GENETIC DIVERSITY IN RAPESEED MUSTARD (*Brassica rapa* L.) GENOTYPES

BY

MONIKA SONOM

REGISTRATION NO. 06-02059

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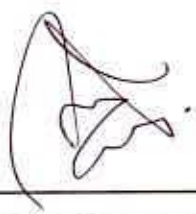

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Supervisor

Dr. Mohammad Saiful Islam
Professor
Co-supervisor

Prof. Dr. Md. Sarowar Hossain
Chairman
Examination Committee

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department Of Genetics and Plant Breeding
Sher-e Bangla Agricultural University
Dhaka-1207, Bangladesh
Mob: +8801552467945
e-mail:ipbscfc2009@gmail.com

CERTIFICATE

This is to certify that thesis entitled, **"GENETIC DIVERSITY IN RAPESEED MUSTARD (*Brassica rapa* L.) GENOTYPES"** 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 **MONIKA SONOM**, Registration NO. 06-02059 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2014
Place: Dhaka, Bangladesh

Prof. Dr. Md. Shahidur Rashid Bhuiyan
Supervisor

DEDICATED

TO

MY PARENTS

ACRONYMS

Abbreviation	Full word
%	Percent
°C	Degree Celsius
@	At the rate
σ^2p	Phenotypic variance
σ^2g	Genotypic variance
σ^2e	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
cm.	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

Abbreviation	Full word
J.	Journal
Kg	Kilogram
m	Meter
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
PHT	Plant height
NPB	Number of primary branches per plant
NSB	Number of secondary branches per plant
NSP	Number of siliqua per plant
SL	Siliqua length
D50%F	Days to 50% flowering
D50%M	Days to 50% maturity
NSS	Number of seeds per siliqua
TSW	Thousand seed weight
YPP	Yield per plant

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The Author

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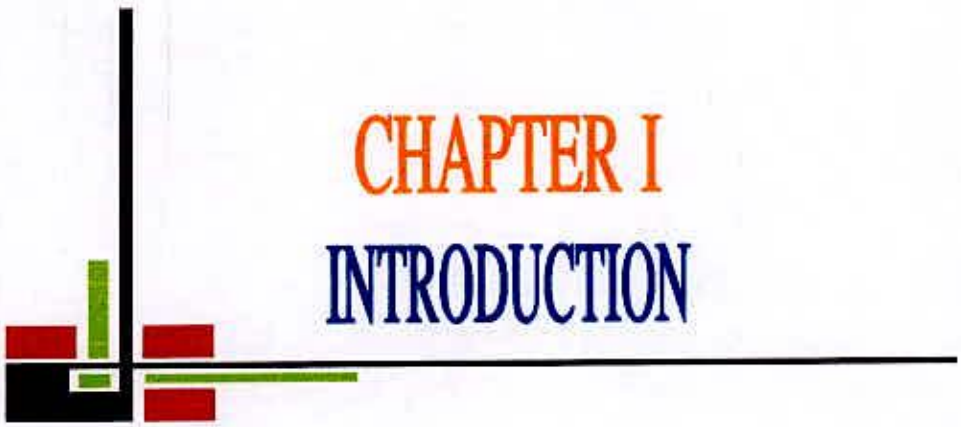
ABSTRACT

