GENETIC VARIABILITY, CORRELATION AND PATH COEFFICIENT ANALYSIS IN BC_1F_3 GENERATION OF *Brassica napus* L.

BY

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic variability, correlation and path coefficient analysis in BC_1F_3 generation of Brassica napus L."*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***MST. MOKA SHEFA****, Registration No.* ***07-02228*** *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: December, 2013
Place: Dhaka, Bangladesh

(Dr. Firoz Mahmud)
Professor
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DEDICATED
TO
MY PARENTS
AND
MY SON

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ABSTRACT

A field experiment was conducted with 31 BC_1F_3 genotypes of *Brassica napus* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the genetic diversity, variability, correlation and path coefficient analysis during November 2012 to March 2013. The genotypes were found significantly variable for all the characters. Comparatively phenotypic variances were higher than the genotypic variances for all the characters studied. The high GCV value was observed for number of secondary branches per plant. Plant height, number primary branches per plant, days to 50% flowering, and seed yield per plant showed high broad base heritability. The significant positive correlation with seed yield per plant was found in plant height, the number primary branches per plant, number of secondary branches per plant and number of siliqua per plant. Path coefficient analysis revealed that number primary branches per plant, number of secondary branches per plant and number of siliqua per plant had the positive direct effect on yield per plant. The genotypes were grouped into five clusters. The highest inter cluster distance was observed between cluster I and V and the maximum intra cluster distance was found in cluster IV. Considering group distance and other agronomic performance genotypes G1, G2, G3, G20, and G28 might be suggested for future hybridization program.

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LIST OF ABBREVIATED TERMS

Abbreviation	Full word
%	Percent
^{o}C	Degree Celsius
@	At the rate
$\sigma^2 p$	Phenotopic variance
$\sigma^2 g$	Genotypic variance
$\sigma^2 e$	Environmental variance
$h^2 b$	Heritability in broad sense
AEZ	Agro-Ecological Zone
Agric.	Agriculture
Agril.	Agricultural
Agron.	Agronomy
Anova	Analysis of variance
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
BD	Bangladesh
CN	Centi-meter
CV%	Percentage of Coefficient of Variation
cv.	Cultivars
Df	Degrees of Freedom
et al.	And others
etc.	Etcetera
F_3	The third generation of a cross between two dissimilar homozygous parents
FAO	Food and Agricultural Organization
g	Gram
G	Genotype
GA	Genetic Advance
GCV	Genotypic coefficient of variation
HI	Harvest Index
IARI	Indian Agricultural Research Institute
ICARDA	International Center for Agricultural Research in Dry Areas
J.	Journal
Kg	Kilogram
m	Meter

Abbreviation	Full word
MS	Mean sum of square
MP	Murate Potash
MOA	Ministry of Agriculture
m^2	Square meter
PCV	Phenotypic coefficient of variation
RCBD	Randomized Complete Block Design
SAU	Sher-e-Bangla Agricultural University
TSP	Triple Super Phosphate

CHAPTER I
INTRODUCTION

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INTRODUCTION

Brassica oil is the world's third most important sources of edible vegetable oils. *Brassica* is an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. It is originated in either the Mediterranean area or northern Europe. Scientific interest in rapeseed and its economic importance has lately increased largely due to the use of the high-grade oil for food purposes and as a source for the production of biodiesel.

In Bangladesh various species of *Brassica* are grown. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica campestris*, BB for *Brassica nigra* and CC for *Brassica oleracea* having diploid chromosome number of 20, 16 and 18 respectively. On the other hand the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the amphidiploids. Approximately, 70% of the total cultivated mustard in Bangladesh is the variety of either *Brassica rapa* or *Brassica napus*.

Brassica oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2000). Mustard and rapeseed seeds contain 42% oil, 25% protein (Khaleque, 1985). Rape seed and mustard is the third highest source of edible oils supply in the world after soybean and palm (FAO, 2000). The mustard oil is used not only for edible purpose but also is used in hair dressing, body massaging and in different types of pickles preparation. The oil cake contains proteins of high biological value and applicable quantities of calcium and phosphorus. It is used as a very good animal feed as well as organic manure for various crops.

The per capita consumption of edible oil in our country is 8 g/day as compared to a need of 40 g/day (Kaul and Das, 1978). The shortage of edible oil has become a chronic problem for the nation. In Bangladesh two third of the total annually consumed edible oil are imported. Productivity of oilseed crops in Bangladesh is comparatively lower than the oil seed growing countries of the world. The major reasons for such poor yield in Bangladesh may be attributed due to lack of improved

varieties and poor management practices. The average per hectare yield of oilseed crops in Bangladesh was 733 kg and world average production was 1575 kg (FAO, 2005).

A plant breeding program can be divided into three steps viz. building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Kempthorne, 1957). The knowledge of genetic variability present in the population, heritability of economically important characters and correlation coefficients of those characters is very important before launching an effective breeding program.

There is plenty of scope to increase yield per unit of area through breeding superior varieties. Information on genetic variability and character association is a prerequisite for initiating a successful breeding program aiming to develop high yielding varieties.

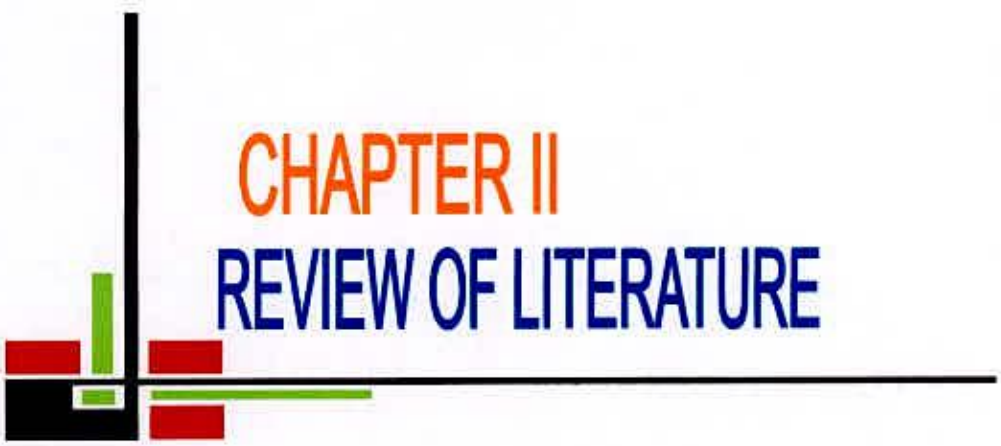
Determination of correlation co-efficient between the characters has a considerable importance in selecting breeding materials. The path co-efficient analysis has been found to give more specific information on the direct and indirect influence of each of the component characters upon seed yield (Behl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

Variability and genetic diversity are the fundamental law of plant breeding which is major tool being used in parent selection for efficient hybridization program (Bhatt, 1973). Genetic diversity is one of the criteria of parent selection. Inclusion of more diverse parents (within a limit) in hybridization is supposed to increase the chance of obtaining maximum heterosis and give broad spectrum of variability in segregating generations.

Keeping these in mind, this research was undertaken with the following objectives:

Objectives:

- To study the variability in BC_1F_1 generation for selection of desired plant types,
- To study the interrelationships of yield contributing characters among themselves and with seed yield; and their direct and indirect effects,
- To assess the contribution of different traits towards divergence, and
- To select promising genotypes considering early maturity, high yielding plants.



CHAPTER II
REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Extensive researches on *Brassica* breeding have been performed in many countries for its improvement in respect of yield and yield contributing characters. A large number of literatures are available on variability, correlation and path analyses of yield and yield contributing characters of *Brassica* grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely -

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

2.1 Genetic variability, heritability and genetic advance

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

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

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

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

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

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

Hosen (2008) conducted a study by using 5 parental genotype of *Brassica rapa* and their ten F_3 progenies including reciprocals. There are large numbers of variations present among all the genotypes used in the experiment. The plant height, days to 50% flowering, and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

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

Nanda *et al.* (1995) observed that days to first flowering varied both by genotypes and date of sowing, while working with 65 strains of *B. napus*, *B. juncea*, *B. carinata* and *B. rapa*. Many other researchers like Kumar and Singh (1994), Kumar *et al.* (1996), Kachroo and Kumar (1991), Andrahernnadi (1991), Lebowitz (1989), Biswas (1989), Singh *et al.* (1987), Chaudhury and Singh (1985), Yadava (1983) and Thakral (1982)

found significant variations for this character while working with different genotypes of *Brassica napus*.

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

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

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

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

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

Generally high number of seeds per siliqua is desirable. On the variability of this trait a good number of literatures are available. Significant variability in number of seeds/siliqua in oleiferous *Brassica* materials of diverse genetic base was observed by Kudla (1993) and Kumar and Singh (1994). Similar significant variability in the genotypes of *Brassica napus*, *B. campestris* and *B. juncea* were studied by them.

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

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

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

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

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

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

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

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

In every breeding program yield is the important character among various traits for oil crops. It is a complex trait which is influenced by various factors of production. A good number of literatures are available on the variability of this trait. High variability in different genotypes of *B. rapa* was reported by Sharma *et al.* (1994). Thakral (1982) also reported significant genetic variability in genotypes of *B. napus*. Similar high variability in different genotypes of *B. napus* was found by Khera and Singh (1988).

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

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

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

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

Malik *et al.* (2000) observed very high broad sense heritability (h^2_b>90%) for number of primary branches per plant, days to 50% flowering and oil content while working with different strains of *B. napus*. They also observed low heritability (h^2_1, 50%) for

plant height, number of siliqua/plant, number of seeds siliqua and seed yield. But high heritability for all these characters were found by Lodhi *et al.* (1979) while working with 55 genotypes of *B. napus*, *B. rapa* and *B. juncea*.

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

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

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

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

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

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

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

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

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

According to Knott (1972), Seitzer and Evans (1978) and Whan *et al.* (1982), selection for yield in early segregating generations was effective in developing high yielding cultivars of self pollinated crops. Selection for bold seed size from F_2 to F_5 generations was highly effective was observed by Gupta and Labana (1985) in Indian mustard.

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

2.2 Correlation among different characters

Rameeh (2012) aimed at finding out the planting date effect on yield associated traits and also determining the variations of correlations among the traits in different planting dates of rapeseed genotypes. Significant planting dates and genotypes effect for phonological traits, yield components, seed yield and oil percentage revealed significant differences of planting dates genotypes for these traits. The variation of

correlation between duration of flowering and pods per plant was less than the correlation of duration of flowering to other traits in different planting dates.

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

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

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

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

Pankaj *et al.* (2002) studied four parental cultivars and the F_4 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of the characters. The number of siliquae per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliqua and test weight at both levels. The number of seeds per siliqua was positively associated with siliqua length and yield per plant at both levels.

Srivastava and Singh (2002) studied correlation in Indian mustard [*Brassica juncea* L. Czern and Coss] for 10 characters was conducted with 24 strains of Indian mustard along with 2 varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and oil percent were positively associated with seed yield.

Shalini *et al.* (2000) evaluated 81 genotypes of Indian mustard for the magnitude of association between their quantitative characters of secondary branches, plant height, number of siliquae and seeds per siliquae were highly associated with seed yield.

Khulbe and Pant (1999) carried out a study of correlation in 8 Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids and revealed that the number of siliqua per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and harvest index were positively associated with seed yield.

The number of siliquae per plant, number of seeds per siliqua and plant height was significantly positively correlated with seed yield was observed by Masood *et al.* (1999) while studied 7 genotypes of B. campestris and standard cultivar of *B. napus* to calculate correlation co-efficient.

Thakaral *et al.* (1999) studied correlation co-efficient on seed yield and yield contributing characters in 8 Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids grown at Hisar. The data indicated that higher seed yield could be obtained by selecting for increased plant height.

According to Kumar *et al.* (1999) genotypic correlation co-efficient were higher in magnitude than corresponding phenotypic correlation co-efficient for most characters. The plant height, siliquae on main shoot, siliquae per plant and thousand seed weight were positively correlated with seed yield. Gurdial and Hardip (1998) carried out and experiment with gobhi sarson (*B. nigra*) and reported that dwarf plant gave higher yield.

Zajac *et al.* (1998) studied phenotypic correlation between yield and its component and reported that strong positive correlation occurred between seeds per siliqua and actual yield. Positive but a weaker correlation was observed between seed yield and

siliquae per plant. The number of seeds per siliqua had the greatest influence and siliquae number per plant had the smallest effect on yield.

