to seed yield, followed by primary branches per plant, 1000-seed weight, number of siliqua on main shoot and number of seeds per siliqua.

Goswami and Behl, (2006) studied 43 genotypes of Indian mustard using D^2 statistics. They recorded data for plant height, primary branches, secondary branches, main shoot length, number of siliqua on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant and oil content. The genotypes were grouped into six clusters. The intra cluster distances were almost equal and relatively lower than the inter-cluster distances.

Vivek*et al.*,(2007) studied the genetic diversity in 81 true breeding advanced generation cultivars of Indian mustard based on yield and yield components. They are followed by cluster analysis and showed that out cluster XII, which was most diverse, had very high seed yield and number of siliqua per plant. Cluster VII also represented entries with high seed yield, number of siliqua per plant and highest number of seed per siliqua. Cluster XI with the lowest number of days to maturity could be considered as a good source for earliness.

Hossain*et al.*, (2008) studied the genetic divergence using D^2 statistic in 40 genotypes of rapeseed. The genotypes differed significantly for 10 yield and yield contributing characters, and they grouped then into 9 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.

Zaman*et al.,* (2010) conducted a field experiment for estimation of divergence among 45 advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (six) and the cluster III contained the lowest (three). The highest intra cluster distance was observed in cluster II and the lowest in cluster I. The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between clusters IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82 %), branches per plant (1.91%) and siliqua 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.

Pandey*et al.,* (2013) conducted an experiment with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. D^2 analysis was conducted to measure the genetic diversity among the genotypes. The 45 genotypes were grouped in 8 clusters using Tocher's method. Intra cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. Maximum contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield per plant (20.91%) and number of siliqua on main raceme (8.38%).

CHAPTER III

MATERIALS AND METHODS

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

3.1 Experimental site

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during November 2016 to February 2017. The location of the experimental site was situated at $23^0$74' N latitude and $90^0$35' E longitude with an elevation of 8.6 meter from the sea level. Photograph showing the experimental site (Appendix II).

3.2 Soil characteristics

The soil of the experimental site lies in Agro ecological region of Madhupur Tract (AEZ no. 28) (www.banglapedia.com) of Noda soil series. Soil of the experimental site belongs to the general soil type, Shallow red brown terrace soils under Tejgaon Series. The soil was loam in texture. The experimental site was medium high land and the pH was 5.6 to 5.8 and organic carbon content was 0.82%. Experimental area was flat which facilitated irrigation and drainage system easily.Physicochemical properties of the soil are presented in Appendix III.

3.3 Climate

The experimental site was situated under the subtropical climatic zone, characterized by three distinct seasons**,** the dry or cold season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October (Edris*et al.*, 1979) and also characterized by heavy precipitation during the month of May to August and scanty precipitation from October to March.

The mean of air, temperature, humidity and rainfall during the period of experiment were recorded from the Bangladesh Metrological Department, Agargaon, Dhaka (Appendix III, IV & V).

3.4 Plant materials

The healthy seeds of 30 BC_1F_6 populations collected from the Dept. of Genetics and Plant Breeding, Sher-E-Bangla Agricultural University, Dhaka-1207 which were used as experimental materials. The plant materials used in that experiment is shown in Table 1**.**

3.5 Design and layout

The trial field was laid out in a Randomized Complete Block Design (RCBD) with three replications. The plot size was 8 m long with four rows. Row to row distance was 30 cm and plant to plant to distance was 10 cm. The distance between replications was 0.5 m. The genotypes were randomly distributed in each replication.

Table 1: Materials used for the experiment

Genotype	BC_1F_6 populations	Source
G1	Nap108 X Nap0130 (Nap108)	SAU
G2	Nap108 X Nap0130 (Nap0130)	SAU
G3	Nap108 X Nap205 (Nap108)	SAU
G4	Nap108 X Nap205 (Nap205)	SAU
G5	Nap108 X Nap2066 (Nap108)	SAU
G6	Nap108 X Nap2066 (Nap2066)	SAU
G7	Nap108 X Nap9908 (Nap108)	SAU
G8	Nap108 X Nap9908 (Nap9908)	SAU
G9	Nap205 X Nap0130 (Nap205)	SAU
G10	Nap205 X Nap0130 (Nap0130)	SAU
G11	Nap206 X Nap205 (Nap205)	SAU
G12	Nap2066 X Nap205 (Nap2066)	SAU
G13	Nap2066 X Nap0130 (Nap0130)	SAU
G14	Nap2066 X Nap0130 (Nap2066)	SAU
G15	Nap9901 X Nap 203 (Nap9901)	SAU
G16	Nap9905 X Nap108 (Nap108)	SAU
G17	Nap9905 X Nap108 (Nap9905)	SAU
G18	Nap9905 X Nap0130 (Nap0130)	SAU
G19	Nap9905 X Nap0130 (Nap9905)	SAU
G20	Nap9905 X Nap9908 (Nap9905)	SAU
G21	Nap9905 X Nap9908 (Nap9908)	SAU
G22	Nap9905 X Nap9901 (Nap9905)	SAU
G23	Nap9905 X Nap2066 (Nap9905)	SAU
G24	Nap9906 X Nap2066 (Nap9906)	SAU
G25	Nap9908 X Nap0130 (Nap9908)	SAU
G26	Nap9906 X Nap205 (Nap205)	SAU
G27	Nap9906 X Nap9901 (Nap9906)	SAU
G28	Nap9906 X Nap205 (Nap9906)	SAU
G29	Nap9906 X Nap0130(Nap9906)	SAU
G30	Nap9908 XNap2066 (Nap9908)	SAU

3.4 Operational practice

3.4.1 Plot preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilt. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on 10th November 2016.

3.4.2 Fertilizer application

Organic and inorganic fertilizer viz. cow dung, Urea, TSP and MP fertilizers are required for mustard cultivation. The field was fertilized with 10 ton cow dung per ha on 15 November 2016. The field was also fertilized as the rate shown in Table 2. The entire amount of cow dung was applied seven days before sowing. Half amount of urea, total TSP. MP, Gypsum and Boron were applied during final land preparation and incorporated into the soil. The rest amount of urea was applied as top dressing after 25 days of sowing.

Table 2. List of fertilizer with doses and application procedures

Sl No.	Fertilizer	Doses	application procedure
01	Cowdung	10 ton/ha	as basal
02	Urea	270 Kg/ha	50% basal and 50% at 25 DAS
03	TSP	170 Kg/ha	as basal
04	MP	100 Kg/ha	as basal
05	Gypsum	150 Kg/ha	as basal
06	Zinc oxide	5 Kg/ha	as basal
07	Boron	3 Kg/ha	as basal

3.4.3 Seed sowing

The spacing of row to row was 30 cm and plant to plant in row was 8 cm. Variety to variety distance in each replication was 60 cm. Distance between replication was 50 cm. Seeds were sown in line in the experimental plot on 15

November 2016. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.4.4 Intercultural operations

Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The weeding was done after 15 days of sowing. At the same time, 1st thinning was done and another after 7days of1st thinning for maintaining a distance of 8 cm from plant to plant in rows of 30 cm apart. Total experimental plot was tagging on 1 December 2016 by bamboo stick by maintaining variety cone and replication number. Second weeding was done after 30 days of sowing. Aphid and disease alternaria spot infection was found in the crop during the siliqua development stage. To control pest Malathion-57 EC @ 2ml/liter with Rovral50WP under Iprodione group @ 2gm/lit of water was applied on 12 January 2017 and second time on 16 January 2107. The pesticide was applied in the afternoon.

A **B**

C

D **E**

Plate 1: Photograph showing (**A.** seedling stage, **B.** flowering stage, **C.**siliquae formation stage, **D**. maturity stage, **E.** harvesting stage) experimental field

3.4.5 Crop harvesting

The crop was harvested in different dates according to maturity. Harvesting was started from 2nd week of February 2017 and continued to 3rd week of February 2017 depending upon the maturity. When 80% of the plants showed maturity symptoms like straw color of siliqua, leaves, stem and desirable seed color in the matured siliqua, the crop was assessed to attain maturity. The harvesting was done by my supervision and also present my research supervisor. Ten plants were selected at randomly from each variety in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.

3.5 Parameter recorded

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

3.5.1 Days to 50% flowering

Days to 50% flowering were recorded fromsowing date to the date of 50% flowering of every entry.

3.5.2 Days to maturity

The data were recorded from the date of sowing to siliqua maturity of 80% plants of each entry.

3.5.3 Plant height (cm)

It was measured in centimeter (cm) from the baseof the plant to the tip of the longest inflorescence. Data were taken after harvesting.

3.5.4 Number of primary branches per plant

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

3.5.5 Number of secondary branches per plant

The total number of branches arisen from the primary branch of a plant was counted as thenumber of secondary branches per plant.

3.5.6 Number of siliquae per plant

Total number of siliquae of each plantwas counted and considered as the number of siliqua per plant.

3.5.7 Siliqua length (cm)

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

3.5.8 Number of seeds per siliqua

Well filled seeds were counted from fivesiliqua which was considered as the number of seeds per siliqua.

3.5.9 1000-seed weight (g)

Weight in grams of randomly counted thousand seeds of each entry was recorded.

3.5.10 Seed yield per plant (g)

All the seeds produced by a representative plant was weighed in g and considered as the seed yield per plant.

3.6 Statistical analysis

The mean values of five randomly selected plants were used for recording observations and computed for each of seventeen traits for each genotype in each replication and were subjected to statistical analysis. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2017 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.6.1 Analysis of variance

The analysis of variance for different characters was carried out using mean data in order to assess the genetic variability among genotypes as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using F test. The model of ANOVA used is presented in Table 3.

Table 3. Analysis of variance (ANOVA)

Sources of variation	Degrees of freedom (df)	Mean sum of squares (MSS)	Expected MSS
Replication	(r-1)	Mr	$g\sigma^2_r + \sigma^2_e$
Genotype	(g-1)	Mg	$r\sigma^2_g + \sigma^2_e$
Error	(g-1) (r-1)	Me	σ^2_e
Total	(rg-1)		

Where,

r = number of replications

g = number of treatments (genotypes)

σ^2_r = variance due to replications

σ^2_g = variance due to treatments (genotypes)

σ^2_e = variance due to error

To test significant of the difference between any two-adjusted genotypic mean, the standard error of mean was computed using the formula.

$$\mathbf{S.E} = \sqrt{\frac{2\,Ee}{r}\left(1 + \frac{rqu}{q+1}\right)}$$

Where,

S.E = Standard error of mean

Ee = Mean sum of squares for error (Intra block)

r = Number of replications

q = Number of genotypes in each sub-block

u = Weightage factor computed

3.6.2 Genotypic and phenotypic variances

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

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = Error variance

3.6.3 Genotypic and phenotypic co-efficient of variation

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

Genotypic co-efficient of variation (GCV %) = $\sqrt{\frac{\sigma_g^2}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\frac{\sigma_{ph}^2}{\bar{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

PCV and GCV were classified into three following categories as suggested by Sivasubramanian and Madhamenon (1973).

Categories

Low: Less than 10%

Moderate: 10-20%

High: More than 20%

3.6.4 Heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability estimates in cultivated plants could be placed in the following categories as suggested by Robinson *et al*. (1966).

Categories

Low: 0-30%

Moderate : 30-60%

High:>60%

3.6.5 Genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, $GA = K. h^2. \sigma_p$

Or Genetic advance, $GA = K. \frac{\sigma^2 g}{\sigma^2 p}. \sigma_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Categories

High (>20%)

Moderate (10-20%)

Low (<10%

3.6.6 Genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance}}{\text{Population mean}} X\ 100$$

Genetic advance as per cent mean was categorized into following groups as suggested by Johnson *et al.* (1955).

Categories

Low - <10%

Moderate -10-20%

High - >20%

3.6.7 Genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation, } r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{pv})}}$$

Where,

σ_{pxy} = Phenotypic covariance between the trait x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.6.8 Path co-efficient analysis

Path coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software packages called OPSTAT. These values were obtained by solving the following set of 'p' simultaneous equation using above package.