BY

Monika Sonom

An experiment was carried out with 51 genotypes of *Brassica rapa* including two commercially cultivated varieties as cheeks to study their inter-genotypic variability, correlation, path co-efficient and genetic divergence considering 10 different morphological characters at the experimental farm of SAU, Dhaka during November 2012 to February 2013. 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 low genetic advance in percent of mean were obtained for number of seeds per siliqua, seed yield per plant, number of secondary branches per plant and days to 50% flowering. Highly significant positive association of seed yield per plant was observed with number of siliqua per plant, thousand seed weight,number of seeds per siliqua, number of primary branches per plant.Path analysis showed that , yield per plant had the highest direct effect on number of siliqua per plant, number of seeds per siliqua and thousand seed weight. By using different multivariate analysis techniques all the genotypes were grouped into five cluster. PCA, PCO, CVA analysis gave almost similar result. Cluster III had maximum (19) and Cluster I had minimum (2) number of genotypes. The highest inter-cluster distance was observed between cluster I and cluster V (10.43). The highest intra cluster distance was cluster V (0.459). The lowest intra cluster distance was cluster I (0.0). Moderate or intermediate inter cluster distance was found between cluster I and cluster IV (4.47) and cluster III and cluster V (4.86). Considering the magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster mean for different characters and field performance the genotypes G-35 and G-47 from cluster III and G-I, G-18, G-41 and G-46 from cluster V would be suitable for highest yield per plant for future hybridization programme.Involvement of such diverse genotypes in crossing program produces desirable segregates. So, divergent genotypes are recommended to use as parent in hybridization program.



CHAPTER I

INTRODUCTION

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INTRODUCTION

Mustard has been grown the Indian sub-continent for hundreds of years as an oil seed crop (Labana and Gupta, 1993). Rapeseed mustard crop account for almost 14 percent of the edible vegetable oil supply of the world demand (Kour and Singh 2004). The annual production of rapeseed mustard in our country is 203 thousand metric tons from 578 thousand acres of land during 2008-09 (BBS, 2010). The seed of rapeseed mustard contain 42% oil and 25% protein (Khaleque, 1985). Its oil is mainly used for food cooking purpose its oil and fat are not only the source of energy but also contain fat-soluble vitamins A, D, E, and K (Mahmud *et al.*, 2008). The oil cake is used as a very good animal feed as well as fertilizer for better improvement of soil status because of its high biological protein value as well as source of calcium and phosphorus.

Brassica is a genus under the family Brassicaceae contributes approximately 10% of the world's vegetable and 12% of the worldwide edible oil supply (USDA, 2014). *Brassica* can be grouped into rapeseed, mustard and cole. The group includes diploid *brassica rapa* (AA, 2n = 20) that is also known as turnip and amphidiploid *Brassica napus* (AACC, 2n = 38) (yarnell *et al.*, 1956). It is the top ranking oil seed crop in Bangladesh that covers about 60% of the total acreage land (BBS, 2010). The oil seed production in world is 199.3 million ton. The utilization of oil seed in Bangladesh is 102.7 million ton where 44 million ton is important (FAO, 2013). Because of their ability to germinate and grow at low temperature they can grown in the cooler agricultural regions and at higher elevations, as well as winter crops in the temperate zones.

Recent data indicate that oil crops produces 0.16 million tons of edible oil in every year as against the total requirements of 0.5 million tons for a population of 130 million in Bangladesh (Anonymous 1999). The share of rapeseed and mustard was 253640 tons, which comes to 52 percent of the total edible oil production (Anonymous, 2007). The yield of rapeseed and mustard is generally low in

Bangladesh as compared with the world average. The present seed yield per hectare of mustard in Bangladesh is far below the level attained in the developed countries of the world (BBS, 2008). It occupies first position in oil crops with cultivated area 252238.13 ha which produced 0.246494 million tons seed and average yield was 0.997 t / ha during 2010-2011 (BBS, 2011). In Bangladesh mustard occupies the first position in respect of area and producing among the oil crops grown (Anonymous, 2008). *Brassica rapa* is well suited in cropping pattern with rice variety i.e Aman-Mustrad-Boro as the growing period of this mustard is reduced from 0.784730 (Karim *et al.*,2014). But the area and production has been increased in 2012-2013-2014 as 0.518 million hectare and 1.10 ton hectare to 0.532 million hectare and 1.12 ton per hectare due to high yielding varieties of mustard (MOA, 2014).