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

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

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

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

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

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

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

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

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

Gosh and Mukhopadhyay (1994) studied Tori-7 (*B. campestris var. toria*) for evaluation of seed yield and 5 seed yield contributing characters and found that plant height, siliqua per plant, seeds per siliqua and thousand seed weight was significant and positively correlated with seed yield.

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

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

Ahmed (1993) worked with 8 cv. of *B. campestris* and *B. juncea* for study of nature and degree of interrelationship among yield components and observed that siliqua length, number of siliqua per plant, number of seeds per siliqua and seed weight per siliqua was positively and linearly associated with seed yield per plant. He also observed that seed oil content was positively correlated with seed weight, but negatively correlated with number of seeds per siliqua.

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

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

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

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

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

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

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

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

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

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

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

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

2.3 Path co-efficient analysis

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

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

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

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

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

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

Khulbe and Pant (1999) studied path co-efficient analysis in eight Indian mustard (*B. juncea*) parents and their 28 F_1 hybrids. The results revealed that harvest index, siliqua length, seeds per siliqua, siliqua per plant, thousand seed and days to initial flowering were the major traits influencing seed yield.

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

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

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

Uddin *et al.* (1995) studied path analysis in 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and thousand seed weight had high positive direct effect on seed yield per plant. Chauhan and Singh (1995) observed that plant height, siliqua per plant and seeds per siliqua had high positive direct effect on seed yield. Kachroo and Kumar (1991) studied path co-efficient analysis in *B. juncea* and found that thousand seed weight had positive direct effect but days to flowering and number of primary branches had negative indirect effect via seeds per siliqua on seed yield.

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

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

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

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

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

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

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

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

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

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

2.4 Genetic Diversity analysis

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

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

Choudhary and Joshi (2001) determined genetic diversity among the 88 entries including eighty F_4 derivatives i.e., 20 each selected from *Brassica crosses* viz., *B. juncea*×*B. napus*, *B. juncea* × *B. rapa* var. toria, *B. juncea*×*B. rapa* var. yellow sarson and *B. tournefortii* × *B. juncea*, and eight parent genotypes through multivariate analysis (D^2 statistic). The genetic distances calculated among different *Brassica* species revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus*, *B. rapa* var. toria and *B. rapa* var. yellow sarson. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. The characters, namely, plant height, secondary branches per plant, days to flowering and 1000-seed weight was contributed maximum towards genetic divergence.

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

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

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

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

The D^2 analysis allowed the 36 genotyped/variety of linseed to be identified into five distinct clusters by Begum *et al.* (2007). The cluster I included 11 genotypes that had medium mean values for 1000-seed weight (g) and seed yield/plant. The cluster II contained 6 genotypes, which had the highest mean values for number of seeds/capsule, number of branches/plant and seed yield/plant. They also showed the highest mean value for plant height. It is also related with medium mean values for rest of the characters. The cluster IV included 3 genotypes having the highest mean values for number of capsules/plant and days to maturity. The cluster V included single genotype, which had the lowest mean values for days to maturity and plant height. The highest inter cluster distance was observed among clusters V, IV and II, while the lowest between III and I. The highest intra cluster distance was observed in cluster III that revealed maximum variability within the clusters. In this study, two traits such as number of branches/plant and number of seeds/capsule contributed the maximum towards divergence in the existing germplasm.

Islam and Islam (2000) reported the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were grouped into four clusters. The inter-cluster distances were larger than the intra-cluster distances. The characters contributed maximum in divergence analysis is days to 50% flowering, plant height, primary branches/plant and number of siliquae/plant.

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

Uddin (1994) conducted an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The inter-cluster

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

CHAPTER III

MATERIALS AND METHODS

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3.1 Experimental site:

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka – 1207 during November 2012 to February 2013. The location of the experimental site was situated at 230 74' N latitude and 900 35' E longitude with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix 1).

3.2 Soil and Climate:

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

3.3 Experimental materials:

The healthy seeds of thirty one BC_1F_3 of *Brassica napus* collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

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

Table 1. Materials used for the experiment

Gentypes	BC_1F_3 Populations	Source
G1	108×9908(108)	SAU
G2	905×0130(0130)	SAU
G3	905×0130(9905)	SAU
G4	2066×205(205)	SAU
G5	108×0130(0130)	SAU
G6	066×0130(0130)	SAU
G7	906×0130(9906)	SAU
G8	205×0130(0130)	SAU
G9	908×0130(0130)	SAU
G10	9906×205(9906)	SAU
G11	108×205(108)	SAU
G12	066×0130(2066)	SAU
G13	9908×108(9908)	SAU
G14	9905×9901(9901)	SAU
G15	9906×205(205)	SAU
G16	9906×2066(9906)	SAU
G17	9908×0130(9908)	SAU
G18	108×2066(2066)	SAU
G19	9901×203(9901)	SAU
G20	9905×9908(9908)	SAU
G21	108×2066(108)	SAU
G22	9906×2066(2066)	SAU
G23	9905×9908(9905)	SAU
G24	2066×205(2066)	SAU
G25	9908×2066(9908)	SAU
G26	205×0130(205)	SAU
G27	9905×108(108)	SAU
G28	9905×9901(9905)	SAU
G29	108×0130(108)	SAU
G30	108×9908(9908)	SAU
G31	9906×9901(9901)	SAU

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of Cowdung, 250 kg Urea, 175 kg Triple Super Phosphate (TSP), 85 kg Muriate of Potash (MP), 250 kg Gypsum, 3 kg Zinc Oxide and Boron 1 kg per hectare. The half amount of urea, total amount of Cowdung, TSP, MP, Gypsum, Zinc Oxide and Boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 56m×14m = 784m^2. Each replication size was 56m×3.5m, and the distance between replication to replication was 1m. The spacing between lines to line was 30cm. Seeds were sown in lines in the experimental plots on 13 November, 2012. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. A pictorial view of experimental field at flowering stage is presented in plate 1.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. One post sowing

Plate 1: Photograph showing the experimental field at SAU at flowering stage

irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm. apart. Second weeding was done after 35 days of sowing. Aphid infection was found in the crop during the siliqua development stage. To control aphids Malathion-57 EC @ 2ml/liter of water was applied. The insecticide was applied in the afternoon.

3.4.5 Crop harvesting

Harvesting was done from 4th to 20th February, 2013 depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. Ten plants were selected at random from the parental line and BC_1F_3 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. A pictorial view of experimental field at harvesting stage is presented in plate 2.

3.4.6 Data collection

For studying different genetic parameters and inter-relationships, ten characters were taken into consideration. The data were recorded on ten selected plants for each cross and ten selected plants for each parent on the following traits-

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

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

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

Plate 2. Photograph showing the experimental field at SAU at harvesting stage

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

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

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

vii. **Siliqua length (cm):** This measurement was taken in centimeter (cm) from the base to the tip of a siliqua without beak of the ten representative siliquae.

viii. **Number of seeds per siliqua:** Well filled seeds were counted from ten representative siliquae, which was considered as the number of seeds per siliqua.

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

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

3.4.7 Statistical analysis

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Simple correlation coefficient was obtained using the formula suggested by Clarke (1973); Singh and Chaudhary (1985) and path co-efficient analysis was done following the method outlined by Dewey and Lu (1995).

i) Estimation of genotypic and phenotypic variances:

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

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

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

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

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

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

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

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

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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

iii) Estimation of heritability:

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

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

Where, h^2_b = Heritability in broad sense.

δ^2_g = Genotypic variance

δ^2_p = Genotypic variance

iv) Estimation of genetic advance: The following formula was used

to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

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

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

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

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

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

vi) Estimation of simple correlation co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

vii) Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1995) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

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

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

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

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

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

Total correlation, say between x1 and y is thus partitioned as follows:

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

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

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

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

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

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

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

Riy = Correlation of the character with yield.

viii) Estimation of Genetic Diversity

a. Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jager *et al.* 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

b. Principal Coordinate Analysis (PCO)

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

c. Canonical Vector Analysis (CVA)

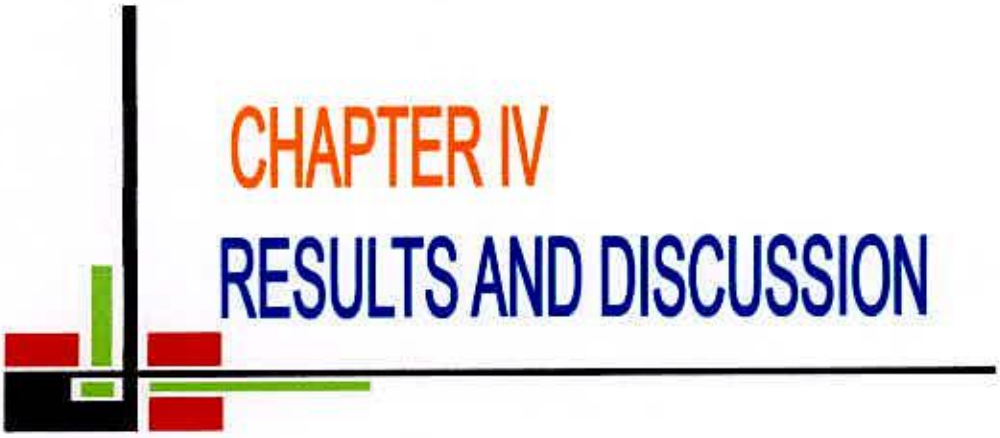
The canonical vector analysis compute a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Finally, a series of orthogonal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

d. Average Intra-cluster Distances

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

e. Clustering

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



CHAPTER IV

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among thirty one BC_1F_3 materials of *Brassica napus* genotypes and also to study the correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different characters such as plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, days to 50% flowering, no. of siliqua per plant, days to maturity, no. of seeds per siliqua, siliqua length (cm) thousand seed weight (g) and seed yield per plant (g). The data were statistically analyzed and thus obtained results are described below under the following heads:

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

4.1 Variability study in *Brassica napus*

4.1.1 Variability among the thirty one BC_1F_3 materials for *Brassica napus* and one check variety

Significant variations were observed for most of the characters among thirty one BC_1F_3 materials of *Brassica napus*. Table 2a & 2b showed the values of mean, range CV%, phenotypic variances, genotypic variances, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters.

4.1.1.1 Plant height (cm)

In this study the highest plant height was observed in Nap-9905 × Nap-0130 (0130) (105.83cm) (Plate 4) where as the minimum plant height was observed in Nap-9906 × Nap-205 (9906) (73.00cm) (Plate 13) (Table 2a). Phenotypic variance and genotypic

variance were observed as 89.01and 65.26, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The estimates of PCV (10.5%) and GCV (8.99%) also indicated presence of considerable variability among the genotypes for this trait (Table 2b). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al.* (2001).

4.1.1.2 Number of primary branches per plant

Among the 31 BC_1F_3 populations the highest number of primary branches per plant was observed in 9905×0130 (0130) (3.05) (Plate 4) where as the minimum number of primary branches/plant was observer in 9906×205 (205) (1.14) (Plate 16 and Table 2a). Relatively large differences between them indicating large environmental influences on these character and relatively high difference between PCV (27.65%) and GCV (21.69%) value indicating the apparent variation not only due to genotypes but also due to the large influence of environment (Table 2b).

Chowdhury *et al.* (1987) also found significant differences for number of primary branches per plant.

Table 2a Estimation of genetic parameters in ten characters of 31 genotypes in *Brassica napus* L.

Parameters	Range	Mean	MS	CV (%)	σ^2 p	σ^2g	σ^2 e
PH	73-105.83	89.81	219.54**	5.43	89.01	65.26	23.76
NPB	1.14-3.05	1.99	0.67**	17.16	0.30	0.19	0.12
NSB	0.18-1.58	0.68	0.31**	36.55	0.15	0.08	0.06
D50%F	27.67-38.33	36.03	9.96**	3.27	4.24	2.86	1.38
NSP	52.86-119.51	74.53	691.78**	9.93	267.15	212.33	54.83
NSS	16.33-25.78	20.66	13.25**	8.87	6.65	3.30	3.36
DM	83-96.33	89.33	24.28**	2.80	12.28	6.01	6.27
SL	6.77-9.67	8.11	1.14**	5.55	0.52	0.31	0.20
TSW	3.27-4.78	4.16	0.38**	6.31	0.17	0.11	0.07
SYP	32.76-84.54	44.56	317.04**	16.05	139.78	88.63	51.15

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

PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondary branches per plant, D50%F = Days to 50% flowering, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, DM = Days to 80% maturity, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, MS = mean sum of square, CV (%) = Coefficient of Variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance.

Table 2b Estimation of genetic parameters in ten characters of 31 genotypes in *Brassica napus* L.