$P_{01}+ P_{02}\ r_{12} + ...+ P_{0p}\ r_{1p} = r_{01}$

$P_{01}+ P_{12}\ r_{02} + ...+ P_{0p}\ r_{2p} = r_{02}$

$P_{01}+ r_{1p} + P_{02}\ r_{2p} +\ldots\ldots\ldots\ldots+P_{0p} = r_{0p}$

Where, P_{01}, P_{02}, ……. P_{0p} are the direct effects of variables 1, 2……P on the dependent variable 0 and r_{12}, r_{13},.....r_{1p}……$r_{p(p+1)}$ are the possible correlation coefficient between various independent variables and r_{01}, r_{02}, r_{03}..... r_{0p} are the correlation between dependent and independent variables. The indirect effects of the i^{th} variable via j^{th} variable was attained as (P_{0j} * r_{ij}). The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below.

$P^2_{ox} = 1- (P^2_{01} + 2P_{01}P_{02}r_{12} + 2P_{01}\ P_{03}r_{13} +\ldots..+ P^2_{02} + 2P_{02}\ P_{03}r_{13} +\ldots\ldots.. +P^2_{0P})$

Categories

Negligible - 0.00 to 0.09; Low- 0.10 to 0.19; Moderate 0.20 to 0.29; High – 0.30 to 1.0; Very High- >1.00

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

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} +\ldots\ldots\ldots\ldots\ldots.+ r_{8.y}P_{8.y})$

Where,

$P^2_{RY} = R^2$

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

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the ith character with yield y.

3.7 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents' selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao, (1952). suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.7.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity.Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.7.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby*et al.,* 1989).

3.7.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.7.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variability that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.7.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.7.6 Average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster

n = Number of all possible combinations between the populations in cluster

3.7.7 Average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

Average inter-cluster distance= $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possiblecombinations of the populations in cluster i and j

n_i= Number of populations in cluster i

n_j= Number of populations in cluster

3.7.8 Cluster diagram

Using the values of intra and inter-cluster distances (D = $\sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSIONS

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

4.1 Varietal performance and genetic parameters

4.2 Correlation studies

4.3 Path co-efficient analysis

4.4 Genetic diversity through D^2statistics

4.1 VARIETAL PERFORMANCE AND GENETIC PARAMETERS

The achievement in any crop improvement program depends on the capability of the breeder to define and accumulate the required genetic variability and to select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather, 1949). Therefore, it is necessary to have prior information on both PCV and GCV, so that the estimate of heritability that helps the breeder to predict the expected GA possibly by selection for a character can be computed.

The results are pertained to analysis of variance (ANOVA), range, grand mean, CV%, mean performance, genotypic and phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2_b) and expected genetic advance as per cent of mean (GA) for all the eleven traits are furnished in Table 4 to Table 7. Genotypic and phenotypic coefficient of variation is shown in Figure 1; heritability and genetic advance as per cent of mean is represented in Figure 2. Out of the eleven traits studied, plant height, no. of primary branches per plant,

no. of secondary branches per plant are considered as growth attributing characters. Days to 50% flowering and days to maturity were regarded as earliness attributes. No. of siliqua per plant, length of siliqua, no. of seeds per siliqua and 1000 seed weight were considered as reproductive traits. Yield per plant was the economic trait. The character wise details of these variability are discussed below of the genotypes evaluated for 11 characters are presented in below**.**

4.1.1 Days to 50% flowering

Highly significant mean sum of square was observed in days to 50% flowering with the value of 1.66 (Table 4). The maximum duration to days to 50% flowering was found in G6 with 42.00 DAS which was followed by G4, G9, G11, G17 with the value of 41.33. The minimum days to 50% flowering was observed in G29 with 39.00 DAS which was followed by G15 and G19 with the value of 39.33(Table 5). The mean value of days to 50% flowering was 40.40 (Table 6).

The genotypic variance (0.27) is lower than phenotypic variance (1.12) (Table 7). Thus, genes controlling this trait possessed considerable influence of environment on the expression of the character. The Genotypic co-efficient of variation and Phenotypic co-efficient of variation were moderate with value of 1.29 and 2.62 percent respectively, along with low heritability of 24.38% with low genetic advance as percent of mean 1.32% and low genetic advance 0.53% (Table 7). In the contrary, Niraj and Srivastava (2004) and Hosen (2008). Reported that days to 50% flowering showed high heritability with genetic advance in percentage of mean. The flowering trait of the plant is moderate sensitive and influenced by the environmental temperature fluctuation which is reflected in the present study.

Table 4. Analysis of variance for different characters in *Brassicanapus* genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 29**	**Error (r-1)(g-1) = 58**
Days to 50% flowering	0.1333	1.6644*	0.8460
Days to 80% maturity	2.1444	2.0444**	0.8801
Plant height (cm)	23.7865	125.5208**	14.8728
No. of primary branches /plants	0.2671	0.8319**	0.2965
No. secondary branches /plants	0.0028	1.8246**	0.3016
No. of siliqua per plant	156.7000	1,330.1839**	70.2632
Length of siliqua (cm)	0.0034	0.7403**	0.1109
No.of seed/siliqua	1.0111	6.2973**	1.1031
1000 seed wt.	0.0412	0.4004**	0.0613
Seed yield per plant (g)	0.7361	19.1688**	0.9489

** Denote Significant at 1% level of probability

Table 5. Mean performance of different characters of 30 *Brassica napus* genotypes

Genotype	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
G1	41.00	86.67	111.33	2.47	2.00	111.33	7.82	18.33	4.45	9.07
G2	40.33	89.00	111.80	2.67	2.00	129.67	8.48	20.67	4.30	11.53
G3	40.00	88.33	96.50	2.33	2.00	105.00	7.17	19.00	4.05	8.08
G4	41.33	89.00	99.47	2.60	1.67	103.00	7.40	20.00	4.26	8.74
G5	40.33	89.00	99.95	1.67	1.33	117.00	7.26	19.67	4.14	9.53
G6	42.00	86.33	91.09	2.33	2.50	119.00	6.81	18.67	4.35	9.65
G7	40.33	88.67	105.54	2.00	1.67	83.00	8.21	21.67	3.74	6.72
G8	41.00	87.00	103.81	3.67	1.00	124.67	8.08	21.33	4.77	12.72
G9	41.33	89.00	115.54	3.00	2.00	130.33	7.91	20.33	4.82	12.70
G10	39.67	88.33	111.70	4.00	3.67	181.33	6.61	19.67	4.98	17.74
G11	41.33	87.67	93.17	2.33	2.50	95.00	7.50	17.00	5.00	8.08
G12	39.67	88.67	115.27	2.67	2.67	126.00	6.74	19.33	4.80	11.69
G13	41.33	88.33	102.33	2.67	2.33	113.67	7.76	19.67	4.95	11.10
G14	40.00	88.33	112.43	2.67	2.67	110.67	7.59	20.67	4.71	10.76
G15	39.33	90.00	106.91	2.67	2.00	114.00	7.23	19.67	4.34	9.75
G16	40.33	88.33	101.07	3.33	2.33	101.67	8.73	20.33	4.60	9.49
G17	41.33	88.67	109.33	2.67	3.50	129.33	7.53	21.00	4.69	12.74
G18	39.67	89.33	104.09	2.67	3.00	118.00	7.99	24.67	4.11	11.67
G19	39.33	89.00	110.67	2.67	4.00	135.00	7.45	20.33	4.62	12.71
G20	40.33	88.67	98.92	2.00	1.33	79.67	7.59	20.00	4.77	7.57
G21	40.00	89.00	102.17	2.67	2.67	86.67	8.52	20.00	4.50	7.80
G22	40.00	89.00	104.33	3.00	3.00	130.33	7.77	20.33	4.95	13.11
G23	40.67	89.00	94.78	3.00	2.33	107.67	7.39	20.00	4.81	10.38
G24	41.00	88.67	95.33	2.33	1.33	96.67	7.33	17.67	4.70	8.01
G25	41.00	89.33	108.37	3.00	1.33	93.67	7.49	17.00	4.23	6.87
G26	39.67	89.00	107.23	2.67	1.00	97.33	8.02	19.00	4.82	8.93
G27	40.33	88.67	103.27	3.67	2.33	89.67	7.68	19.00	4.22	7.17
G28	39.67	89.33	101.57	2.33	1.00	74.33	7.46	19.00	4.49	6.34
G29	39.00	90.00	107.67	2.00	2.00	110.33	7.53	19.67	4.76	10.34
G30	40.67	89.00	104.90	2.00	1.67	106.00	7.26	19.00	3.57	7.17

D50%F: days to 50% flowering, DM: days to maturity: PH: plant height (cm), PBP: no. of primary branches per plant, SBP: no. of secondary branches per plan, SPP: no. of siliqua per plant, LS: length of siliqua (cm), SPS: no. of seeds per siliqua, TSW: 1000 seed weight (g) and SYP: seed yield per plant (g)

Table 6. Range, mean and CV (%) of 30 *Brassica napus* genotypes

Parameters	Range		Mean	CV (%)
	Min	Max		
Days to 50% flowering	39.00	42.00	40.40	2.28
Days to 80% maturity	86.33	90.00	88.64	1.06
Plant height (cm)	91.09	115.54	104.35	3.70
No. of primary branches /plants	1.67	4.00	2.66	20.49
No. secondary branches /plants	1.00	4.00	2.16	25.41
No. of siliqua per plant	74.33	181.33	110.67	7.57
Length of siliqua (cm)	6.61	8.73	7.61	4.37
No.of seed/siliqua	17.00	24.67	19.76	5.32
1000 seed wt.	3.57	5.00	4.52	5.48
Seed yield per plant (g)	6.34	17.74	9.94	9.80

CV (%) = coefficient of variation

Table 7. Estimation of genetic parameters for different characters in *Brassica napus*

Parameters	**σ^2p**	**σ^2g**	**σ^2 e**	**PCV**	**GCV**	**ECV**	**Heritability**	**GA (5%)**	**GAM**
Days to 50% flowering	1.12	0.27	0.85	2.62	1.29	2.28	24.38	0.53	1.32
Days to 80% maturity	1.27	0.39	0.88	1.27	0.70	1.06	30.60	0.71	0.80
Plant height (cm)	51.76	36.88	14.87	6.89	5.82	3.70	71.26	10.56	10.12
No. of primary branches /plants	0.48	0.18	0.30	25.93	15.90	20.49	37.57	0.53	20.07
No. secondary branches /plants	0.81	0.51	0.30	41.63	32.97	25.41	62.73	1.16	53.79
No. of siliqua per plant	490.24	419.97	70.26	20.01	18.52	7.57	85.67	39.07	35.31
Length of siliqua (cm)	0.32	0.21	0.11	7.40	6.04	4.29	66.46	0.77	10.14
No.of seed/siliqua	2.83	1.73	1.10	8.52	6.66	5.32	61.08	2.12	10.72
1000 seed weight	0.17	0.11	0.06	9.22	7.42	5.48	64.73	0.56	12.30
Seed yield per plant (g)	7.02	6.08	0.95	26.67	24.80	9.80	86.49	4.72	47.51

σ^2p : Phenotypic variance

σ^2g : Genotypic variance

σ^2 e : Environmental variance

PCV : Phenotypic coefficient of variation

GCV : Genotypic coefficient of variation

ECV : Environmental coefficient of variation

h^2b : Heritability

GA (5%) : Genetic advance (5%)

GA (% mean) : Genetic advance (% mean)