The targeted yield of oil seed in 2015-2020, 2020-2025 and 2025-2030 is 1730, 2141 and 2572 kg / ha in Bangladesh that is now 1186 k g / ha only. In present, there are total 14 varieties of *B. rapa* in the country. Among them 8 are released from Bangladesh Agricultural Research Institute (BARI) , 3 from Institute of Nuclear Agriculture (BINA) , 2 from Sher-e-Bangla Agricultural University (SAU) and 1 from Bangladesh Agricultural University (BAU) (Rahman and Chowdhury, 2010).

In Bangladesh, *Brassica rapa* is the main oil yielding species of *Brassica* (FAOSTAT, 2013). Though the local cultivars of *Brassica juncea* and *Brassica napus* are high yielding, they are not short durable. That's why *Brassica rapa* is grown widely in the country (Islam, 2013). The yield potentialities of the commonly used varieties are in stagnant position (Sathi *et al.*, 2012). Farmers still use the low yielding varieties with smaller seed size (2-2.5 g in thousand seed wt. (Farhana, 2012). At present the leading short duration *Brassica rapa* genotype is Tori-7 in Bangladesh. But it has lower yield like 1.1-1.3 t / ha (Karim *et al.*,2014).

Hybridization is one of the major tools for achieving variability aiming at improvement of a crop. Before hybridization genetic diversity of the existing varieties or entries needs to be known. Information about the relationship among elite breeding populations and the genetic diversity in available germplasm is important for the optimal design of any breeding program. This helps to choice desirable parents establishing new breeding population. Besides better knowledge on genetic diversity

or genetic similarity could help to sustain long term selection gain (Chowdhury *et al.*, 2002).

Information on genetic variability is necessary for initiating a successful breeding program. Determination of correlation co-efficient between the characters has a considerable importance in selecting breeding materials. The path co-efficient analysis gives more specific information on the direct and indirect influence of each of the component characters upon seed yield (Behl *et al.*, 1992)

Genetic diversity arises either due to geographical separation or due to genetic barriers to cross ability. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination in the segregating generations. Selection of parents based on genetic divergence has become successful in several crops (Ashana and pandey,1980 ; Ananda and Rawat, 1984).

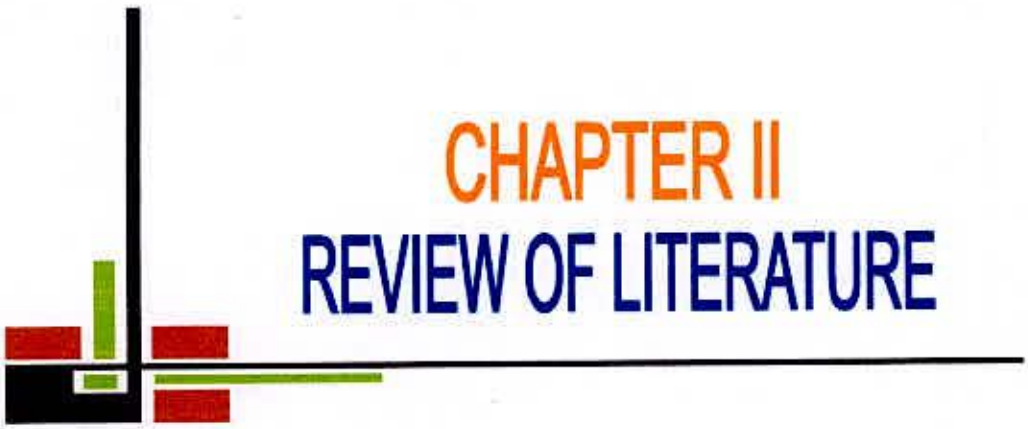
According to Sharma and Jana (2002), assessment of genetic variation in a species is a prerequisite for initiating an efficient breeding program , as it provides a basis for tailoring desirable genotypes.

Genetic diversity within a population depends on the number and frequency of all loci and the genetic constitution of the population (Crossa *et al.*, 1993).Genetically diverse parents are likely to segregates and or to produce high heterotic F_1 and broad spectrum of variability in segregating generations (Arunachalam, 1981).