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
PH	10.51	8.99	5.43	73.31	14.25	15.87
NPB	27.65	21.69	17.14	61.56	0.70	35.05
NSB	56.03	42.53	36.47	57.63	0.45	66.78
D50%F	5.72	4.69	3.27	67.37	2.86	7.94
NSP	21.93	19.55	9.93	79.48	26.76	35.91
NSS	12.49	8.79	8.87	49.58	2.63	12.75
DM	3.92	2.74	2.80	48.91	3.53	3.95
SL	8.86	6.89	5.56	60.61	0.90	11.06
TSW	10.04	7.81	6.31	60.53	0.52	12.52
SYP	26.53	21.13	16.05	63.41	15.44	34.66

PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, D50%F = Days to 50% flowering, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, DM = Days to 80% maturity, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation.

4.1.1.3 Number of secondary branches per plant

Among the 31 BC_1F_3 populations the highest number of secondary branches/plant was observed in 108×9908 (108) (1.58) (Plate 32) whereas the minimum number of secondary branches/plant was observed in Nap-2066 × Nap-205 (205) (0.18) (Plate 5 and Table 2a). Higher estimate of PCV (56.03%) and GCV (42.53%) values indicated presence of considerable variability among the genotypes for this trait (Table 2b). Lekh *et al.* (1998) found highest genotypic coefficient of variation for number of secondary branches while working on 24 genotypes of *Brassica napus*. Chowdhury *et al.* (1987) found significant differences for number of secondary branches per plant. Genotypic and phenotypic variability in mustard are shown in Figure 1.

4.1.1.4 Days to 50% flowering

Considerable variations were observed among 31 BC_1F_3 populations for days to 50% flowering. The days to 50% flowering were observed the lowest (27.67 days) in Nap-9905 × Nap-9901 (9901) and highest (38.33 days) was observed in Nap-9908 × Nap-2066 (9908) (Table 2a).

Phenotypic and genotypic variance for days to 50% flowering was observed as 4.24 and 2.86, respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (5.72%) was higher than the genotypic coefficient of variation (4.69%) (Table 2b), which suggested that environment has a significant role on the expression of this trait. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.* (1998).

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

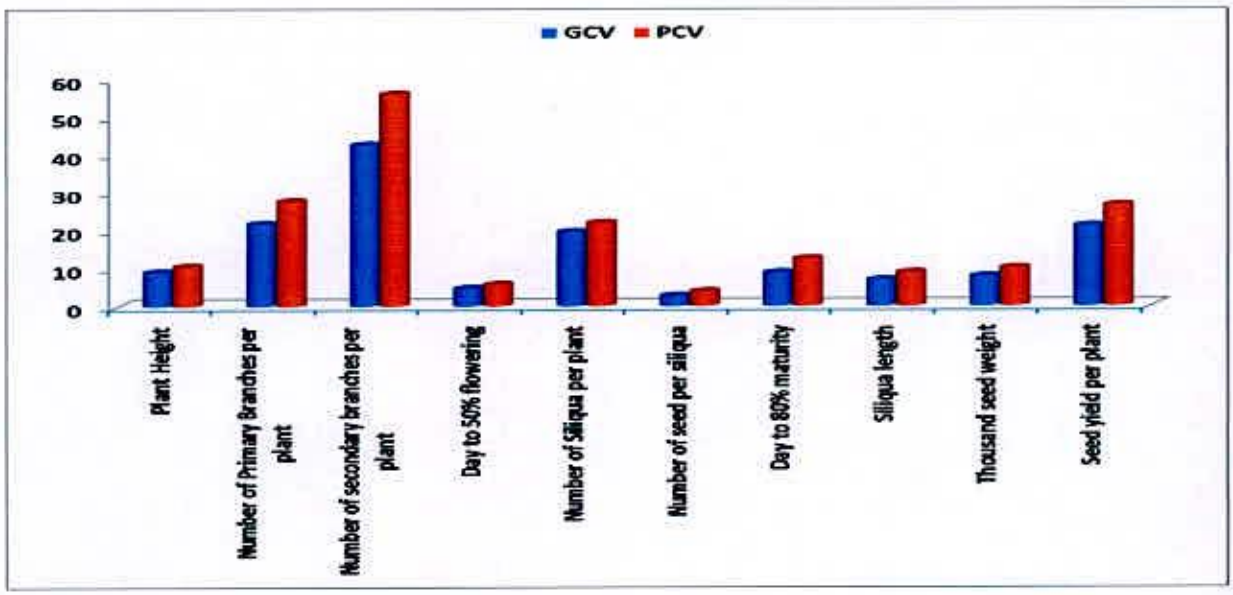


Fig. 1. Genotypic and phenotypic coefficient of variation in *Brassica napus*.

4.1.1.5 Days to maturity

The highest days to maturity was observed in Nap-9905 × Nap-9908 (9908) (96.33 days) and the minimum days to maturity was observed in Nap-9905× Nap 9901 (9905) (Table 2a). Phenotypic and genotypic variance for days to maturity was observed 0.76 and 0.05, respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (12.28%) was higher than the genotypic coefficient of variation (6.01%) (Table 2b), which suggested that environment has a significant role on the expression of this trait. Higher genotypic variances indicated the better transmissibility of a character from parent to the offspring. Similar result for this trait was also observed by Katiyar *et al.* (1974).

4.1.1.6 Number of siliqua per plant

The number of siliqua per plant was observed the highest in Nap 9905 × Nap 0130 (0130) (119.51) (Plate 4) and the lowest in Nap 108×2066 (2066) (52.86) (Plate 21). Number of siliqua per plant showed the highest phenotypic variance (267.15) and genotypic variance (212.33) with large environmental influence and the difference between the PCV (21.93%) and GCV (19.55%) indicated existence of adequate variation among the genotype (Table 2b). High genetic variation was also found by Kudla (1993).

Plate 3: NAP 108× 9908(108)

Plate 4: NAP 9905×0130(0130)

Plate 5: NAP 2066× 205(205)

Plate 6: NAP 9905× 0130(9905)

Plates 3- 33: Photographs showing the plants with siliqua of different lines of *Brassica napus* L.

Plate 7: NAP 2066×0130(0130)

Plate 8: NAP 9906×0130(9906)

Plate 9: NAP 108×0130(0130)

Plate 10: NAP 205×0130(0130)

Plate 11: NAP 9908×0130(0130)

Plate 12: NAP 108×205(108)

Plate 13: NAP 9906×205 (9906)

Plate 14: NAP 2066×0130(2066)

Plate 15: NAP 9908×108(9908)

Plate 16: NAP 9906×205 (205)

Plate 17: NAP 9905×9901 (9901)

Plate 18: NAP 9906×2066 (9906)

Plate 19: NAP 9908×0130(9908)

Plate 20: NAP 9901×205(9901)

Plate 21: NAP 108×2066(2066)

Plate 22: NAP 9905×9908(9908)

Plate 23: NAP 108×2066(108)

Plate 24: NAP 9905×9908(9905)

Plate 25: NAP 9906×2066(2066)

Plate 26: NAP 2066×205(2066)

Plate 27: NAP 9908×2066(9908)

Plate 28: NAP 9905×108(108)

Plate 29: NAP 205×0130(205)

Plate 30: NAP 9905×9901(9905)

Plate 31: NAP 108×0130(108)

Plate 32: NAP 9906×9901(9901)

Plate 33: NAP 108×9908(9908)

4.1.1.7 Length of siliqua (cm)

Length of siliqua was observed the highest in Nap-9905 × Nap-0130 (9905) (9.67 cm) and the minimum length of pod was observed in Nap-2066 × Nap-0130 (2066) (6.77 cm) (Table 2a). Length of siliqua showed phenotypic variance (0.52) and genotypic variance (0.31) with little difference between them indicating that they were less responsive to environmental factors for their phenotypic expression and relatively medium PCV (8.86%) and GCV (6.89%) indicating that the genotype has moderate variation for this trait (Table 2b). High co-efficient of variation for this trait for both genotypic and phenotypic variability was recorded by Masood *et al.* (1999). High genetic variability for this trait was also found by Olson (1990).

4.1.1.8 Number of seeds per siliqua

The number of seeds per siliqua was observed highest in Nap-9905 × Nap-9908 (9908) (25.78). The minimum number of seeds per siliqua was observed in Nap-2066 × Nap-0130 (2066) (16.33) (Table 2a). The phenotypic and genotypic variances for this trait were 6.65 and 3.30 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 12.49% and 8.79% respectively for number of seeds per siliqua which indicating that medium variation exists among different genotypes (Table 2b). Similar variability was also recorded by Kumar and Singh (1994).

4.1.1.9 Thousand seed weight (g)

Thousand seed weight was found maximum in Nap-9905 × Nap-0130 (0130) (4.78 g) where as the minimum thousand seed weight was found in Nap-108 × Nap-2066 (108) (3.27 g) (Table 2a). Thousand seed weight showed very low genotypic (0.11) and phenotypic (0.17) variance with high differences indicating that they were high responsive to environmental factors. The phenotypic coefficient of variation (10.04%) and genotypic coefficient of variation (7.81%) were close to each other (Table 2b). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Significant variability for this trait was also found by Kumar and Singh (1994). Masood *et al.*

(1999) found high coefficient of variation for thousand seed weight while working with seven genotypes of *Brassica napus* to study genetic variability.

4.1.1.10 Yield per plant (g):

Yield per plant was found maximum in Nap-108 × Nap-9908 (108) (84.54 g) when it was the minimum yield per plant was found in Nap-9905 × Nap-108 (108) (32.768g) (Table 2a). The phenotypic variances and genotypic variances for this trait were 139.78 and 88.63 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The values of GCV and PCV were 21.13% and 26.53% indicating that the genotype has considerable variation for this trait (Table 2b). Similar variability was also found by Khera and Singh (1988).

4.1.2 Heritability, genetic advance and selection

4.1.2.1 Plant height (cm):

Plant height of BC_1F_3 showed high heritability 73.31% with moderately high genetic advance of 14.25 and genetic advance in percentage of mean of 15.87% (Table 2b), revealed the possibility of predominance of additive gene action in the inheritance of this trait and indicating that this trait could be improved through selection process. High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *et al.* (1986). Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *Brassica rapa.* Heritability and genetic advance in percentage of mean are shown in Figure 2.

4.1.2.2 Number of primary branches per plant:

Number of primary branches per plant exhibited low heritability 61.56 with low genetic advance of 0.70 and genetic advance in percentage of mean of 35.05%, which revealed that this trait was controlled by non-additive gene. As a whole, the low heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also

found by Singh *et al.* (1987). Yadava *et al.* (1985) found high heritability and genetic advance for number of primary branches per plant.

4.1.2.3 Number of secondary branches per plant:

Number of secondary branches per plant exhibited moderately high heritability (57.63%) with low genetic advance 0.45 and genetic advance in percentage of mean (66.78%), such results revealed that this trait was controlled by non-additive gene. As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes. Moderately high heritability coupled with low genetic advance was also found by Singh *et al.* (1987). Sheikh *et al.* (1999) found high heritability coupled with high genetic advance for number of secondary branches per plant while working with 24 genotypes of toria.

4.1.2.4 Days to 50% flowering:

Days to 50% flowering exhibited low heritability (67.37%) with low genetic advance (2.86) and genetic advance in percentage of mean (7.94%) indicated that this trait was controlled by non-additive gene. This results support the reports of Malik *et al.* (1995).

4.1.2.5 Days to maturity:

Days to maturity shows low heritability (48.91%) with low genetic advance (3.53) and genetic advance in percentage of mean (3.95%) indicated that this trait was controlled by non-additive gene and medium possibility of selecting genotypes that would mature earlier. In some of the crosses the frequency of the segregating plants showing reduced maturity was comparatively higher than the other crosses. Low heritability coupled with low genetic advance for this trait was also observed by Sharma (1984).