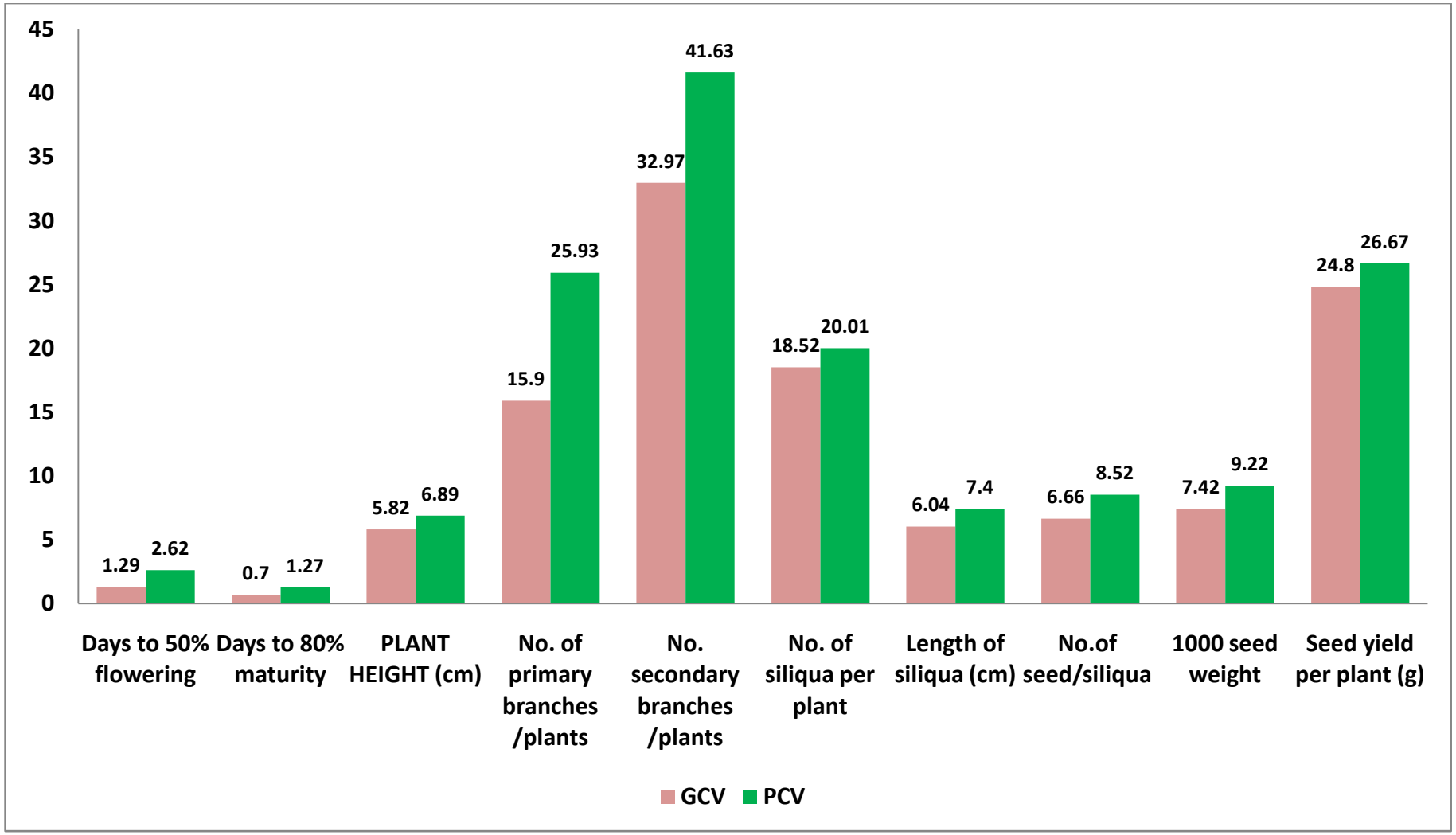


Figure 1: Genotypic and phenotypic variability in *Brassica napus*

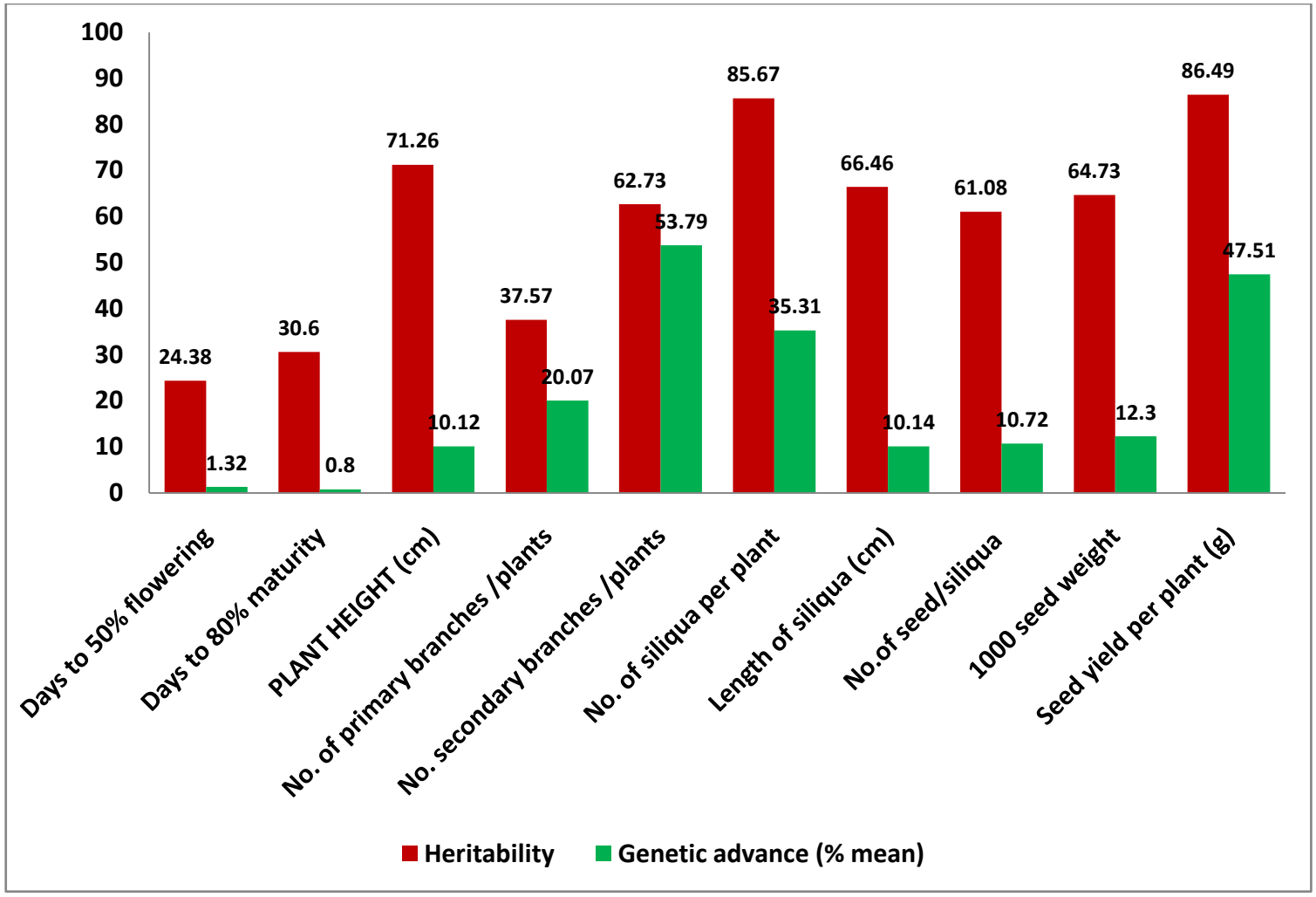


Figure 2: Heritability and genetic advance as percent over mean in *Brassica napus*

4.1.2 Days to maturity

The average day to maturity was recorded 88.64 with a range of 86.33 to 90.00 day (Table 6). G6 required least number of days to maturity (86.33 days). whereas the maximum number of days to maturity was observed in the both genotypes G15 and G29 (90.00 days) (Table 5).

Days to maturity exhibited low GCV and PCV of 0.70 and 1.27 percent respectively, along with moderate heritability of 30.60 percent, low genetic advance 0.71 and low genetic advance as percent of mean 0.80 percent (Table 7). Naznin (2013) also found low difference between PCV (22.15) and GCV (19.74) in *B. rapa*L. In the contrary, heritability was high for days to maturity reported by Niraj and Srivastava (2004). This moderate heritability with low genetic advance suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non-additive genetic effects for the control of this character. Jahan (2008) found high heritability with low genetic advance in percent of mean was observed for days to maturity and selection for such trait might not be rewarding. The genotypic and phenotypic variances were recorded as 0.39 and 1.27, respectively (Table 7). As phenotypic variance is larger than genotypic variance proving that considerable influence of environment is present in the expression of genes for this trait.

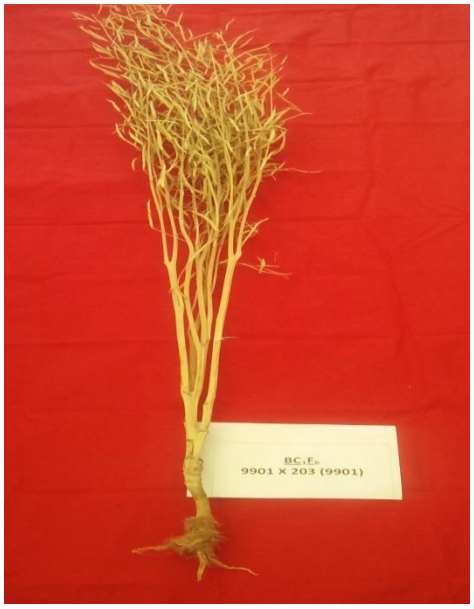
4.1.3 Plant height (cm)

Plant height was observed the highest in G9 (115.54 cm) which was followed by G12 (115.27 cm). The lowest plant height was observed in G6 (91.09 cm) and this was followed by G11 (93.17 cm) (Table 5). The mean value was recorded as 104.35 cm and mean of sum of square was 125.52 indicating significant differences among the genotypes for this trait. It ranged from 91.09 to 115.54 cm (Table 6).

G6 **G28**

(Nap108 X Nap2066 (Nap108)) **(Nap9906 X Nap0130 (Nap9906))**

Plate 2: Photograph of selected genotype showing maximum and minimum days to maturity



G9 **G12**

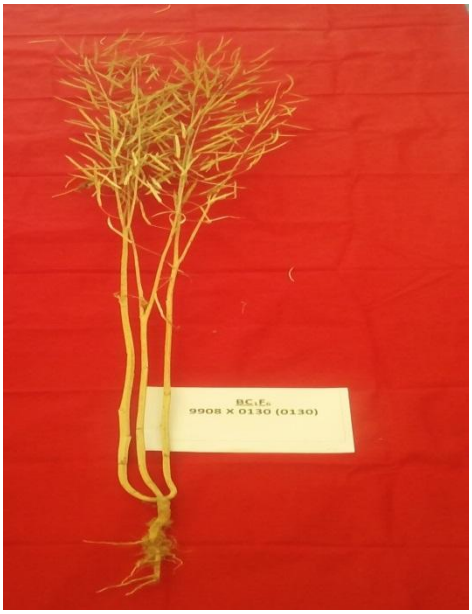
(Nap205 X Nap0130 (Nap205) **(Nap2066 X Nap205 (Nap2066))**

Plate 3: Photograph of selected genotype showing Maximum and Minimum Plant height

The highest genotypic, phenotypic and environmental variances were observed in plant height reported by Khan *et al.* (2013). The plant height exhibited low genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 5.82 and 6.89 percent respectively (Table 7). Low phenotypic coefficient of variation and genotypic coefficient of variation was found by Ghosh and Gulati (2001). High heritability of 71.26 percent, moderate genetic advance 10.56 along with moderate genetic advance as percent of mean (10.12%) was recorded (Table 7). Afrin *et al.* (2011) found that the plant height showed the highest value of broad sense heritability. High heritability with the moderate genetic advance shows that it is controlled by additive and non-additive gene effects and the selection maybe effective for improvement of *Brassica*. Jahan (2008) also found the same result that high heritability with moderate genetic advance in percent of mean for plant height.

4.1.4 Number of primary branches per plant

Number of primary branches per plant ranged from 1.67 to 4.00 in different genotypes (Table 6). The maximum number of primary branches per plant was recorded in the genotype G10 (4.00) which was followed byG16 (3.33).However, minimum number of primary branches per plant exhibited in genotype G5 (1.67) (Table 5). The mean observed for this trait was 2.66 (Table 6).The genotypic variance (0.18) and phenotypic variance (0.48) were least diverse to each other that was supported the result of Hosen (2008). Moderate GCV and high PCV were observed as 15.90% and 25.93% respectively (Table 7). This indicates moderate influence of environment upon the character. According to Mekonnen*et al.*, (2014) assessed that number of primary branches per plant exhibited comparatively high genotypic and phenotypic coefficient of variation.Whereas, it showed moderate heritability (37.57%), low genetic advance (0.53) and high genetic gain as percent of mean (20.07%) for this trait (Table 7). In contrary, Parveen (2007),Ghosh and Gulati (2001) found the high heritability coupled with high genetic advance for this trait.Moderate



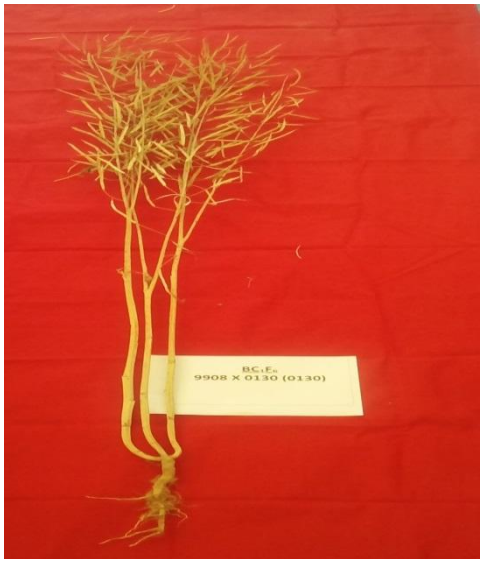
G10

(Nap205 X Nap0130 (Nap0130))

G5

(Nap108 X Nap2066 (Nap108))

Plate 4: Photograph of selected genotype showing maximum and minimum number of primary branches



G19
(Nap9905 X Nap0130 (Nap9905))

G5
(Nap108 X Nap2066(Nap108))

Plate 5: Photograph of selected genotype showing maximum and minimum number of secondary branches

heritability with low genetic advance revealed the possibility of predominance of both additive and non- additive gene action in the inheritance of this trait.

4.1.5No. of secondary branches per plant

The mean of sum of square for number of secondary branches per plant was significantly recorded as 1.82 (Table 4). Maximum number of secondary branches per plant was found in the back cross genotype G19 (4.00). The minimum number of secondary branches per plant was found in both the genotype G8, G26& G28 (1.00). (Table 5). These variations might be due to difference in genetically constituents as well as environmental effects. The genotypic and phenotypic variance was recorded as 0.51 and 0.81, respectively. High genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were observed 32.97 and 41.63 percent respectively (Table 7). High GCV and PCV also observed for number of secondary branches per plant by Choudhary*et al.* (2003); The variation is caused not only due to genotypes but also the influence of environment. High heritability 62.73% and high genetic advance as percent mean 53.79% shows that additive gene effects were present, making selection effective for this trait. Findings of Parveen (2007); Shalini*et al.* (2000); Choudhary*et al.* (2003) were also in agreement with this result.The genetic advance was recorded as 1.16 (Table 7).

4.1.6 No. of siliqua per plant

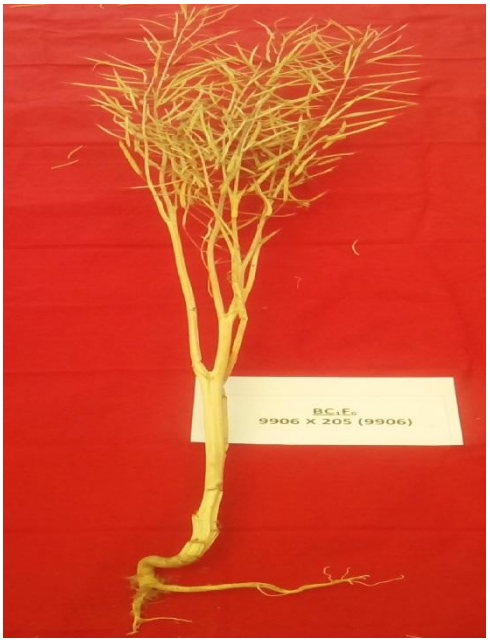
Number of siliqua per plant ranged from 74.33 to 181.33 with mean value 181.33 in different *Brassica* varieties (Table 6). The maximum number of siliqua per plant was noticed in the back cross genotype G10 (181.33). The back cross population G28 (74.33) recorded minimum number of siliqua per plant (Table 5). The mean sum of square reported significantly for this trait was 1330.18 (Table 4). The phenotypic variance (490.24) is higher than genotypic variance (419.97) (Table 7). This indicates high influence of environment on this character. The high phenotypic coefficient of variation (20.01%) and genotypic coefficient of variation (18.52%) (Table 7) indicated presence of

considerable variability among the genotypes. Similar result was also reported by Khan *et al*. (2013).

Mekonnen*et al.* (2014) observed comparatively high GCV for this trait. The heritability (85.67%) estimates for this trait was high, high genetic advance (39.07) and high genetic advance in percent of mean (35.31) were found (Table 7). So, these traits could be exploited for further improvement through selection procedures. It was also reported by Mekonnen*et al.* (2014), Alam (2010) founded that pods per plant had moderately high GCV and genetic advance and high heritability.

4.1.7 Length of siliqua (cm)

The mean of siliqua length was 7.61 cm and ranged from 6.61 to 8.73 cm (Table 6). The back cross population of G16 (8.73 cm) had long siliqua which was followed by G21 (8.52 cm), G2 (8.48 cm) and G7 (8.21 cm). The siliqua was shorter in G10 (6.61 cm) and it was followed by G12 (6.74 cm) and G6 (6.81 cm) (Table 5). The mean sum of square was significant (0.74) which indicated considerable amount of variation for this trait in the varieties (Table 4). The genotypic and phenotypic variance for siliqua length was seen as value of 0.21 and 0.32, respectively. Siliqua length exhibited low GCV (6.04%) and PCV (7.40%) values (Table 7). Similar result was seen by Khan *et al.* (2013). As PCV is higher than GCV thus we can conclude that the trait is controlled by its genotype as well as influence of environment. A high heritability estimates of 66.46%, low genetic advance 0.77 and a medium genetic advance as percent of mean 10.14% were observed (Table 7). High heritability with combination of medium genetic advance as percent of mean suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non- additive genetic effects for the control of this character.



G10 **G28**

(Nap205 X Nap0130 (Nap0130)) **(Nap9906 X Nap205 (Nap9906))**

Plate 6: Photograph of selected genotype showing maximum andminimum number of siliquae per plant

G16 **G10**

(Nap9901 X Nap203 (Nap9901)) **(Nap205 X Nap0130 (Nap0130))**

Plate 7: Photograph of selected genotype showing long and short siliqua length

4.1.8 No. of seed per siliqua

Number of seeds per siliqua ranged from 17.00 to 24.67 in different population (Table 6).The maximum number of seeds per siliqua was recorded in population of G18 (24.67). However, minimum number of seeds per siliqua exhibited in population of G25 (17.00) (Table 5). The mean observed for this trait was 19.76 (Table 6). The genotypic variance (1.73) was lower than the phenotypic variance (2.83). Low GCV and PCV were observed as 6.66 and 8.52 respectively (Table 7). This indicates little influence of environment upon the character. It showed high heritability (61.08%), low genetic advance (2.12) and medium genetic gain as percent of mean (10.72%) for this trait (Table 7). High heritability with low genetic advance and moderate genetic advance as percent of mean indicates that this trait was under additive gene control and selection for genetic improvement for this trait would be effective

4.1.9 1000 seed weight (g)

1000 seed weight of different genotypes ranged from 3.57 g to 5.00 g (Table 6). The population of G11 was exhibited maximum 1000 seed weight (5.00 g). Whereas, the population of G30 was recorded minimum seed weight (3.57 g) (Table 5). The grand mean found for this trait was 4.52 g. The mean sum of square was significant (0.40) in *Brassicanapus* which allows showing the presence of considerable variation for this trait.

1000 seed weight was recorded low PCV (9.22%) and GCV (7.42%). As PCV is greater than GCV, there is considerable influence of environment on this trait. While it recorded high heritability (64.73%), very low genetic advance (0.56) and moderate genetic gain as percent of means (12.30%) was found for this trait (Table 7). High heritability with moderate genetic advance as percent mean suggests that the character is governed by the additive and no additive gene action. Thus, selection may be effective in this trait for the improvement of the crop.

4.1.10 Seed yield per plant (g)

Seed yield per plant ranged from 6.34 g to 17.74 g, with a mean value of 9.94 g (Table 6). Maximum yield was recorded by the population of G10 (17.74 g). The lowest yield was recorded by the population of G28 (6.34 g) (Table 5). The mean sum of square was significant (19.16) (Table 4).

Seed yield per plant exhibited high estimates of PCV (26.67%) and GCV (24.80%) in Table 7. whereas; it also recorded high heritability (86.49%), low genetic advance (4.72) and high genetic gain as percent of mean (47.51%) for this trait (Table 7). Selection would be effective for this trait as there are additive gene effects on the gene controlling this trait.

Plate 9 : Photograph showing seed yield per plant

4.2 CORRELATION ANALYSIS

Improvement of a specific trait in all the breeding programs can be achieved by indirect selection via other characters. This needs a good understanding of the association of different characters with the target character and among the different characters themselves. It is necessary to have the estimates of correlation of yield with other characters for which the genotype could be assessed visually. The phenotypic and genotypic correlation reveals the extent of association between different characters, thus, it helps to base selection procedure to a required balance, when two opposite desirable characters affecting the principal characters are being selected. A positive correlation occurs due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of genes controlling different traits. No correlation indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes. Yield being a complex character is governed by a large number of genes. The influence of each character on yield could be known through correlation studies with a view to determine the extent and nature of relationships prevailing among yield and yield attributing characters. So, the Pearson correlation (Table 8) and the correlation partition into genotypic and phenotypic correlation co-efficient values for 10 characters in *Brassicanapus* genotypes studied are presented in Table 9.

In Pearson correlation seed yield per plant had positively significant correlation with plant height (0.462), primary branches per plant (0.528), and secondary branches per plant (0.625). no. of siliquae per plant (0.941), seeds per siliqua (0.401) and 1000 seed weight (0.519) (Table 8). The genotypic and phenotypic correlations are discussed in below.

Table 8. Pearson correlation coefficient

	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
D50%F	1									
DM	-0.596**	1								
PH	-0.364*	0.254	1							
PBP	0.003	-0.147	0.267	1						
SBP	-0.162	-0.042	0.255	0.323	1					
SPP	-0.076	-0.125	0.455*	0.453*	0.605**	1				
LS	-0.003	0.063	0.102	0.107	-0.166	-0.327	1			
SPS	-0.272	0.191	0.248	0.119	0.291	0.246	0.384*	1		
TSW	-0.002	-0.130	0.092	0.377*	0.264	0.314	-0.052	-0.133	1	
SYP	-0.132	-0.080	0.462*	0.528**	0.625**	0.941**	-0.172	0.401*	0.519**	1

* p< .05, ** p < .01

D50%F : days to 50% flowering, DM : days to 80% maturity, PH : plant height (cm), PBP : no. of primary branches per plant, SBP : no. of secondary branches per plant, SPP : no. of siliqua per plant, LS : length of siliqua (cm), SPS : no. of seed per siliqua, TSW : 1000 seed weight (g) and SYP : seed yield per plant (g).

4.2.1 Days to 50% flowering

At genotypic level only days to 50% flowering showed insignificant and positive association with 1000 seed weight (0.086) (Table 9). It was significant negative correlation with days to maturity (-0.975, plant height (-0.523) and seeds per siliqua (-0.464) at genotypic level (Table 9). In the contrary, significant positive correlation was found between days to 50% flowering and plant height (Afrin *et al.* (2011). Significant positive correlation was found between days to 50% flowering and thousand grain weight founded by Maurya*et al.* (2012). Negative and insignificant association of days to 50% flowering with secondary branches per plant (-0.172 and -0.160), siliqua per plant (-0.089 and -0.071) and seed yield per plant (-0.117 and -0.084) at both genotypic and phenotypic and genotypic level (Table 9). In the contrary, Parveen (2007) observed that days to 50% flowering were positively correlated with seed yield per plant.