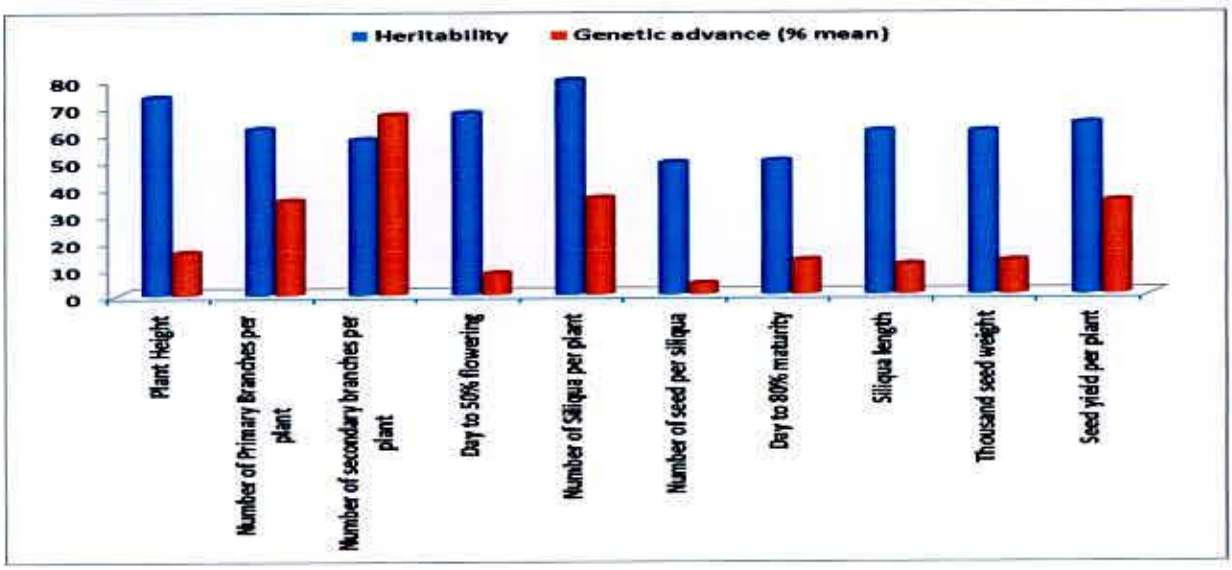


Fig. 2. Heritability and genetic advance over mean in *Brassica napus*.

4.1.2.6 Number of siliqua per plant:

Number of siliqua per plant exhibited very high heritability 79.48% with high genetic advance 26.76 and genetic advance in percentage of mean 35.91%. These results revealed the possibility of predominance of additive gene action in the inheritance of this trait. This trait possessed high variation; it is high potential for effective selection for further genetic improvement of this character. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). Mahmud *et al.* (2003) reported that the number of siliqua per plant were highly heritable coupled with high genetic advance. Akbar *et al.* (2007) also found higher GCV, higher heritability and genetic advance for this trait.

4.1.2.7 Siliqua length:

Siliqua length showed high heritability (60.61%) with low genetic advance (0.98) and low genetic advance in percentage of mean 11.06% indicated that this trait was controlled by non-additive gene. High heritability for this trait was observed by Chaudhury *et al.* (1989). Similar results were also found by Kwon *et al.* (1989) and Rao (1977).

4.1.2.8 Number of seeds per siliqua:

Number of seeds per siliqua showed high heritability 49.58% coupled with high genetic advance 2.63 and high genetic advance in percentage of mean 12.75%, indicated that this trait was controlled by additive gene and selection for this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Singh (1986).

4.1.2.9 Thousand seed weight:

Thousand seed weight exhibited high heritability 60.53% with low genetic advance 0.52 and genetic advance in percentage of mean 12.52%, revealed that this trait was controlled by non-additive gene. Liang and Walter (1968) reported that moderate values of heritability and the genetic advance may be due to non-additive gene action which includes dominance and epistasis. Johnson *et al.* (1955) reported that heritability estimates along with genetic group were more useful in prediction

selection of the best individual. High heritability for this trait was also observed by Yadava *et al.* (1993). Singh *et al.* (2002) reported the high heritability and genetic advance for thousand seed weight.

4.1.2.10 Seed yield per plant:

Seed yield per plant showed high heritability 63.41% with high genetic advance (15.44) and moderately high genetic advance in percentage of mean 34.66% indicated this trait was controlled by additive gene and selection for this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). High heritability and genetic advance for seed yield per plant was reported by Singh (1986) while working with 22 genotypes of *Brassica napus*.

Significant variability was found in almost all the BC_1F_3 materials *Brassica napus* for most of the characters studied. The performance of the crosses also compared with the one character variety, BS-13 as per objectives, selection was carried out among the 31 BC_1F_3 materials different cross combinations. Most promising 31 plants with short duration and high yield/plant were selected from the BC_1F_3 materials (Table 2a). There were large variations of the twenty selected BC_1F_3 materials for siliqua per plant ranging from 53 to 120 siliqua. One plant from Nap-9905×Nap-0130 (0130) produced 4.78 g thousand seed weight. One plant from Nap-108 × Nap 9908 (108) produced exceptionally high yield/plant 84.54 g (Table 2a).

4.2 Correlation coefficient

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for BC_1F_3 materials of *B. napus* are shown in (Table 3 & 4).

4.2.1 Plant height (cm)

Plant height showed highly significant and positive interaction with number of primary branches (G = 0.311, P = 0.369), number of secondary branches (G = 0.284, P= 0.276), number of siliqua per plant (G = 0.620, P = 0.577), number of seed per siliqua (G = 0.410, P = 0.348), siliqua length (G = 0.480, P = 0.426) and seed yield per plant (G = 0.286, P = 0.198) (table 3 & 4). Highly significant positive associations between plant height and other characters indicate that the traits were governed by same gene and simultaneous improvement would be effective. It had positive and insignificant interaction with date of maturity (G = 0.430, P = 0.203). However, it had insignificant and negative interaction with thousand seed weight (G = -0.228, P = -0.198) (Table 8). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showed resemblance to the reports of Parveen (2007). Shalini *et al.* (2000) also observed that plant height was highly associated with seed yield. Similar result was reported by Srivastava et al. (2983). Significant positive correlation between plant height and seed yield was found by Khan and Khan (2003). Chaudhary *et al.* (1990) found positive correlation of plant height with number of seed per siliqua, number of siliqua per plant. Basalma (2008) reported opposite result for this trait.

4.2.2 Number of primary branches per plant

Number of primary branches per plant showed positive and significant interaction with number of secondary branch (G = 0.816, P = 0.707), number of siliqua per plant (G = 0.629, P = 0.545) and seed yield per plant (G = 0.731, P = 0.468). These suggesting if number of primary branches increases then yield per plant also increases. Malik *et al.* (2000) reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. It had insignificant and positive correlation with number of seeds per siliqua (G = 0.122, P = 0.0238) and siliqua length (G = 0.178, P = 0.191). However, it had insignificant and negative interaction was found in days to 50% flowering (G = -0.065, P = -0.108), thousand seed weight (G = -0.131, P = -0.098) (Table 3 & 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Similar results were obtained by Rashid (2007).

4.2.3 Number of secondary branches per plant

Number of secondary branch showed highly significant and positive interaction with number of siliqua per plant (G = 0.696, P = 0.564) and seed yield per plant (G = 0.839, P = 0.556) indicated that the traits were governed by same gene and simultaneous improvement would be effective and branching was an important contributor to yield , independent of its association with plant size. It had significant and positive correlation with number of seed per siliqua (G = 0.265, P = 0.160) and siliqua length (G = 0.212, P = 0.222) indicated that if number of secondary branches increased than number of seed per siliqua and siliqua length decreased. However, it had insignificant and negative interaction with days to 50% flowering (G = -0.066, P = -0.103), days to maturity (G = -0.015, P = -0.016). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showing similar to the reports of Chowdhary *et al.* (1987).

4.2.4 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity (G = 0.513, P = 0.282) indicated that if days to 50% flowering increased then days to maturity also increased. It also exhibited insignificant and positive interaction with number of seed per siliqua (G = 0.032, P = 0.014), siliqua length (G = 0.110, P = 0.084) and yield per plant (G = 0.112, P = 0.001). However, it had insignificant and negative interaction with number of siliqua per plant (G = -0.032, P = -0.014) (Table 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Parveen (2007) also revealed that days to 50% flowering had insignificant and positive interaction with yield per plant.

4.2.5 Number of siliqua per plant

Siliqua per plant showed significant and positive correlation with days to maturity (G = 0.285, P = 0.139), yield per plant (G = 0.593, P = 0.472) and seed length (G = 0.397, P = 0.403). Malik *et al.* (2000) reported positive correlation between siliqua per plant and seed yield. Whereas the insignificant and positive interaction was found in

number of seed per siliqua (G = 0.277, P = 0.259), thousand seed weight (G = 0.036, P = 0.012) (Table 3 & 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Tyagi *et al.* (1996) reported that no. of seed per siliqua had positive and insignificant effect on seed yield per plant.

4.2.6 Days to maturity

Days to maturity showed significant and positive correlation with number of seeds per siliqua (G= 0.281, P= 0.220) and siliqua length (G = 0.211, P = 0.132). It had insignificant and positive correlation with yield per plant (G = 0.049, P = -0.065). However, it had insignificant and negative interaction with thousand seed weight (G = -0.101, P = -0.060) (Table 3 & 4). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Parveen (2007) also revealed that days to maturity had insignificant and positive interaction with yield per plant.

Table 3 Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different Genotype of *Brassica napus* L.

	NPB	NSB	D50%F	NSP	DM	NSS	SL	TSW	SYP
PH	0.311**	0.284**	0.463**	0.620**	0.430**	0.410**	0.480**	-0.228*	0.286**
NPB		0.816**	-0.065	0.629**	0.100	0.122	0.178	-0.131	0.731**
NSB			-0.066	0.697**	-0.015	0.265*	0.212*	0.145	0.839**
D50%F				0.092	0.513**	-0.032	0.110	0.005	0.112
NSP					0.285**	0.277**	0.397**	0.036	0.593**
DM						0.281**	0.211*	-0.101	0.049
NSS							0.595**	-0.001	0.274**
SL								-0.106	0.149
TSW									0.127

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

PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, D50%F = Days to 50% flowering, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, DM = Days to 80% maturity, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yeild per plant.

Table 4 Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus* L.

	NPB	NSB	D50%F	NSP	DM	NSS	SL	TSW	SYP
PH	0.369**	0.276**	0.310**	0.577**	0.203	0.348**	0.426**	-0.198	0.198
NPB		0.707**	-0.108	0.545**	0.082	0.238*	0.191	-0.098	0.468**
NSB			-0.103	0.564**	0.035	0.160	0.222*	0.094	0.556**
D50%F				0.050	0.282**	0.014	0.084	-0.048	0.001
NSP					0.139	0.259*	0.403**	0.012	0.472**
DM						0.220*	0.132	-0.060	-0.065
NSS							0.488**	0.032	0.112
SL								-0.088	0.113
TSW									0.078

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

PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, D50%F = Days to 50% flowering, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, DM = Days to 80% maturity, SL=Siliqua length, TGW = Thousand Grain Weight (g), SYP=Seed yield per plant.

4.2.7 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant and positive interaction with seed length (G = 0.595, P = 0.488). Highly significant positive associations between number of seeds per siliqua and seed length indicated that the traits were governed by same gene and simultaneous improvement would be effective. It had insignificant and positive interaction with thousand seed weight (G = -0.001, P = 0.032). However, it had insignificant and negative interaction with yield per plant (G = 0.274, P = -0.112) (Table 3 & 4). Insignificant association of these traits indicated that the association between these traits sis largely influenced by environmental factors. Nasim *et al.* (1994) reported that no. of seeds per siliqua had negative and significant effects on seed yield per plant. Ahmed (1993) also found similar results for this trait.

4.2.8 Siliqua length (cm)

Siliqua length showed insignificant and negative correlation with thousand seed weight (G=-0.106, P=-0.088) indicated that the traits were governed by same gene and simultaneous improvement would be effective. It also showed highly significant and positive correlation with yield per plant (G=0.149, P=0.113) (Table 3 & 4) indicated that if siliqua length increased then yield per plant decreased. Nasim *et al.* (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.2.9 Thousand seed weight

Thousand seed weight showed insignificant and positive interaction with yield per plant (G=0.127, P=0.078) (Table 3 & 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Saini and Kumar (1995), Kakroo and Kumar (1991) and Olsson (1990) found positive associations which support the results. Tuncturk and Ciftci (2007) reported positive correlation between seed yield with 1000-seed weight which does not support the present findings.

4.2.10 Seed yield per plant (g)

Seed yield per plant had highest significant positive correlation with number of secondary branches per plant (G = 0.839, P = 0.556), number of primary branches per plant (G = 0.731, P = 0.468), number of siliqua per plant (G = 0.593, P= 0.472), and plant height (G = 0.286, P = 0.198) at both phenotypic and genotypic level suggesting, if the number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant increase then seed yield per plant also increase. Yield per plant had also non-significant positive correlation with days to 50% flowering (G = 0.112, P = 0.001), number of seed per siliqua (G = 0.274, P = 0.112) and siliqua length (G = 0.149, P = 0.113) at both genotypic and phenotypic levels. This trait had also negative insignificant correlation with days to maturity (G = 0.049, P = -0.065). Kumar *et al.* (1999) reported that seed yield had positive correlation with plant height, number of siliqua per plant and thousand seed weight. Jeromel *et al.* (2007) found complete positive correlation between plant height and yield. Siddikee (2006) revealed that yield per plant had highest significant positive correlation with number of siliqua per plant. Srivastava and Singh (2002) revealed that number of primary branches per plant and number of secondary branches per plant were positively associated with seed yield.