4.2.2 Days to maturity

At genotypic and phonotypic level days to maturity displayed insignificant positive association with plant height (0.315 and 0.207), length of siliqua (0.019 and 0.103) and seeds per siliqua (0.314 and 0.089) at genotypic and phenotypic. It showed negative insignificant association with primary branches per plant (-0.190 and -0.118), secondary branches per plant (-0.080 and -0.009), siliqua per plant (-0.164 and -0.092), 1000 seeds weight (-0.232 and -0.043) and seed yield per plant (-0.077 and -0.039) at genotypic and phenotypic level (Table 9). It indicates if days to 80% maturity increased then yield/plant decreased. Similar result was found by Zahan (2006) but Parveen (2007) reported insignificant and positive interaction with yield per plant for this trait.

4.2.3 Plant height (cm)

At both level plant height had positive and high significant correlation with siliqua per plant (0.476 and 0.424) and seed yield per plant (0.346 and 0.305). It had positive correlation with days to maturity (0.315 and 0.207), primary branches per plant (0.296 and 0.239), secondary branches per plant (0.278 and 0.222), length of siliqua (0.057 and 0.16), seeds per siliqua (0.282 and 0.204)

Table 9. Genotypic (G) and phenotypic (P) correlation coefficients of yield and yield component traits of *Brassica napus*

		DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
D50%F	G	-0.975**	-0.523**	0.064	-0.172	-0.089	-0.053	-0.464*	0.086	-0.117
	P	-0.335	-0.254	-0.033	-0.160	-0.071	0.037	-0.136	-0.072	-0.084
DM	G		0.315	-0.190	-0.080	-0.164	0.019	0.314	-0.232	-0.077
	P		0.207	-0.118	-0.009	-0.092	0.103	0.089	-0.043	-0.039
PH	G			0.296	0.278	0.476*	0.057	0.282	0.128	0.346*
	P			0.239	0.222	0.424*	0.160	0.204	0.040	0.305*
PBP	G				0.417	0.564**	0.131	0.180	0.565**	0.484*
	P				0.236	0.344*	0.084	0.060	0.194	0.270
SBP	G					0.655**	-0.177	0.387	0.294	0.486*
	P					0.536**	-0.154	0.171	0.226	0.389*
SPP	G						-0.354	0.287	0.369*	0.674**
	P						-0.289	0.190	0.232	0.666**
LS	G							0.447*	-0.058	-0.132
	P							0.302*	-0.047	-0.109
SPS	G								-0.167	0.281
	P								-0.093	0.297
TSW	G									0.379*
	P									0.358*

D50%F : days to 50% flowering, DM : days to 80% maturity, PH : plant height (cm), PBP : no. of primary branches per plant, SBP : no. of secondary branches per plant, SPP : no. of siliqua per plant, LS : length of siliqua (cm), SPS : no. of seed per siliqua, TSW : 1000 seed weight (g) and SYP : seed yield per plant (g).

and 1000 seed weight (0.128 and 0.04). It had negative association with days to 50% flowering (-0.523 and -0.254) (Table 9).

4.2.4 Number of primary branches per plant

At genotypic and phenotypic level number of primary branches per plant were positive and significant correlation with siliqua per plant (0.564 and 0.344) but only positive significant correlation at genotypic level with 1000 seed weight (0.565) and seed yield per plant (0.484). It had negatively association with days to maturity (-0.190 and -0.118). Number of primary branches per plant was positively correlated with plant height (0.296 and 0.239), secondary branches per plant (0.417 and 0.236), length of siliqua (0.131 and 0.084) and seeds per siliqua (0.180 and 0.060) (Table 9).

4.2.5 Number of secondary branches per plant

At genotypic and phenotypic level numbers of secondary branched per plant were positive and significant associated with siliqua per plant (0.655 and 0.536) and seed yield per plant (0.486 and 0.389). Positive correlation was observed of secondary branches per plant with plant height (0.278 and 0.222), primary branches per plant (0.417 and 0.236), seeds per siliqua (0.387 and 0.171) and 1000 seeds weight (0.294 and 0.226) at genotypic and phenotypic levels. Number of secondary branches per plant was negatively associated with days to 50% flowering (-0.172 and -0.160), days to maturity (-0.08 and -0.009), length of siliqua (-0.177 and -0.154) at both level (Table 9).

4.2.6 Number of siliqua per plant

Number of siliqua per plant displayed significant and positive correlation with plant height (0.476 and 0.424), primary branches per plant (0.564 and 0.344), number of secondary branches per plant (0.655 and 0.536) at both genotypic and phenotypic level but only significantly correlated with 1000 seed weight (0.369) at genotypic level. It showed negatively association with days to 50% flowering (-0.089 and -0.071), days to maturity (-0.164 and -0.092), length of

siliqua (-0.354 and -0.289) at both level. It represented significant positive association with seed yield per plant (0.674 and 0.666) at both genotypic and phenotypic level (Table 9).

4.2.7 Siliqua length (cm)

Siliqua length is one of the main yield components in *Brassicanapus*. Siliqua length showed similar association in case of both genotypic and phenotypic levels. It was recorded that siliqua length had positive and significant correlation with seeds per siliqua (0.447, 0.302) and insignificant positive correlation with days to maturity (0.019 and 0.103), plant height (0.057 and 0.160), primary branches per plant (0.131 and 0.084) at both levels (Table 9). Siliqua length was negatively associated with secondary branches per plant (-0.177 and -0.154), siliqua per plant (-0.354 and -0.289), 1000 seeds weight (-0.058 and -0.047) at genotypic level and phenotypic levels. Siliqua length showed negative correlation with seed yield per plant (-0.132 and -0.109) at genotypic and phenotypic level (Table 9).

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua was found in significant and positive association with length of siliqua (0.447 and 0.302) at genotypic and phenotypic level. Seeds per siliqua had positive association with days to maturity (0.314 and 0.089), plant height (0.282 and 0.204), primary branches per plant (0.180 and 0.060), secondary branches per plant (0.387 and 0.171), siliqus per plant (0.287 and 0.190) at both genotypic and phenotypic levels. At genotypic and phenotypic level it was negative correlation with days to 50% flowering (-0.464 and -0.136) and 1000 seed weight (-0.167 and -0.093). Positive association was observed of seeds per siliqua with seed yield per plant (0.281 and 0.297) at genotypic and phenotypic level (Table 9).

4.2.9 1000 seed weight (g)

1000 seed yield had positive and significant correlation with primary branches per plant (0.565) and siliqua per plant (0.369) at genotypic level. At genotypic

and phenotypic level 1000 seeds weight showed positive and significant correlation with seed yield per plant (0.379 and 0.358) (Table 9). It was negative correlation with days to maturity (-0.232 and -0.043), length of siliqua (-0.058 and -0.047) and seeds per siliqua (-0.167 and -0.093) at genotypic and phenotypic level

4.2.10 Seed yield per plant

Seed yield per plant was significant and positively correlated with plant height (0.346 and 0.305), number of secondary branches per plant (0.486 and 0.389), siliqua per plant (0.674, 0.666) and 1000 seeds weight (0.379 and 0.358) at both genotypic and phenotypic levels. At genotypic level it showed significant positive association with primary branches per plant (0.484). It showed positive association with seeds per siliqua (0.281 and 0.297) at genotypic and phenotypic level (Table 9). These character association studies suggest that plant height, number of secondary branches per plant, number of siliqua per plant and 1000 seed weight may be the most important yield attributes in *Brassicanapus*. Based on phenotypic and genotypic correlation between yield and yield attributing characters, it is suggested that selection should made for the characters, which are having positive significant association to improve the seed yield per plant in *Brassicanapus*. The inter-correlations estimated for the yield components indicate the probability of simultaneous improvement of these traits by selection. If the correlation existing between the characters is positive, simultaneous improvement of these traits by a single selection program is possible, but when negative association exists, it would be difficult to exercise simultaneous selection of these characters in developing a variety (Newell and Eberhart, 1961). Since the characters are inter correlated among themselves, selection in any one of these traits will result in the improvement of other character thereby, resulting in increasing in seed yield

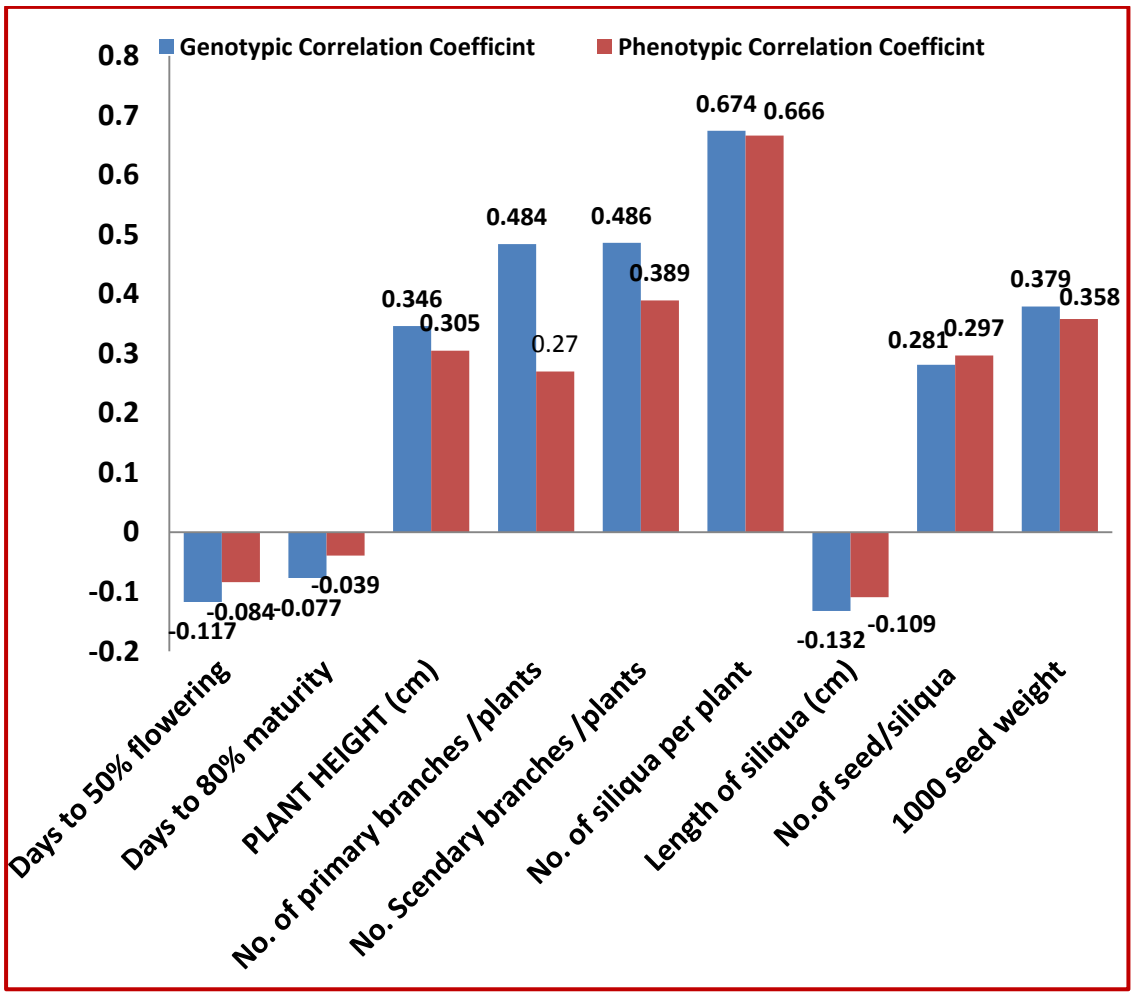


Figure 3. Genotypic and phenotypic correlation coefficient of nine characters with yield in *Brassica napus L.*

4.3 PATH COEFFICIENT ANALYSIS

Simple correlation does not consider the complex relationships between the various traits related to the dependent variable. Correlation coefficients show relationships among independent variables and the linear relationship between these variables. But it is not sufficient to describe these relationships when the causal relationship among variables is needed. It has been suggested that yield components have either a direct or an indirect effect on seed yield, or both. Therefore, it was essential to determine the effects of yield components on seed yield. Consequently, path coefficient analysis is the most common statistical method used for this purpose. Thus, it is possible to calculate both direct and indirect effects of yield components on seed yield through the other components. Genotypic path was worked out in the present study (Table 10) considering yield per plant as dependent character and its attributes as independent characters viz., days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, length of siliqua (cm), no. of seeds per siliqua and 1000 seed weight (g). Each component has two path actions viz., direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.3.1 Days to 50% flowering

Days to 50% flowering showed positive direct effect (0.007) towards yield per plant. Further, it showed negligible positive indirect effect towards yield per plant via primary branches per plant (0.0001) secondary branches per plant (0.0008). However, it was recorded negligible negative indirect effect to yield per plant via days to maturity (-0.0077), plant height (-0.0062), siliqua per plant (-0.0579) and number of seeds per siliqua (-0.0675). It showed negative and non-significant genotypic correlation (-0.132) with yield per plant (Table 10).