4.3 Path Co-efficient analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on seed yield per hector. In order to find out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and days to 50% flowering, days to maturity, plant height, number of primary braches per plant, number of siliqua per plant, length of siliqua, number of seeds per siliqua and thousand seed weight were causal (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* is presented in Table 5. Figure 3 showing path

diagram of yield and its contributing traits in thirty one BC_1F_3 genotypes in *Brassica napus*.

4.3.1 Plant height

Path analysis revealed that plant height had negative direct effect (-0.172) on yield per plant. It had positive indirect effect on number of primary branches per plant (0.097), number of secondary branches (0.143), days to 50% flowering (0.158), number of siliqua per plant (0.094) and days to maturity (0.116) (Table 5). Varshney (1986) worked with several strains of Brassica rapa and observed that plant height had the negative direct effect on yield. Plant height had negative indirect effect via number of seed per siliqua (-0.077) and thousand seed weight per plant (-0.003) (Table 5). Plant height finally made significant positive correlation with seed yield (0.286). These results indicated that if plant height increases than seed yield also increases mostly through the positive indirect effect of plant height with other characters. Han (1990) and Singh (2004) also reported direct positive result for this character.

4.3.2 Number of primary branches per plant

Number of primary branches per plant had the positive direct effect on yield per plant (0.312). This trait had positive indirect effect on number of secondary branches per plant (0.411), number of siliqua per plant (0.096) and days to maturity (0.035). On the other hand, negative indirect effect was found on days to 50% flowering (-0.022), number of seed per siliqua (-0.016), siliqua length (-0.029), plant height (-0.053) and thousand seed weight (-0.002) (Table 5). Number of primary branches per plant finally makes significant positive correlation with see yield (0.731). Mahla *et al.* (2003) and Singh *et al.* (2001) reported that number of primary branches per plant had direct positive effect on seed yield. Gupta *et al.* (1987) observed that primary branching had the direct effect on seed yield.

4.3.3 Number of secondary branches per plant:

Path co-efficient analysis revealed that number of secondary branches had positive direct effect (0.504) on yield per plant. It had positive indirect effect via number of primary branches per plant (0.255), number of siliqua per plant (0.106), number of seed per siliqua (0.002), days to maturity (0.075) and thousand seed weight (0.002) on

seed yield per plant. On the other hand, plant height (-0.049), days to 50% flowering (-0.023), and seed length (-0.034) had negative indirect effect on yield per plant (Table 5). The genotypic correlation with seed yield was positive and significant (0.839). Yadava *et al.* (1996) found the number of secondary branch had the highest positive direct effect on seed yield. Rashid (2007) observed that number of secondary branches per plant had the highest direct effect on seed yield per plant.

4.3.4 Days to 50% flowering:

Path co-efficient analysis revealed that, days to 50% flowering had positive direct effect (0.341) on yield per plant. Number of siliqua per plant (0.014) had positive direct effect on yield per plant. Number of primary branches (-0.020), number of secondary branch (-0.033), days to maturity (-0.009), plant height (-0.080), number of seed per siliqua (-0.084), siliqua length (-0.018) and thousand seed weight (0.000) (Table 5). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant.

Table 5 Path coefficient analysis showing direct and indirect effects of different characters on yield of mustard

Characters	Direct effect	Indirect effect									Genotypic correlation with yield
		PH	NPB	NSB	D50%F	NSP	NSS	DM	SL	TSW	
PH	-0.172	-	0.097	0.143	0.158	0.094	-0.070	0.116	-0.077	-0.003	0.286**
NPB	0.312	-0.053	-	0.411	-0.022	0.096	-0.016	0.035	-0.029	-0.002	0.731**
NSB	0.504	-0.049	0.255	-	-0.023	0.106	0.002	0.075	-0.034	0.002	0.839**
D50%F	0.341	-0.080	-0.020	-0.033	-	0.014	-0.084	-0.009	-0.018	0.000	0.112
NSP	0.152	-0.107	0.196	0.351	0.031	-	-0.046	0.078	-0.064	0.001	0.593**
NSS	-0.163	-0.074	0.031	-0.008	0.175	0.043	-	0.080	-0.034	-0.002	0.049
DM	0.283	-0.071	0.038	0.134	-0.011	0.042	-0.046	-	-0.096	0.000	0.274**
SL	-0.161	-0.083	0.056	0.107	0.038	0.060	-0.034	0.168	-	-0.002	0.149
TGW	0.015	0.039	-0.041	0.073	0.002	0.005	0.016	0.000	0.017	-	0.127

Residual effect: **0.222**

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

PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, D50%F = Days to 50% flowering, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, DM = Days to 80% maturity, SL=Siliqua length, TGW = Thousand Grain Weight (g), SYP=Seed yeild per plant.

4.3.5 Number of siliqua per plant:

Path co-efficient analysis revealed that number of siliqua per plant had the positive direct effect (0.152) on seed yield followed by positive indirect effect on number of primary branches (0.196), number of secondary branches(0.351), days to 50% flowering (0.031), days to maturity (0.078) and thousand seed weight (0.001). This trait had negative indirect effect on yield via plant height (-0.107), number of seed per siliqua (-0.046) and siliqua length (-0.064) (Table 5). This trait had significant positive genotypic correlation with yield per plant. Shalini *et al.* (2000) found the number of siliqua per plant had the highest direct effect on seed yield. Sheikh *et al.* (1999) revealed that siliqua per plant had highly positive direct effect on seed yield.

4.3.6 Days to maturity:

Path co-efficient analysis revealed that, days to maturity had positive direct effect (0.283) on yield per plant. This trait had positive indirect effect through number of primary branches (0.058), number of secondary branches (0.134) and number of siliqua per plant (0.042). On the other hand, days to maturity had negative indirect effect via plant height (-0.071), days to 50% flowering (-0.011), number of seed per siliqua (-0.046) and siliqua length (-0.096) (Table 5). Rashid (2007) revealed that days to maturity had positive direct effect on yield. Alam *et al.* (1986), Singh *et al.* (1985) and Srivastava *et al.* (1983) observed that days to maturity had positive direct and indirect effect on seed yield.

4.3.7 Number of seeds per siliqua:

Path analysis revealed that number of seeds per siliqua had direct negative effect (-0.163) on yield per plant. This trait had also indirect positive effect on number of primary branches per plant (0.031), days to 50% flowering (0.175), number of siliqua per plant (0.043) and days to maturity (0.080). On the other hand, this trait showed indirect negative effect on and plant height (-0.074), number of secondary branches (-0.008), siliqua length (-0.034) and thousand seed weight (-0.002) (Table 5). The direct effect was negative and the total effect was positive. The negative direct effect was mainly counter balanced by indirect positive effect of different characters. Rashid

(2007) reported that number of seeds per siliqua had direct positive effect on yield per plant. Parveen (2007) also found similar results for this trait.

4.3.8 Siliqua length:

Path analysis revealed that siliqua length had direct negative effect (-0.161) on yield per plant. This trait had also indirect positive effect on number of primary branches (o.056), number of secondary branches (0.107), days to 50% flowering (0.038), number of siliqua per plant (0.060) and days to maturity (0.168). On the other hand, length of siliqua showed indirect negative effect on number of seeds per siliqua (-0.034), plant height (-0.083) and thousand seed weight (-0.002) (Table 5). The genotypic correlation with seed yield was positive (0.149). Hence, selection should be practiced for this trait which had longer siliquae in order to improve seed yield. Han (1990) and Singh *et al.* (1978) reported that siliqua length had negative direct effect on yield per plant.

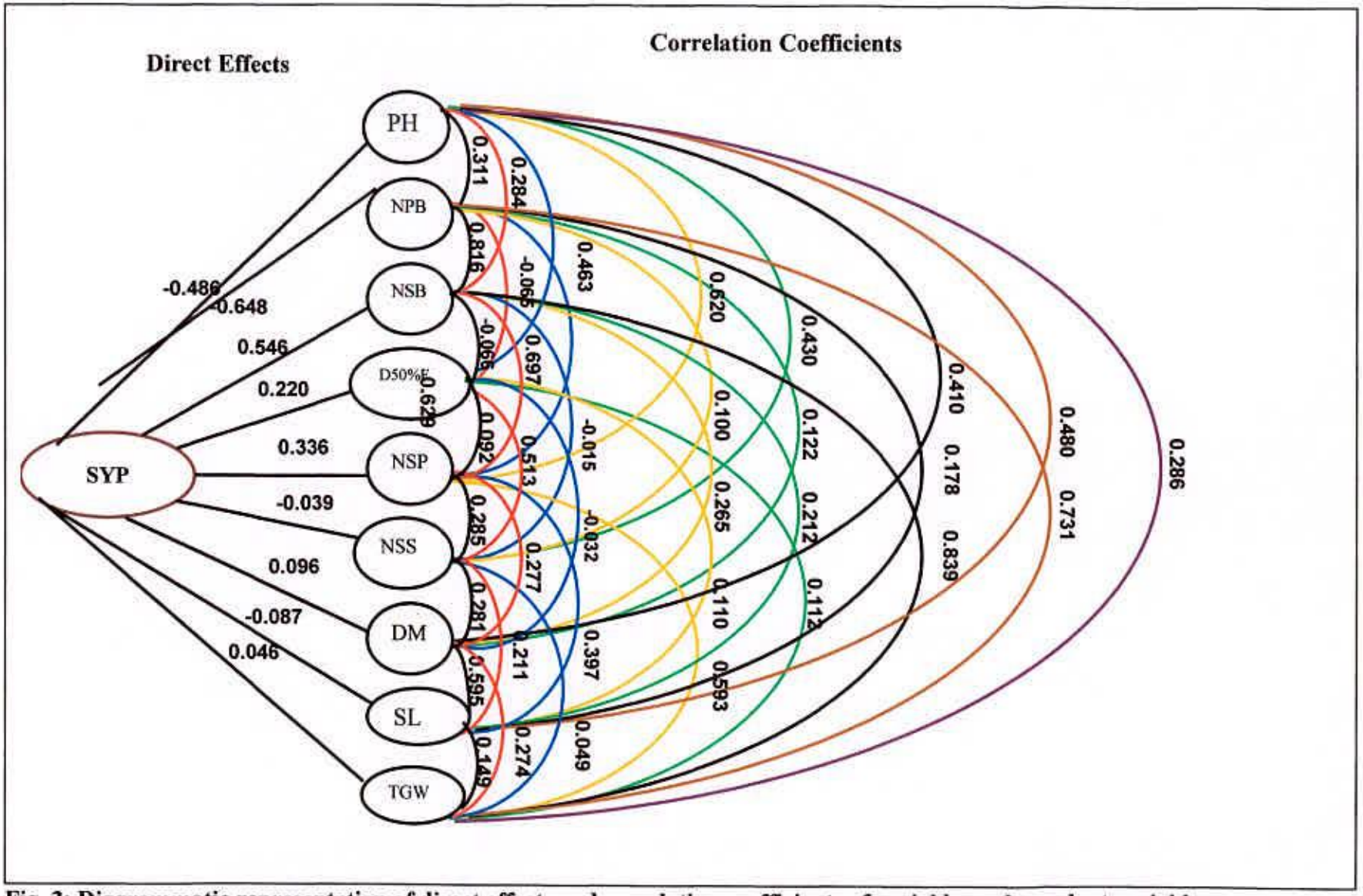


Fig. 3: Diagrammatic representation of direct effects and correlation coefficients of variable on dependent variable

4.3.9 Thousand seed weight:

Thousand seed weight had positive direct effect on yield per plant (0.015) and positive indirect effect on plant height (0.039), number of secondary branch (0.073), days to 50% flowering (0.002), number of siliqua per plant (0.022), number of seed per siliqua (0.016) and siliqua length (0.017) (Table 5). On the other hand, this trait showed negative indirect effect on number of primary branches (-0.041) (Table 5). This trait had positive genotypic correlation with yield (0.127). Siddikee (2006) reported that thousand seed weight had the highest positive direct effect on seed yield per plant. Kachro and Kumar (1991) reported that thousand seed weight had positive direct effect on seed yield. Kudla (1993) reported that thousand seed weight had positive direct effect on seed yield.