4.3.2 Days to maturity

Days to maturity found positive direct effect (0.013) towards yield per plant. Further, it recorded positive indirect effect towards yield per plant via plant height (0.0043) and seeds per siliqua (0.0474) (Table 10). However, it was recorded negative indirect effect towards yield per plant via days to 50% flowering (-0.0042), primary branches plant (-0.0062), siliqua per plant (-0.0953) and 1000 seed weight (-0.0387). It showed negative correlation (-0.08) with yield per plant.

4.3.3 Plant height

Plant height recorded positive direct effect (0.017) towards yield per plant. Whereas, in the present study the correlation was positive and significant (0.462) with yield per plant (Table 10). Further, it was recorded positive indirect effect towards yield per plant via days to maturity (0.0033), number of primary branches (0.0112), number of siliqua per plant (0.3467), seeds per siliqua (0.0615) and 1000 seed weight (0.0274). However, it was found negative indirect effect towards yield per plant via days to 50% flowering (-0.0025) and secondary branches per plant (-0.0013) (Table 10).

4.3.4 Number of primary branches

Number of primary branches positive direct effect (0.042) towards yield per plant. Further, it was recorded positive indirect effect towards yield per plant via plant height (0.0045), number of siliqua per plant (0.3452), seeds per siliqua (0.0295) and 1000 seed weight (0.1123) (Table 10). However, it was found negative indirect effect towards yield per plant via days to maturity (-0.0019), number of secondary branches (-0.0016) and length of siliqua (-0.0011). The correlation of number of primary branches was significant (0.528^{*}) with yield per plant.

Table 10. Partitioning of genotypic correlations into direct and indirect effects of 10 important characters by path analysis of *Brassica napus*

	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	Correlation with SYP
D50%F	**0.0070**	-0.0077	-0.0062	0.0001	0.0008	-0.0579	0.0000	-0.0675	-0.0006	-0.132
DM	-0.0042	**0.0130**	0.0043	-0.0062	0.0002	-0.0953	-0.0006	0.0474	-0.0387	-0.080
PH	-0.0025	0.0033	**0.0170**	0.0112	-0.0013	0.3467	-0.0010	0.0615	0.0274	0.462*
PBP	0.0000	-0.0019	0.0045	**0.0420**	-0.0016	0.3452	-0.0011	0.0295	0.1123	0.528**
SBP	-0.0011	-0.0005	0.0043	0.0136	**-0.0050**	0.4610	0.0017	0.0722	0.0787	0.625**
SPP	-0.0005	-0.0016	0.0077	0.0190	-0.0030	**0.7620**	0.0033	0.0610	0.0936	0.941**
LS	0.0000	0.0008	0.0017	0.0045	0.0008	-0.2492	**-0.0100**	0.0952	-0.0155	-0.172
SPS	-0.0019	0.0025	0.0042	0.0050	-0.0015	0.1875	-0.0038	**0.2480**	-0.0396	0.401*
TSW	0.0000	-0.0017	0.0016	0.0158	-0.0013	0.2393	0.0005	-0.0330	**0.2980**	0.519**

Residual effect: 0.047** = Significant at 1%. * = Significant at 5%.

D50%F : days to 50% flowering, DM : days to 80% maturity, PH : plant height (cm), PBP : no. of primary branches per plant, SBP : no. of secondary branches per plant, SPP : no. of siliqua per plant, LS : length of siliqua (cm), SPS : no. of seed per siliqua, TSW : 1000 seed weight (g) and SYP : seed yield per plant (g)

4.3.5 Number of secondary branches

Number of secondary branches recorded negative direct effect (-0.005) towards yield per plant. Further, it was recorded positive indirect effect towards yield per plant via plant height (0.0043), number of primary branches (0.0136), siliqua per plant (0.461), number of seeds per plant (0.0722) and 1000 seed weight (0.0787) (Table 10). However, it was found negative indirect effect towards yield per plant via days to 50% flowering (-0.0011) and days to maturity (-0.0005). The correlation of number of secondary branches was positive significant (0.625) with yield per plant.

4.3.6 Number of siliqua per plant

Number of siliqua per plant recorded positive direct effect (0.762) towards yield per plant. Further, it was recorded positive indirect effect towards yield per plant via plant height (0.0077), number of primary branches (0.019), length of siliqua (0.0033), number of seeds per siliqua (0.061) and 1000 seed weight (0.0936) (Table 10). However, it was found negative indirect effect towards yield per plant via days to 50% flowering (-0.0005), days to maturity (-0.0016) secondary branches per plant (-0.003). The correlation of number of siliqua per plant was positive significant (0.941) with yield per plant.

4.3.7 Siliqua length

Siliqua length observed negative direct effect (-0.01) towards yield per plant. It was also recorded negative indirect effects to yield per plant via number of siliqua per plant (-0.2492) and 1000 seed weight (-0.0155) (Table 10). On the other hand, it was found negligible positive indirect effect toward yield per plant via plant height (0.0017), number of primary branches (0.0045), number of seeds per siliqua (0.0952). The correlation of siliqua length (-0.172) with yield per plant was negative and non-significant.

4.3.8 Number of seeds per siliqua

Number of seed per siliqua showed positive direct effect (0.248) towards yield per plant. Further, it was recorded negligible positive indirect effect towards yield per plant via days to maturity (0.0025), plant height (0.0042), primary branches (0.005) and siliqua per plant (0.1875) (Table 10). It was found negative indirect effect towards yield per plant via days to 50% flowering (-0.0019), number of secondary branches per plant (-0.0015), length of siliqua (-0.0038) and 1000 seed weight (-0.0396). The correlation of seeds per siliqua (0.401) with yield per plant was positive and significant.

4.3.9 1000 seed weight

1000 seed weight found positive direct effect (0.298) towards yield per plant. Further, it was recorded positive indirect effect towards yield per plant via plant height (0.0016), primary branches per plant (0.0158), number of siliqua per plant (0.2393) (Table 10). It also reported high negative indirect effect towards yield per plant via days to maturity (-0.0017) and number of secondary branches per plant (-0.0013) and seeds per siliqua (-0.033). The trait was positive and significant (0.519) correlated with yield per plant. It suggested that for selecting genotypes with higher yield the indirect influence of different traits should be given due weight age along which exerted direct effects.

4.3.10 Residual effect

The magnitude of residual effect (0.047) indicated that traits included in the path analysis explained about 95.3% of the variation in seed yield. However, the remaining variation in seed yield (4.7%) can be attained by incorporating other yield related traits in the path analysis as far as studies involving association of traits is concerned.

4.4 GENETIC DIVERSITY ANALYSIS

4.4.1 Mahalanobis' generalized distance (D^2)

Conservation of genetic diversity is an essential prerequisite for developing new cultivars with desirable agronomic traits. Although a large number of germplasm collections have been established worldwide, many of them face major difficulties due to large size and a lack of adequate information about population structure and genetic diversity. The development of new varieties is mainly governed by the magnitude of genetic variability in the base material and extent of variability for the desired characters. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. D^2 analysis is a maybe useful tool in identifying the best parents and their combinations for generating variability with respect to various traits under study. The results of D^2 analysis may be useful tool in identifying the best parental combination for generating variability with respect to various traits under study. Progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability providing greater scope for isolating high yielding segregants in the succeeding generations. The genetic diversity among 30 genotypes was measured by employing D^2 statistics.

4.4.2 Principal component analysis (PCA)

Principal component analysis was carried out with 30 genotypes of *Brassicanapus*. The first three Eigen values for three principal coordination axes of genotypes accounted for 67.52% variation. Out of 10 characters studied, Component I contributed maximum towards the total diversity with the value 34.64%, followed by Component II 19.89% and Component III 12.99% (Table 11).

4.4.3 Clustering of the genotypes

The correlated unstandardized mean values (X) for all genotypes for 10 characters under consideration were transferred to the uncorrelated standardized value (Y). The D^2 value which being the sum of squares for each (Y) value was calculated for all combinations.

Based on D^2 values the genotypes were grouped into five clusters using Tocher's methods given by Rao (1952). Clustering of genotypes is presented in the (Table 12). Among five clusters, cluster III was the largest comprising of 30% with nine genotypes followed by cluster V, 26.67% with eight genotypes, cluster I & IV, both same 20% with six genotypes and Cluster II is the solitary cluster.

Cluster I was composed of G2, G9, G12, G17, G19 and G22. Cluster II comprised of only one genotype G10. Cluster III possesses nine genotypes G1, G3, G4, G14, G16, G23, G26, G29 and G30. Cluster IV consists of six genotypes like G5, G6, G8, G13, G15 and G18. Cluster V consist of eight genotypes G7, G11, G20, G21, G24, G25, G27 and G28 (Table 12).

The present investigation shows that there is no perfect relationship between genetic diversity and geographical diversity. This may be attributed since the genotypes of the present study were indigenously developed. The genotypes have overlapped in different clusters with some distinctness.

4.4.4 Cluster mean analysis

Cluster means were computed for all the 10 characters studied and presented in Table 13. Genotypes grouped within cluster II were relatively early to days to 50% flowering (39.67 days) and days to maturity (88.33 days) whereas; genotype grouped under cluster IV was relatively late (40.61 days) and genotype under cluster I was late in days to maturity (88.89 days). Cluster II exhibited the highest mean for plant height with 111.70 cm, whereas the cluster V had the lowest average of plant height 101.04cm. The highest number of primary branches per plant was found in cluster II (4.00) and the lowest number of primary branches per plant was observed in cluster V (2.54).

Table 11. Latent root (Eigen values) and yield percent contribution of ten characters of 30 genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	3.464	34.64	34.64
II	1.989	19.89	54.53
III	1.299	12.99	67.52
IV	0.979	9.79	77.31
V	0.715	7.15	84.46
VI	0.535	5.35	89.81
VII	0.456	4.56	94.37
VIII	0.370	3.70	98.07
IX	0.191	1.91	99.98
X	0.001	0.01	99.99

Table 12.Distribution of 30 genotypes in different clusters

Cluster no.	Genotypes	No. of populations	Percent
I	G2, G9, G12, G17, G19, G22	6	20
II	G10	1	3.33
III	G1, G3, G4, G14, G16, G23, G26, G29, G30	9	30
IV	G5, G6, G8, G13. G15, G18	6	20
V	G7, G11, G20, G21, G24, G25, G27, G28	8	26.67
	Total	30	100

In case of secondary branches per plant genotypes of cluster V (1.77) was less and genotypes under cluster II (3.67) was relatively high. Maximum number of siliqua per plant was found in cluster II (181.33) whereas the minimum number of siliqua was found in cluster V (87.33). Cluster V comprised of genotypes with long siliqua (7.72) while cluster II consisted of genotype with shorter siliqua (6.61). Cluster IV with six genotypes exhibited the highest mean for number of seeds per siliqua (20.61), whereas the cluster V had the lowest average (18.92). Cluster II with three genotypes exhibited the highest mean for 1000 seed weight (4.98 g), whereas the cluster IV had the lowest average (4.44g). Genotypes grouped under cluster II recorded highest mean value for seed yield per plant (17.74 g) and the lowest by the genotypes of cluster V (7.32g).

4.4.5 Canonical variate analysis

4.4.5.1 Inter and intra cluster distances

Genotypes grouped into the same cluster presumably diverged little from one another. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or segregants. However theoretically, a general notion exists that the larger is the divergence between the genotypes, higher will be the heterosis (Falconer, 1981).

From Table 13 it is observed that cluster II showed the maximum inter-cluster distance with the cluster V (19.638), followed by cluster II and cluster III (15.735); and minimum inter cluster distance between cluster III and cluster IV (3.081). Figure 4 is shown to present different clusters. All clusters showed intra cluster distances except cluster II whose constitute one genotype. Intra cluster distance was highest in the cluster V (2.54) followed by the cluster IV (1.542). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses. However, the crosses involving parents from clusters with high inter cluster distance are likely to yield desirable recombinants in the advanced generations which could be developed as traditional homozygous varieties.

Table 13. Cluster mean for ten yield and yield related characters in 30 *Brassica napus* genotypes

Characters	I	II	III	IV	V
Days to 50% flowering	40.33	39.67*	40.30	40.61**	40.50
Days to 80% maturity	88.89**	88.33*	88.63	88.33*	88.75
Plant height (cm)	111.16	111.70**	103.93	101.36	101.04*
No. of primary branches /plants	2.78	4.00**	2.56	2.61	2.54*
No. Secondary branches /plants	2.86	3.67**	1.96	2.03	1.77*
No. of siliqua per plant	130.11	181.33**	105.89	117.72	87.33*
Length of siliqua (cm)	7.65	6.61*	7.66	7.52	7.72**
No.of seed/siliqua	20.33	19.67	19.56	20.61**	18.92*
1000 seed wt.	4.70	4.98**	4.45	4.44*	4.46
Seed yield per plant (g)	12.41	17.74**	9.22	10.74	7.32*

* Lower value
** Higher value

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The lowest intra cluster was recorded in cluster II (0.00). The highest inter cluster distance (19.638) was observed between cluster II and cluster V. This high inter-cluster distance indicated the wider genetic diversity among the genotypes, which could be used in yield improvement of *Brassicanapus*. The lowest inter cluster distance (3.081) was seen between cluster III and cluster IV. The genotypes from distant clusters exhibit wide diversity. So, genotypes from divergent clusters (II and V) can be selected for hybridization program in order to achieve novel recombinants.

4.4.5.2 Nearest and farthest cluster

Cluster I consist of nearest cluster with D^2 values cluster IV (3.592) & farthest cluster with D^2 values cluster II (11.105) (Table 15). Cluster II consist of nearest cluster with D^2 values cluster I (11.105) & farthest cluster with D^2 values V (19.638). Cluster III consist of nearest cluster with D^2 values cluster IV (3.081) & farthest cluster with D^2 values II (15.735). Cluster IV consist of nearest cluster with D^2 values cluster III (3.081) & farthest cluster with D^2 values II (13.265) (Figure 5). Cluster V consist of nearest cluster with D^2 values cluster III (4.169) & farthest cluster with D^2 values II (19.638).

Table 14. Intra (Bold) and inter cluster distances (D^2) for 30 genotypes

Cluster	I	II	III	IV	V
I	**0.450**	11.105	5.265	3.592	9.130
II		**0.000**	15.735	13.265	19.638
III			**0.871**	3.081	4.169
IV				**1.542**	7.065
V					**2.540**

Table 15. The nearest and farthest clusters from each cluster between D^2 values in *Brassica napus*

Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
I	IV (3.592)	II (11.105)
II	I (11.105)	V (19.638)
III	IV (3.081)	II (15.735)
IV	III (3.081)	II (13.265)
V	III (4.169)	II (19.638)

Z1-Z2 Graph

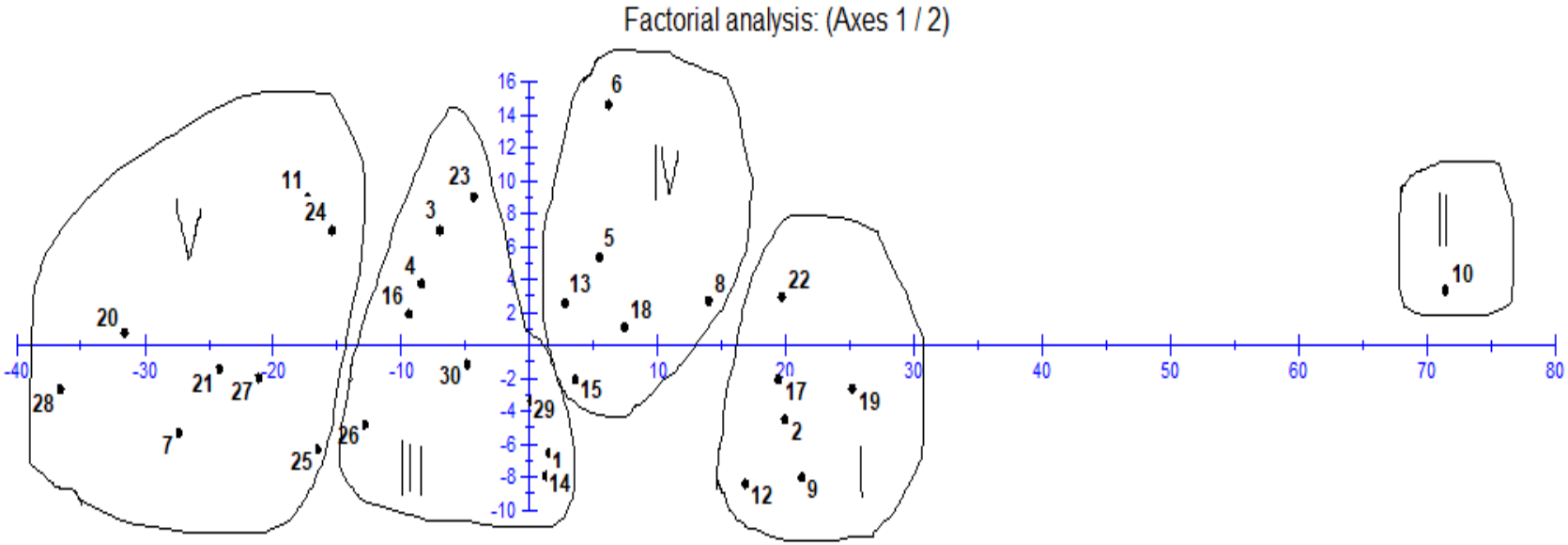

Figure 4: Scatter diagram of *Brassicanapus* genotypes based on their principal component scores by using Darwin 6.0 software

4.4.5.3 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 14. Vector I obtained from PCA expressed that Days to maturity (0.1177), plant height (0.0079), no. of siliqua per plant (0.2304), no. of seeds per siliqua (0.4583) and 1000 seed weight (0.9230) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II primary branches per plant (0.8086), no. of siliqua per plant (0.3621), no. seeds per siliqua (2.0745) and 1000 seeds weight (6.8408) showed their important role toward genetic divergence. The value of Vector I and Vector II revealed that both Vectors had positive values for no. of siliqua per plant, no. of seeds per siliqua and 1000 seed weight indicating the highest contribution of these traits towards the divergence among 30 genotypes of *Brassicanapus*. Negative values in both vectors for days to 50% flowering, no. of secondary branches per plant, length of siliqua and seed yield per plant had lower contribution towards the divergence. In the present study, 30 genotypes of *Brassicanapus* were grouped into five clusters. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated. No. of siliqua per plant, no. of seeds per siliqua and 1000 seed weight were the maximum contributors for divergence in the present study should be given utmost importance for selecting the genotypes for crossing program.

Cluster I showing the highest values of days to maturity, plant height. Cluster II was performed for high value of plant height, primary branches per plant, secondary branches per plant, siliqua per plant, 1000 seed weight and seed yield per plant; and lowest value for days to 50% flowering, days to maturity and length of siliqua. Cluster IV represented high value for days to 50% flowering, no. of seeds per siliqua; and lowest value for days to maturity and 1000 seed weight. Cluster V has shown high value for length of siliqua and lowest value for plant height, primary branches per plant, secondary branches per plant, no. of siliqua per plant, no. of seeds per siliqua and seed yield per plant.

Table 16. Relative contributions of the ten characters of 30 varieties to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days to 50% flowering	-0.2092	-0.3791
Days to 80% maturity	0.1177	-0.4652
Plant height (cm)	0.0079	-0.1135
No. of primary branches /plants	-0.0364	0.8086
No. secondary branches /plants	-0.3974	-1.2337
No. of siliqua per plant	0.2304	0.3621
Length of siliqua (cm)	-0.4952	-0.7609
No.of seed/siliqua	0.4583	2.0745
1000 seed wt.	0.9230	6.8408
Seed yield per plant (g)	-0.2816	-3.6418

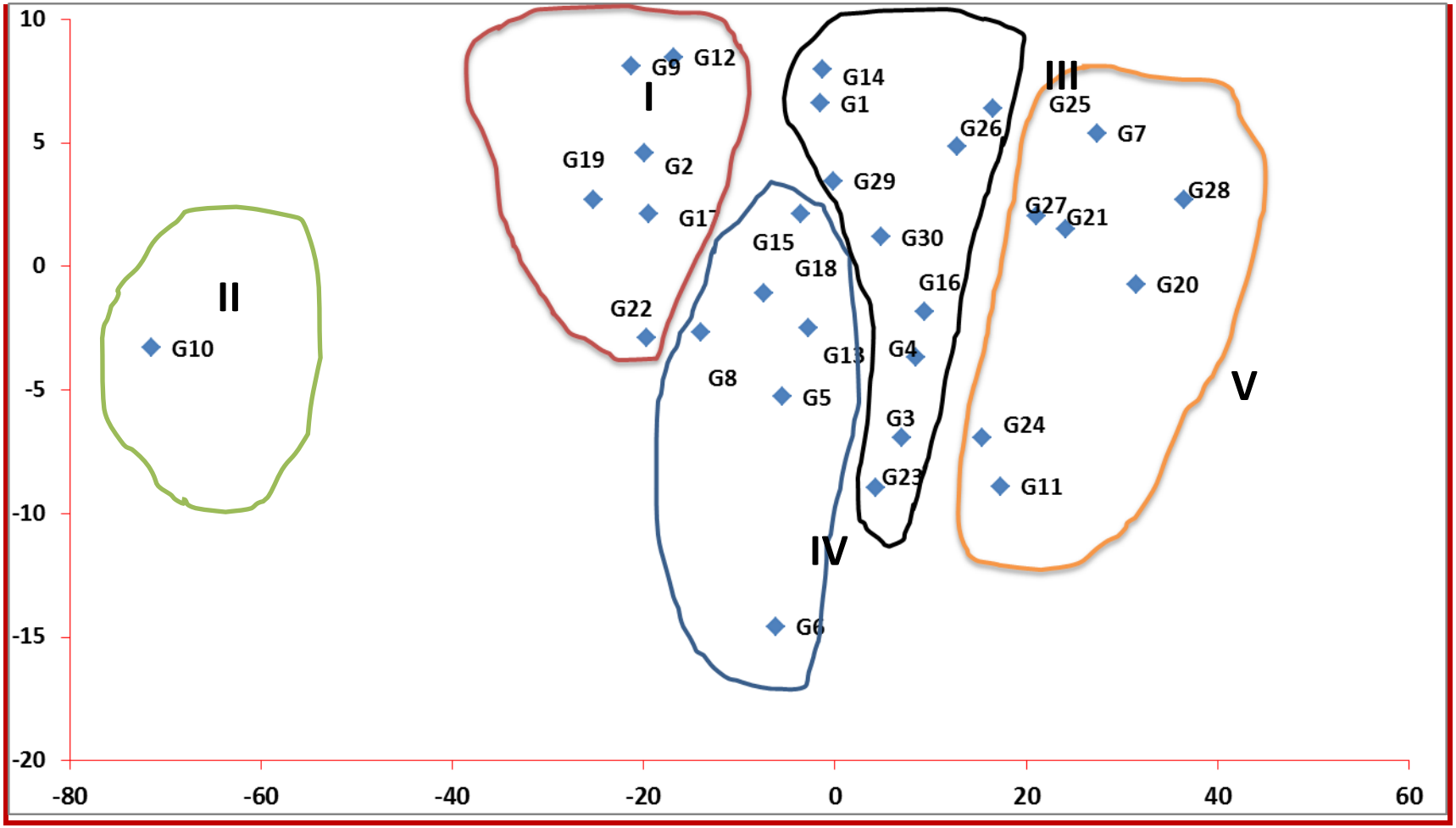

Figure 5. Cluster diagram showing average intra and inter cluster distances of 30 genotypes in *Brassicanapus*.