4.4 Genetic Diversity Analysis

The genetic diversity of *Brassica napus* advanced lines are presented in Table 6 to 10 and Figure 4 to 6.

4.4.1 Principal Component Analysis (PCA)

The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 66.10% (Table 6). The first two principal axes accounted for 54.41% of the total variation among the characters describing 31 advanced lines of *Brassica napus* genotypes. According to the principal axes I and II, a two dimensional chart ($Z_1 - Z_2$) of the genotypes. The scatter diagram revealed that there were four apparent clusters. The genotypes were distantly located from each other (Figure 4).

Table 6 Eigen values and yield percent contribution of 10 characters of 31 germplasm

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Plant Height (cm)	3.5807	35.81	35.81
Number of Primary Branches per plant	1.8604	18.60	54.41
Number of secondary branches per plant	1.1694	11.69	66.10
Day to 50% flowering	1.0562	10.56	76.66
Number of Siliqua per plant	0.6940	6.94	83.60
Number of seed per silique	0.4192	4.19	93.16
Day to 80% maturity	0.5369	5.37	88.97
Siliqua length (cm)	0.3154	3.15	96.31
Thousand seed weight (g)	0.1739	1.75	100.00
Seed yield per plant (g)	0.1939	1.94	98.25

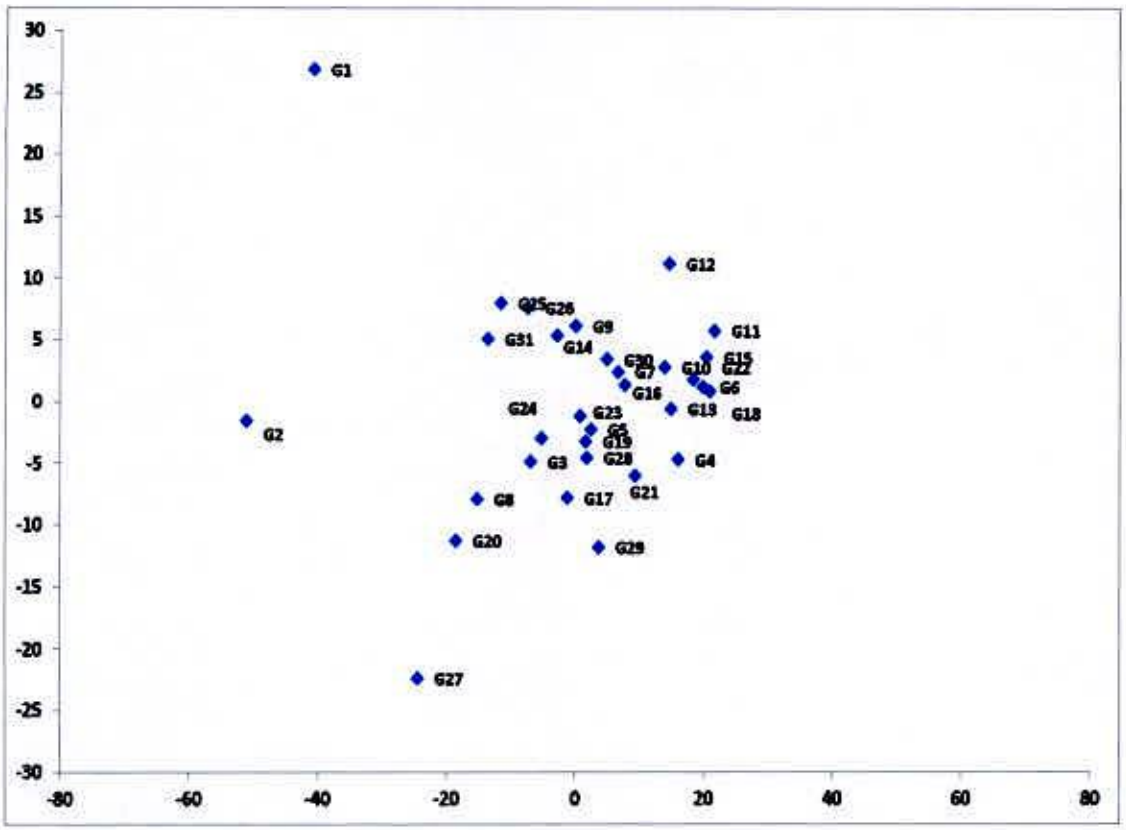


Fig. 4. Scatter diagram of 31 *Brassica napus* genotypes based on their principal component scores.

4.4.2 Non-Hierarchical Clustering

Thirty one *Brassica napus* genotypes were grouped into five different clusters non-hierarchical clustering (Table 7). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Mahmud *et al.* (2008) reported four clusters; Rawhat and Anad (1981) reported seven clusters; Nath *et al.* (2003) five clusters in *Brassica* species and Begum *et al.* (2007) reported five clusters in linseed. Cluster III had the highest number of (11) genotypes followed by I and II which had 9 and 6 genotypes, respectively. On the other hand, Cluster IV and V had 3 and 4 genotypes respectively (Table 7). Cluster V have G1 Nap 108×9908 (108) and G2 Nap 9905×0130(0130) whereas cluster IV composed of G8 Nap 205×0130(0130), G20 Nap 9905× 9908(9908) and G27 Nap 9905×108(108). Interestingly, cluster III represents 11 genotypes.

According to the cluster means (Table 8), cluster I showed better performance in case of early maturity (87.93 days), short plant height (80.52 cm), number of primary branches per plant (1.69), low number of secondary branches per plant (0.45), siliqua length (7.77 cm), number of seeds per siliqua (19.77), number of siliqua per plant (60.22) and seed yield per plant (38.48). Thus indicates that genotype of this cluster could be used for parent in future hybridization program for early maturity. The genotypes included in cluster II were early flowering (35.33 days), higher number of primary branches per plant (2.26), siliqua length (8.07 cm), plant height (88.83 cm) and also higher seed yield per plant (50.92g). Moreover, Cluster III had higher cluster mean for days to 50% flowering (36.21 days) followed by cluster IV (36.67 days) suggested that this cluster composed of late flowering genotypes. On the other hand, cluster IV showed the highest plant height (99.73 cm), higher number of siliqua per plant (95.70), the highest date of maturity (91.89), the highest siliqua length (8.69) and higher date of 50% flowering (36.67). It indicated the genotype of this cluster could be used for future hybridization program for higher plant height and siliqua length. Cluster V showed higher plant height (99.24 cm), higher number of siliqua per plant (110.92), days to maturity (88.17 days) and highest 1000-seed weight (4.49 g), highest seed yield per plant (73.78 g). It indicates that this cluster could be used as a parent for higher yield, early maturity and higher plant height.

Table 7 Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G4, G6, G10, G11, G12, G13, G15, G18, G22	9	2066×205(205), 2066×0130(0130), 9906×205(9906), 108×205(108), 2066×0130(2066), 9908×108(9908), 9906×205(205), 108×2066(2066), 9906×2066(2066)
II	G9, G14, G24, G25, G26, G31	6	9908×0130(0130), 9905×9901(9901), 2066×205(2066), 9908×2066(9908), 205×0130(205), 9906×9901(9901)
III	G3, G5, G7, G16, G17, G19, G21, G23, G28, G29, G30	11	9905×0130(9905), 108×$(0130)^2$, 9906×0130(9906), 9906×2066(9906), 9908×0130(9908), 9901×203(9901), 108×2066(108), 9905×9908(9905), 9905×9901(9905), 108×0130(108), 108×9908(9908)
IV	G8, G20, G27	3	205×$0130(0130)^2$, 9905×9908(9908), 9905×108(108)
V	G1, G2	2	108×9908(108), 9905×0130(0130)
	Total	31	

Table 8 Cluster mean values of 10 different characters of 31 genotypes

Characters	I	II	III	IV	V
Plant Height (cm)	80.52	88.21	93.86	99.73	99.24
Number of Primary Branches per plant	1.59	2.26	2.03	1.88	2.93
Number of secondary branches per plant	0.45	0.80	0.66	0.68	1.52
Day to 50% flowering	35.96	35.33	36.21	36.67	36.50
Number of Siliqua per plant	60.22	80.03	70.85	95.70	110.92
Number of seed per silique	19.77	21.03	20.40	22.71	21.99
Day to 80% maturity	87.93	90.72	89.24	91.89	88.17
Siliqua length (cm)	7.77	8.07	8.21	8.69	8.40
Thousand seed weight (g)	4.26	4.25	4.07	3.83	4.49
Seed yield per plant (g)	38.48	50.92	42.14	39.48	73.78

4.4.3 Canonical Variate Analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 9. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Islam and Islam (2000) reported that the inter-cluster distances were larger than the intra-cluster distances. Uddin (1994) also reported similar result in mustard. The highest inter-cluster distance was observed between clusters I and V (22.433), followed by between cluster V and III (18.168), II and V (13.661), I and IV (12.390) and V and IV (12.313). In contrast, the lowest inter-cluster distance was observed between cluster II and III (5.015), followed by I and III (5.092), II and IV (5.555), III and IV (8.409), and I and II (9.019) (Figure 5). However, the maximum inter-cluster distance was observed between the clusters II and IV (24.003) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. Dhillon *et al.* (1999) mentioned that maximum inter-cluster distance gave desirable segregants for the development of high yielding varieties with quality of oil for seed yield. On the other hand, the maximum intra-cluster distance was found in cluster IV (0.383), which contained of 3 genotypes, while the minimum distance was found in cluster V (0.04) that comprises 2 genotypes. The different multivariate analysis was superimposed in Figure 5 from which it could be concluded that different multivariate techniques supplemented and confirmed one another.

Table 9 Intra (Bold) and inter cluster distances (D^2) for 31 genotypes

Cluster	I	II	III	IV	V
I	**0.021**	9.019	5.092	12.390	22.433
II		**0.051**	5.015	5.555	13.661
III			**0.013**	8.409	18.168
IV				**0.383**	12.313
V					**0.04**

Table 10 Relative contributions of the ten characters of 31 varieties to the total divergence

Characters	Vector-1	Vector-2
Plant Height	0.0789	-0.0081
Number of Primary Branches per plant	-0.8541	1.8503
Number of secondary branches per plant	1.9613	-0.9433
Day to 50% flowering	-0.2541	-0.0611
Number of Siliqua per plant	0.2632	-0.0790
Number of seed per silique	0.3601	-0.2090
Day to 80% maturity	0.1203	-0.0407
Siliqua length	-1.1408	0.1017
Thousand seed weight	-0.1933	2.3438
Seed yield per plant	0.1879	0.1227

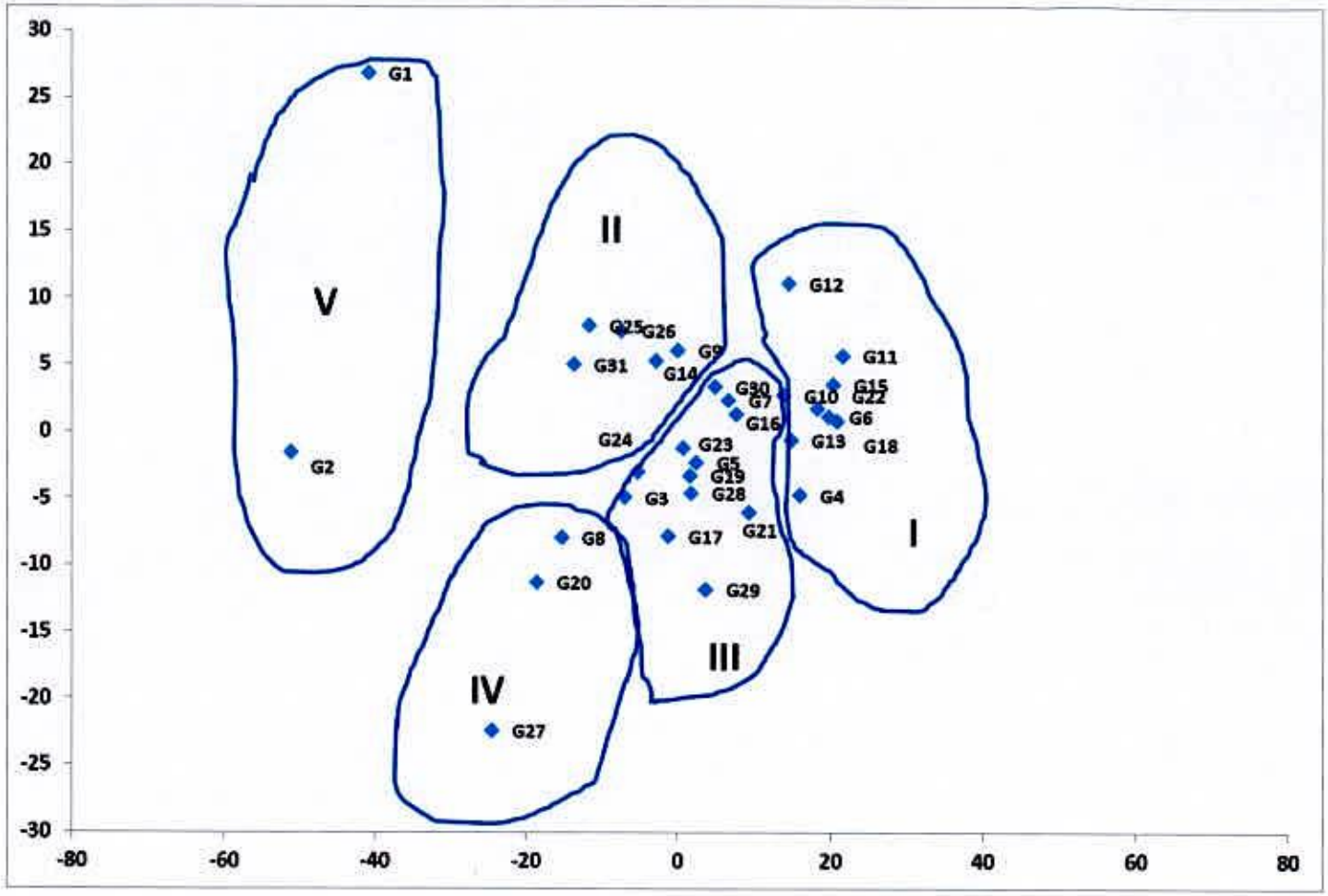


Fig. 5. Intra and inter cluster distances of 31 genotypes in *Brassica napus*.

A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, showing in the relative position (Figure 4). According to scatter diagram all the genotypes were apparently distributed into four clusters. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster I and V. Goswami *et al.* (2006) found moderate genetic diversity between parents had the good general combining ability effect and high specific combining ability as well as high mean values in F_2 in Indian mustard. Main and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis. Keeping this in view, it appears that the crosses between the genotypes belonging cluster I with cluster IV, cluster II with cluster V, cluster IV with cluster V, and cluster V with cluster III might produce high heterosis in respect of yield, earliness, tallness, higher number of siliqua per plant. Also the crosses between genotypes from cluster I with cluster V might produce high level of segregating population. So the genotypes belonging to cluster I and cluster IV, cluster II, cluster V and cluster IV and cluster V, and cluster and cluster III have been selected for future hybridization program.

4.4.4 Contribution of traits towards divergence of the genotypes

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were plant height (0.0789), number of secondary branches per plant (1.9613), number of siliqua per plant (0.2632), number of seed per siliqua (0.1203), days to 80% maturity (0.3601), and seed yield per plant (0.1879). In vector II (Z_2), number of secondary branches per plant (1.8503), siliqua length (0.1017), thousand seed weight (2.3438) and seed yield per plant (0.1227).

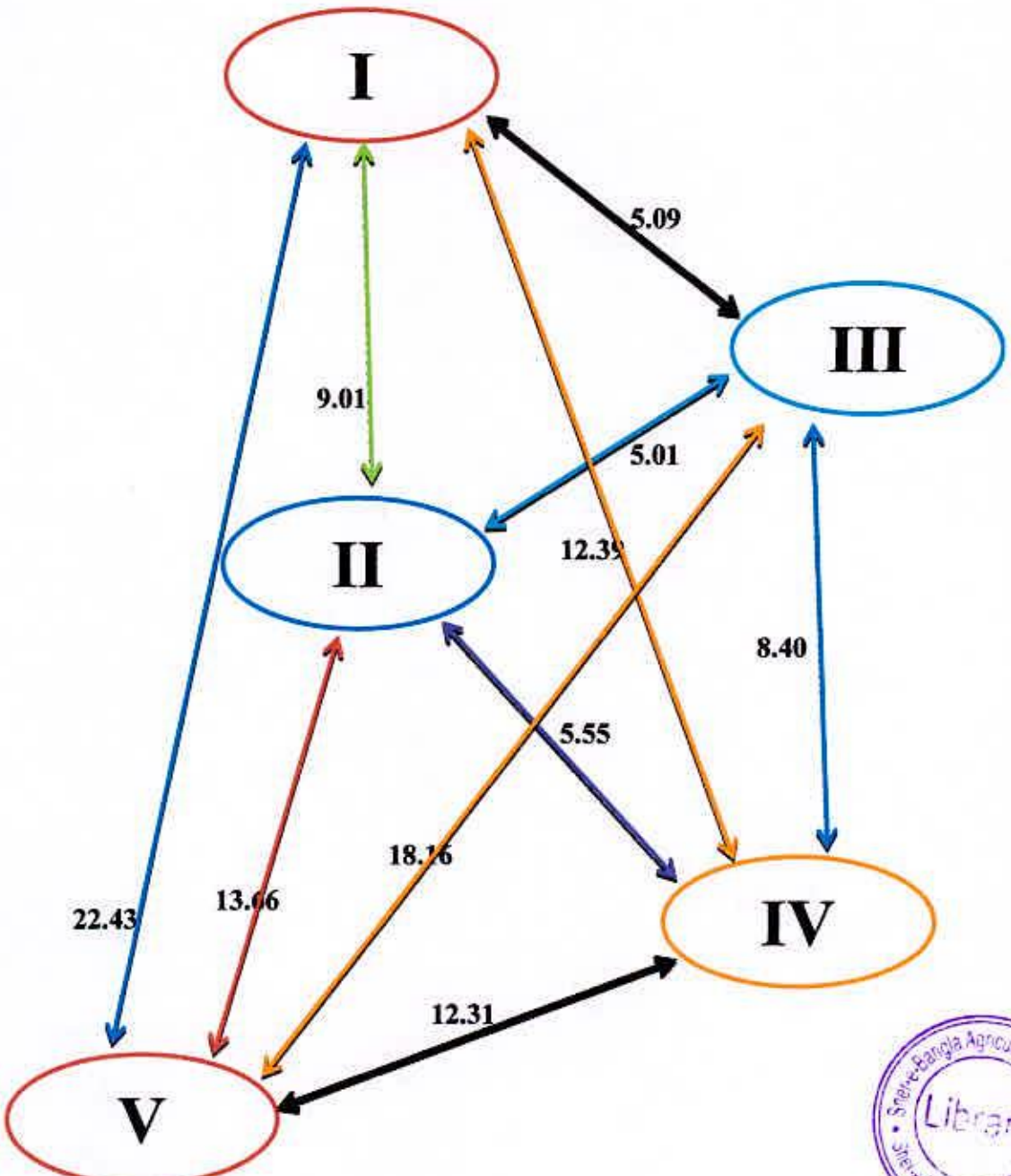
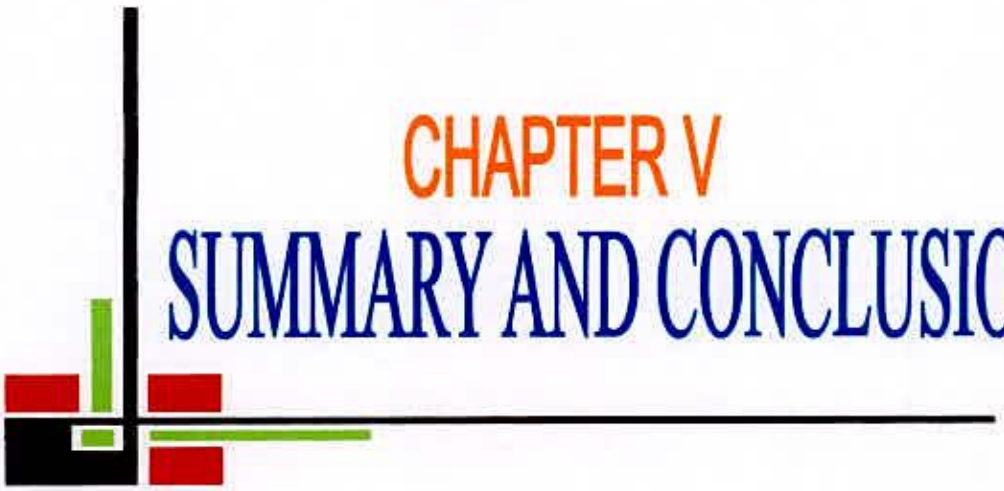


Fig. 6. Intra and inter cluster distances of 31 genotypes of *Brassica napus*.

The role of seed yield per plant in both vectors was important components for genetic divergence in these materials. On the other hand, the role of days to 50% flowering had a minor role in the genetic divergence. Islam and Islam (2000) reported days to 50% flowering, plant height, primary branches per plant and number of siliqua per plant contribute maximum in divergence in rapeseed and mustard. Begum *et al.* (2007) reported that branches per plant and number of number of seeds siliquae contributed the maximum towards divergence in the existing linseed germplasm. Choudhary and Joshi (2001) concluded that plant height, secondary branches per plant, days to flowering and 1000-seed weight contributed the maximum towards genetic divergence.

4.4.5 Selection of parents for future hybridization

Selection of genetically diverse parents is the prime task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G1 Nap 108×Nap 9908(9908) for higher seed yield per plant, and higher number of secondary branches per plant, G2 Nap 9905×Nap 0130(0130) for tallness, highest number of primary branches and the highest number of siliqua per plant, G3 Nap 9905×Nap 0130(9905) for the highest length of siliqua, G20 Nap 9905×Nap 9908(9908) for the highest number of seeds per siliqua, G28 Nap 9905×Nap 9901(9905) for short duration and early maturity. Therefore, considering group distance and agronomic performance the inter-genotypic crosses between G1 and G3, G1 and G28, G2 and G3, G2 and G28, G1 and G20, G2 and G20, G3 and G20, G28 and G20 might be suggested for future hybridization program.



CHAPTER V
SUMMARY AND CONCLUSION

Chapter-V

SUMMARY AND CONCLUSION

The present study was undertaken with 31 BC_1F_3 genotypes of *Brassica napus* L. at the Sher-e-Bangla Agricultural University Farm, Bangladesh during November 2012 to March 2013. Seeds were sown in the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, days to 50% flowering, days to 80% maturity, plant height (cm), number of primary branch per plant, number of secondary branch per plant, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g) and seed yield per plant (g) were recorded.

From variability analysis of BC_1F_3 progenies, it was observed that significant variation exist among all the genotypes used for most of the characters studied. Plant height exhibited highest in G2 Nap 9905×Nap 0130(0130) and lowest in G10 Nap 9906×Nap 205(9906). The highest number of primary branches per plant was recorded in G2 Nap 9905×Nap 0130 (0130) and lowest number was recorded in G15 Nap 9906×Nap 205 (205). The highest number of secondary branches per plant was observed in G1 Nap 108×Nap 9908(108). The minimum days to 50% flowering was found in G28 Nap 9905× Nap 9901 (9905). The lowest days to maturity was observed in G28 Nap 9905× Nap 9901 (9905).

The number of siliqua per plant showed highest in G2 Nap 9905×Nap 0130 (0130) and lowest in G18 Nap 108×Nap 2066 (2066). The highest siliqua length was recorded in G3 Nap 9905×Nap0130 (9905) and the lowest siliqua length was observed in G12 Nap 2066 × Nap0130 (2066). The number of seeds per siliqua was found highest in G20 Nap9905×Nap 9908(9908) and the lowest in G28 Nap 9905×Nap 9901(9905). The seed yield per plant was the highest in G1 Nap 108×Nap 9908(108) and the lowest observed in G27 Nap 9905×Nap 108 (108).

However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. In case of days to 80% maturity, number of primary

branches per plant, number of secondary branches per plant, number of siliqua per plant and seed yield per plant showed higher influence of environment for the expression of these characters.

On the other hand, plant height, days to 50% flowering, number of seeds per siliqua, siliqua length and 1000-seed weight showed least difference phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Number of siliqua per plant (79.48) exhibits the highest value of heritability while number of seeds per siliqua (48.91) exhibits the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed for number of siliqua per plant, plant height, number of primary branches per plant and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.

High heritability with moderate genetic advance was observed for days to 50% flowering and thousand seed weight indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for number of seeds per siliqua and siliqua length indicating that non-additive gene effects were involved for the expression of these characters and selection for such traits might not be rewarding.