4.1.5 Cluster diagram

The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes (Figure 5)

4.2.6. Selection of genotypes as parent for hybridization programme

Among the inter cluster distance, distance II and V (19.638) followed by II and III (15.735) were the highest and other cluster were more or less intermediate distance. Intermediate diverse parents have the more chance to contribute heterosis in the subsequent generations. To select cluster to obtain more heterotic genotype three pairs of clusters to be considered for this purpose, they are II and V (19.638), II and III (15.735), II and IV (13.265). Cluster II had the highest cluster mean for most important yield contributing character. On the other hand the cluster III comprised the intermediate value of maximum traits. Cluster IV had the early days to maturity. Cluster V possessed the maximum lowest value of traits. Selection of genotype from cluster II was G10, from cluster III G14 & G29 and from cluster IV G6 and G8; and from cluster V G11 & G20.

CHAPTER V

SUMMARY AND CONCLUSION

The present research was conducted in the experimental field of Sher -E-Bangla Agricultural University, Dhaka-1207. The analysis of variance showed significant differences among the genotypes for all the traits viz. days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, length of siliqua (cm), no. of seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g). The highest days to 50% flowering was recorded in G6 (42.00) and the lowest was in G29 (39.00). The range of days to maturity was recorded from 86.33 to 90.00 days. G6 required least number of days to maturity (86.33 days). Whereas, the maximum number of days to maturity were observed in the both genotypes G15 and G29 (90.00 days). The maximum plant height was produced by G9 (115.54 cm) which was followed by G12 (115.27 cm). The lowest plant height was observed in G6 (91.09 cm) and this was followed by G11 (93.17 cm) .The maximum number of primary branches per plant was G10 (4.00) which was followed by G8 (3.67). However, minimum number of primary branches per plant exhibited in genotype G5 (1.67).The highest secondary branches per plant was produced by the genotype G19 (4.00). The lowest number of secondary branches per plant was found in both the genotype G8 and G26 (1.00). The back cross G10 (181.33) showed maximum number of siliqua. The back cross population G28 (74.33) recorded minimum number of siliqua per plant .The longest siliqua was found in genotype G16 (8.73 cm) which was followed by G21 (8.52 cm), G2 (8.48 cm) and G7 (8.21 cm). The siliqua was shorter in G10 (6.61 cm) and it was followed by G12 (6.74 cm) and G6 (6.81 cm) .The genotype G18 (24.67) represented the highest no. of seeds per siliqua and the lowest was observed by the genotype G25 (17.00). The

maximum 1000 seed weight was produced by the G11 (5.00 g) and minimum in the G30 (3.57 g). Genotype 10 (17.74g) produced the highest yield per plant and genotype 28 (6.34 g) produced the lowest yield per plant.

Phenotypic variance was higher than the genotypic variances for all the traits. Phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. High PCV and GCV were found for no. of secondary branches per plant (41.63 and 32.97), seed yield per plant (26.67 and 24.80), no. of primary branches per plant (25.93 and 15.90), no. of siliqua per plant (20.01 and 18.52).High heritability was recorded by days to 50% flowering (24.38), days to maturity (30.60), plant height (71.26), no. of primary branches per plant (37.57), no. of secondary branches per plant (62.73), no. of siliqua per plant (85.67), no. of seeds per siliqua (61.08), Length of siliqua (66.46),1000 seed weight (64.73) and seed yield per plant (86.49). Genetic advance in percent of mean was high for Plant height (10.12), days to 50% flowering (1.32), no. of primary branches per plant (20.07), no. of secondary branches per plant (53.79), length of siliqua (10.14), no. of seeds per siliqua (10.72), no. of siliqua per plant (35.31), 1000 seed weight (12.30) and seed yield per plant (47.51) and lowest for days to maturity (0.80). High heritability couple with high genetic advance as percent of mean was noticed for the traits, no. of secondary branches per plant, seed yield per plant, no. of siliqua per plant and provided opportunity for selection of high yielding genotypes.

Genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients in most of the associations which might be due to masking or modifying effect. Very close genotypic and phenotypic correlations were observed the traits, plant height with siliqua per plant, siliqua per plant with seed yield per plant and plant height with seed yield per plant, which might be due to reduction in error (environmental) variance, thus selection for higher yield on the basis of above traits would be reliable. Yield per plant positively and significantly correlate with plant height (0.346 and 0.305), secondary branches per plant (0.486 and 0.389), siliqua per

plant (0.674 and 0.666) and 1000 seed weight (0.379 and 0.358) at bothgenotypic and phenotypic levels. Plant height was correlated positively and significantly in both level with siliqua per plant (0.476 and 0.424). Highly significant positive correlations were recorded for siliqua per plant with primary and secondary braches per plant (0.564 and 0.344) and (0.655 and 0.536) respectively. Positive and highly significant correlation was observed of length of siliqua with seed per siliqua (0.447 and 0.302) at both genotypic and phenotypic levels.

Path analysis revealed siliqua per plant (0.762), 1000 seed weight (0.298), seeds per siliqua (0.248) primary branches per plant (0.0.042) had direct positive effect on yield per plant, indicating these are the main contributors to yield per siliqua. The highest positive indirect effects on yield per plant were obtained by plant height (0.3467), primary branches per plant (0.3452), secondary branches per plant (0.4610) 1000 seed weight (0.2393) via siliqua per plant. Therefore, the present study suggested that plant height, primary branches per plant, secondary branches per plant and 1000 seed weight should be included owing to importance in selecting the genotypes for higher seed yield in *Brassica napus*.

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, canonicalVariate Analysis (CVA). The first three characters of the PCA axes with eigen values above unity contribute a total of 67.52% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. The highest genotypes were included in cluster III (9 genotypes) followed by cluster V (8 genotypes) and cluster I & IV (6). The highest inter-cluster distance was observed between clusters II and V indicating genotypes from these two clusters are diverse, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster III and IV.Cluster II required maximum seed yield per plant, 1000 seed weight, siliqua per plant, primary and secondary branches per plant, plant height as well as lowest days to maturity.

Cluster III required medium of all yield related traits. Cluster II & IV required the lowest days to the maturity. Cluster V showed low value of almost all the traits.

The results of the present investigation revealed that the variability existed among the selected *Brassica napus* genotypes for all the characters studied. Thirty genotypes were grouped in five clusters. Among the genotypes the superior genotypes were G6 (Nap108 X Nap2066 (Nap2066)), G8 (Nap108 X Nap9908 (Nap9908)), G10 (Nap205 X Nap0130 (Nap0130)), G11 (Nap206 X Nap205 (Nap205)), G14 (Nap2066 X Nap0130 (Nap2066)), G20 (Nap9905 X Nap9908 (Nap9905)) and G29 (Nap9906 X Nap0130 (Nap9906)). They might be used as cross pollinated varieties by further purification and parents in future hybridization program.

CHAPTER VI

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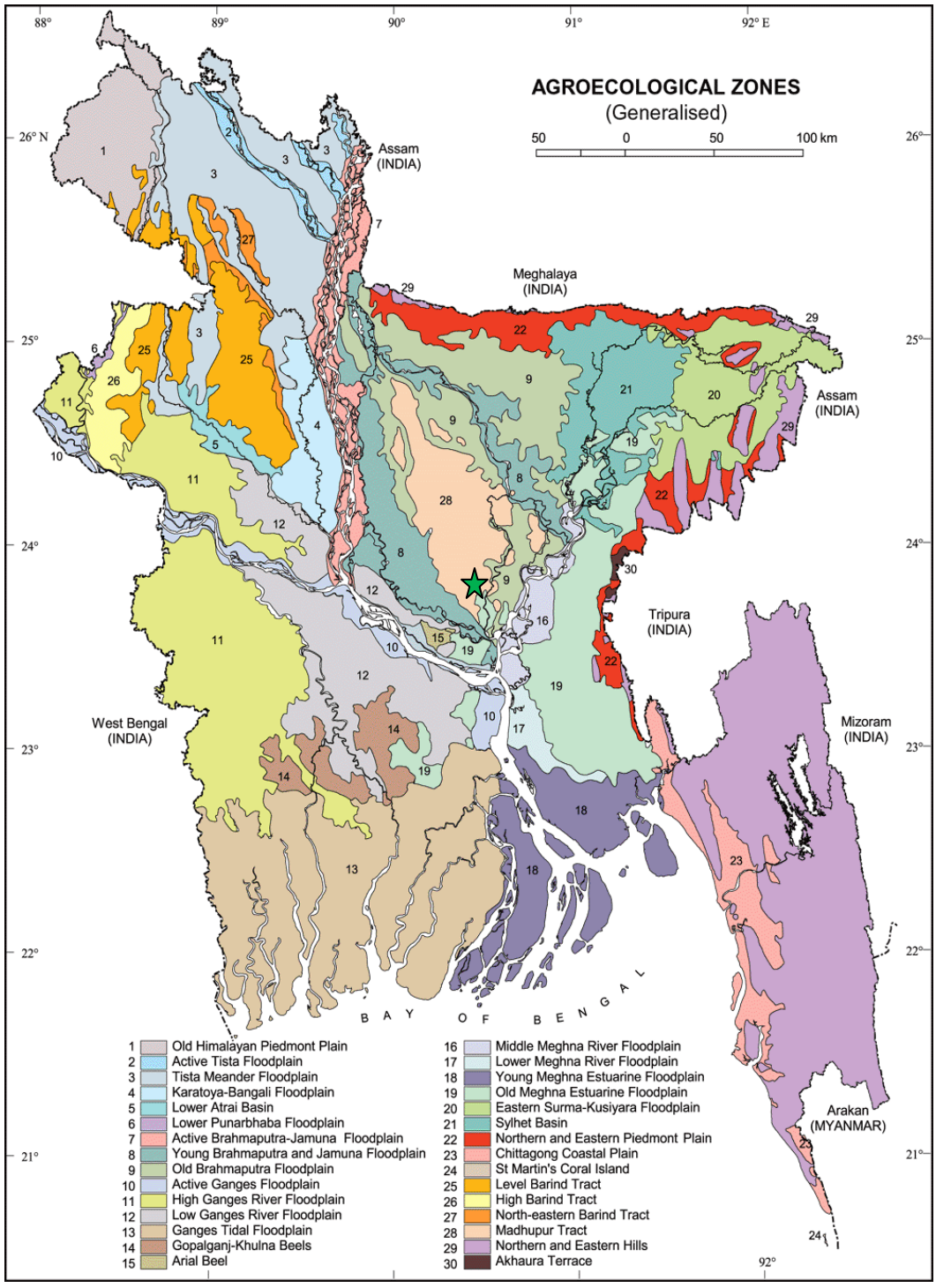
APPENDICES

Appendix I. Principal component score 1 & 2.

Genotypes	PCA 1	PCA 2
G1	-1.56	6.59
G 2	-19.95	4.59
G3	6.95	-6.93
G4	8.40	-3.69
G5	-5.49	-5.27
G6	-6.18	-14.57
G7	27.35	5.39
G8	-14.00	-2.65
G9	-21.28	8.10
G10	-71.42	-3.30
G11	17.29	-8.90
G12	-16.89	8.47
G13	-2.78	-2.50
G14	-1.32	7.99
G15	-3.63	2.14
G16	9.36	-1.85
G17	-19.43	2.12
G18	-7.45	-1.08
G19	-25.20	2.68
G20	31.53	-0.72
G21	24.12	1.49
G22	-19.70	-2.89
G23	4.30	-8.97
G24	15.36	-6.92
G25	16.51	6.39
G26	12.82	4.86
G27	21.09	2.04
G28	36.54	2.71
G29	-0.19	3.45
G30	4.85	1.20

Appendix II. Map showing the experimental site under the study



The experimental site under the study

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

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
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, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1982
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

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

Appendix IV. Monthly average temperature, relative humidity and total rainfall, sunshine of the experimental site during the period from November, 2016 to February, 2017.

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2016	34.7	18.0	77	227	**5.8**
December, 2016	32.4	16.3	69	0	**7.9**
January, 2017	29.1	13.0	79	0	**3.9**
February, 2017	**28.1**	**11.1**	**72**	**1**	**5.7**

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