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

In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per plant were found in plant height (G=0.286, P=0.198), number of primary branches per

plant (G=0.731, P=0.468), number of secondary branches per plant (G=0.839, P=0.556) and number of siliqua per plant (G=0.0.593, P=0.472). In addition, there were non-significant positive correlation with seed yield per plant was also found in days to 80% maturity (G=0.274, P=0.112) and siliqua length (G=0.149, P=0.113).

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

The genotypic correlation of number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant with seed yield per plant was positive and considerably higher in magnitude. It is mainly due to high positive direct effect and positive indirect effects of others characters and selection would be effective for this trait. The path coefficient studies indicated that plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The first three principal component axes accounted for 66.10% variation towards the divergence. Among five clusters cluster III contained maximum number of genotypes (11) while cluster V had only two genotypes. According to PCA, D^2 and cluster analysis, the genotypes grouped into four divergent clusters using Z_1 and Z_2 values obtained from principal component scores. The highest inter-cluster distance was observed between clusters I and V (22.433) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III (5.015).

On the other hand, the maximum intra-cluster distance was found in cluster IV (0.83), which contained of three genotypes, whereas the minimum distance was found in cluster V (0.00) that comprises two genotypes. Therefore, crossing between the

genotypes belonging cluster I with cluster IV, cluster II with cluster V, cluster IV with cluster V and cluster V with cluster III might produce high heterosis in respect of yield, earliness, tallness, higher number of siliqua per plant. Also the crosses between genotypes from cluster I with cluster V might produce high level of segregating population. So the genotypes belonging to cluster I and cluster IV, cluster II and cluster V, cluster IV and cluster, and cluster III and cluster V have been selected for future hybridization program.

The role of seed yield per plant in both the vectors was important components for genetic divergence in these materials. On the other hand, the role of number of seeds per siliqua had a minor role in the genetic divergence.

Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G1 Nap 108×Nap 9908(9908) for higher seed yield per plant, and higher number of secondary branches per plant, G2 Nap 9905×Nap 0130(0130) for tallness, the highest number of primary branches and the highest number of siliqua per plant, G3 Nap 9905×Nap 0130(9905) for the highest length of siliqua, G20 Nap 9905×Nap 9908(9908) for the highest number of seeds per siliqua, G28 Nap 9905×Nap 9901(9905) for short duration and early maturity. Therefore, considering group distance and agronomic performance the inter-genotypic crosses between G1 and G3, G1 and G28, G2 and G3, G2 and G28, G1 and G20, G2 and G20, G3 and G20, G28 and G20 might be suggested for future hybridization program.

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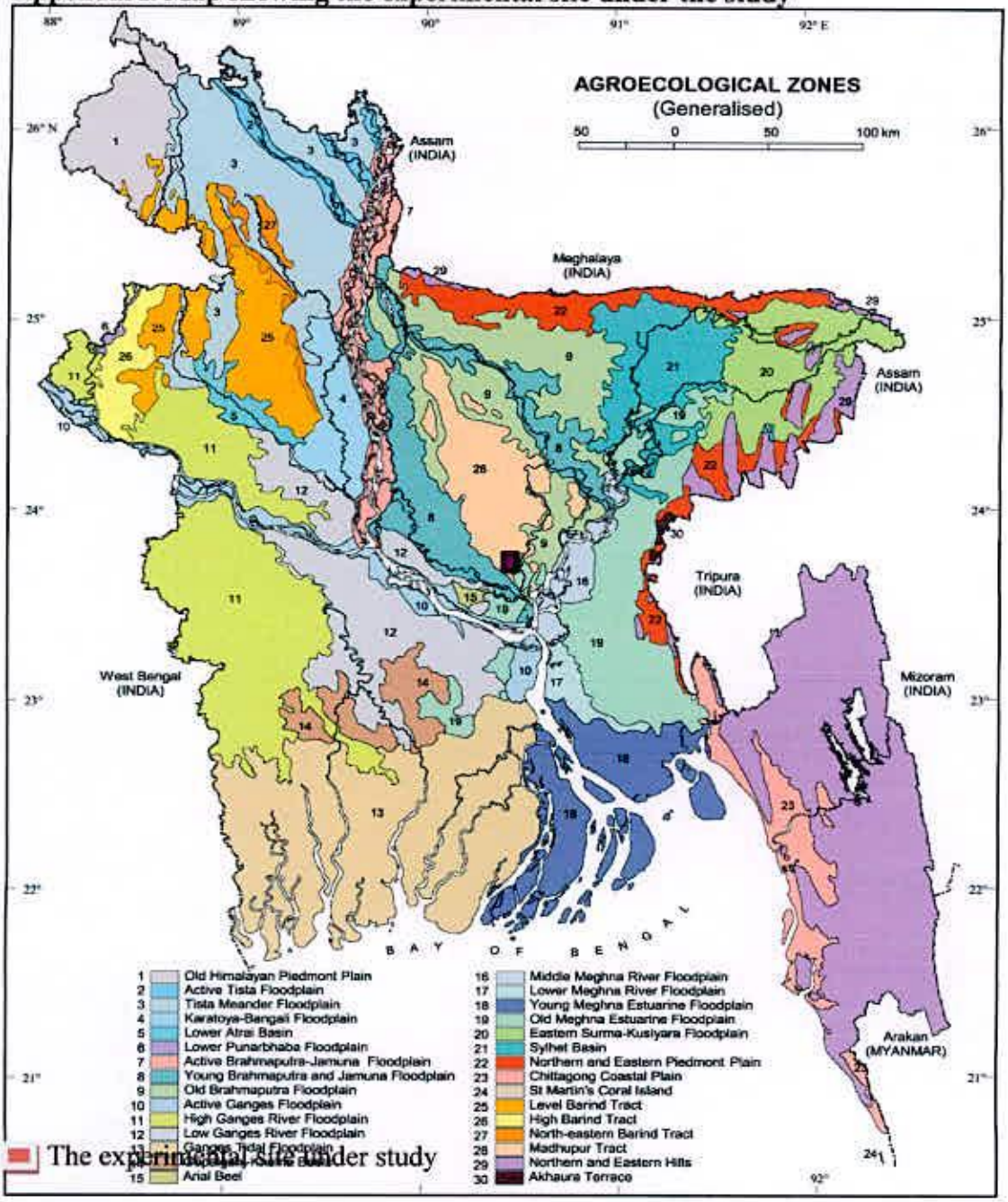
Appendix I. Map showing the experimental site under the study



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

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

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

Appendix III. Monthly average Temperature, Relative Humidity and Total Rainfall and sunshine of the experimental site during the period from November, 2012 to April, 2013

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2012	34.8	18.0	77	227	**5.8**
December, 2012	32.3	16.3	69	0	**7.9**
January, 2013	29.0	13.0	79	0	**3.9**
February, 2013	28.1	11.1	72	1	**5.7**
March, 2013	33.9	12.2	55	1	**8.7**
April, 2013	**34.6**	**16.5**	**67**	**45**	**7.3**

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

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

Genotype	PH	NPB	NSB	D50%F	NSP	DM	NSS	SL	SYP	TSW
G1 108×9908(108)	92.65	2.81	1.58	36.00	102.33	87.00	22.00	8.42	84.54	4.20
G2 9905×0130(0130)	105.83	3.05	1.46	37.00	119.51	89.33	21.99	8.37	63.01	4.78
G3 9905×0130(9905)	98.53	2.48	0.70	36.67	79.20	89.00	19.81	9.67	44.82	3.43
G4 2066×205(205)	84.69	1.62	0.18	36.00	63.25	88.67	18.59	7.32	33.22	4.27
G5 108×(0130)^2	85.69	1.62	0.65	36.00	75.32	91.33	20.93	8.37	40.06	4.63
G6 2066×0130(0130)	82.69	1.46	0.38	34.00	57.58	86.33	22.25	7.82	37.34	4.40
G7 9906×0130(9906)	87.61	2.11	0.63	36.00	67.63	90.33	19.98	7.98	44.49	4.50
G8 205×0130(0130)^2	94.61	1.91	0.78	35.00	91.90	85.67	22.85	8.46	41.95	3.90
G9 9908×0130(0130)	79.32	2.53	1.01	34.67	77.47	90.33	20.84	7.47	46.78	4.13
G10 9906×205(9906)	73.00	1.77	0.25	36.00	68.61	88.00	18.40	7.77	36.86	4.11
G11 108×205(108)	74.82	2.19	0.98	36.67	57.71	90.00	18.99	7.55	38.82	4.27
G12 2066×0130(2066)	77.40	1.58	0.53	35.00	61.42	86.67	16.33	6.77	47.07	3.51
G13 9908×108(9908)	82.73	1.44	0.35	36.00	63.62	86.33	20.85	8.34	36.87	4.66

Continued

G14 9905×9901(9901)	80.07	2.30	0.82	27.67	80.92	86.67	22.26	8.60	46.52	4.23
G15 9906×205(205)	79.96	1.14	0.33	37.00	57.08	88.33	21.88	8.59	38.91	4.34
G16 9906×2066(9906)	91.46	1.72	0.62	36.33	65.01	88.33	19.74	7.32	44.49	3.87
G17 9908×0130(9908)	96.80	2.55	0.56	37.00	75.68	87.00	23.04	8.42	39.39	3.79
G18 108×2066(2066)	88.29	1.24	0.34	37.33	52.86	90.67	22.74	7.92	39.46	4.42
G19 9901×203(9901)	91.83	2.53	1.05	35.00	73.41	88.00	20.99	7.78	41.36	4.40
G20 9905×9908(9908)	102.94	2.17	0.67	38.00	91.03	96.33	25.78	9.56	43.74	3.52
G21 108×2066(108)	97.61	2.22	0.53	35.67	62.97	92.00	21.45	7.71	39.12	3.27
G22 9906×2066(2066)	81.13	1.85	0.69	35.67	59.88	86.33	17.86	7.81	37.74	4.37
G23 9905×9908(9905)	95.79	2.02	1.15	36.00	70.75	89.33	22.32	8.98	45.54	4.20
G24 2066×205(2066)	90.60	2.03	0.82	37.00	80.72	93.00	20.90	8.40	43.52	4.20

Continued

G25 9908×2066(9908)	92.33	1.83	0.64	38.33	80.71	94.00	22.39	8.47	57.56	4.47
G26 205×0130(205)	96.48	2.33	0.67	37.00	74.36	90.67	23.01	7.50	57.34	4.29
G27 9905×108(108)	101.64	1.57	0.59	37.00	104.16	93.67	19.49	8.04	32.76	4.07
G28 9905×9901(9905)	98.39	1.43	0.47	37.00	70.56	83.00	18.84	8.33	42.21	4.10
G29 108×0130(108)	96.60	1.57	0.49	36.33	72.53	91.67	18.87	7.93	34.11	4.27
G30 108×9908(9908)	92.11	2.07	0.42	36.33	66.26	91.67	18.38	7.84	47.96	4.26
G31 9906×9901(9901)	90.47	2.54	0.86	37.33	86.03	89.67	16.76	7.97	53.81	4.16
Mean	89.81	1.99	0.68	36.03	74.53	89.33	20.66	8.11	44.56	4.16
Min.	**73.00**	**1.14**	**0.18**	**27.67**	**52.86**	**83.00**	**16.33**	**6.77**	**32.76**	**3.27**
Max.	**105.83**	**3.05**	**1.58**	**38.33**	**119.51**	**96.33**	**25.78**	**9.67**	**84.54**	**4.78**

PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, D50%F = Days to 50% flowering, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, DM = Days to 80% maturity, SL=Siliqua length, TGW = Thousand Grain Weight (g), SYP=Seed yeild per plant.

Appendix V. Principal component score 1 & 2.

Genotypes	Z_1	Z_2
1	-40.730	26.869
2	-51.112	-1.565
3	-6.966	-4.865
4	16.001	-4.698
5	2.436	-2.270
6	19.789	1.168
7	6.616	2.390
8	-15.245	-7.899
9	0.060	6.131
10	13.876	2.763
11	21.628	5.732
12	14.557	11.168
13	14.848	-0.606
14	-2.846	5.356
15	20.378	3.579
16	7.659	1.338
17	-1.241	-7.789
18	20.863	0.829
19	1.617	-3.249
20	-18.556	-11.277
21	9.320	-6.027
22	18.321	1.789
23	0.751	-1.190
24	-5.267	-2.979
25	-11.614	7.974
26	-7.383	7.589
27	-24.466	-22.395
28	1.772	-4.568
29	3.661	-11.822
30	4.897	3.431
31	-13.626	5.094