Objectives:

The present research work was undertaken with the following objectives:

1. To analyze the genetic diversity of different genotypes in respect of their yield contributing characters.
2. To study the relationship among the different traits and their contribution to the yield and
3. To identify divergent parents for hybridization program which could provide superior segregates.



CHAPTER II
REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

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

2.1 Variability, heritability, genetic advance and selection in *Brassica* species

2.2 Correlation among different characters

2.3 Path co-efficient analysis

2.4 Genetic diversity

2.1 Variability, heritability, genetic advance and selection in *Brassica* species

Genetic variability is a prerequisite for initiating a successful breeding program aiming to develop high yielding varieties. A good number of literatures concerning the variability in the *Brassica* species are availables. Some of those are presented here.

Iqbal *et al.*, (2014) conducted an experiment with ten indigenous variety associated with eight important yield contributing characters of *Brassica rapa* in Pakistan to study variability. The traits showed highly significant differences in almost all traits. The highest heritability with higher genetic advance was reported in plant height while the seed per siliqua was found medium heritability along with lower genetic advance. It was observed that indigenous accessions had great proportion of genetic variability.

Muhammad *et al.*, (2014) studied with four parental genotype along with twelve F_2 generation of *Brassica napus* and reported that days to 50% flowering were significantly different at 5 % level of significance. Plant height and pod length showed high heritability and days to 50 % flowering showed moderate heritability.

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

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

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

Khan *et al.*, (2013) studied twenty genotypes of *Brassica napus* with a cheek variety and it revealed higher broad sense heritability in pods in main receme, seed per siliqua , primary branches per plant , seed yield per plant, seed yield per plant and number of siliqua per plant. Genetic variances were higher than the environmental variances for all traits.

Khan *et al.*, (2013) evaluated thirteen F_7 segregating lines and two parents of *Brassica rapa* to study variability, heritability and genetic advance. The result revealed that except thousand seed weight, significant variation was presented among all the genotypes for all the characters .Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliqu in followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliqua, and siliqua length showed high

heritability along with low genetic advance in percent of mean. Considering important performances, the genotypes G-15, G-19, G-1, G-3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program.

Ahmad *et al.,* (2013) studied thirty five advanced mutant lines along with a cheek variety of *Brassica napus* called Abasin-95 for variability analysis and reported that seed yield and days to flowering showed high genetic variability. High heritability and advance was recorded for seed yield. The mutant lines OA5, G1 and 06 showed their superiority in high seed yield, thousand seed weight and earliness in flowering.

Ali *et al.,* (2013) conducted an experiment with thirty lines of *Brassica carinata* and reported that PCV and GCV ranged from 4.92-48.24 % and3.2-38.1 % respectively. The highest heritability values were recorded for pod length (0.83) followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield / plant and pods on main raceme.

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

Roy *et al.,* (2011) conducted an experiment on rapeseed mustard (*Brassica spp.)* and studied variability and heritability. The result revealed that significant varietal difference except the number of siliqua on main recyme. The PCV and the GCV was high in secondary branches per plant and number of siliqua per plant. High heritability along with high genetic advance as percent of mean was reported in plant height, seed yield, secondary branches per plant, siliqua per plant and seeds per siliqua.

Tahira *et al.,* (2011) conducted an experiment with ten wide genetic ranged variety of *Brassica juncea* to study heritability in broad sense and showed siliqua length, plant height and seed yield had high values.

Patel (2011) experimented with three high yielding varieties and two very low quality varieties and their six generation cross product of *Brassica napus.*The result showed that the heritability in broad sence with high to moderate genetic advance was found in thousand grain weights, seed yield per plant. Moderate to high heritability

associated with low genetic advance was recorded in days to maturity and days to flowering.

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

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

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

A field experiment was conducted by Jahan (2008) to study on inter-genotypic variability and genetic diversity in 10 F_4 lines obtained through intervarietal crosses along with 8 released varieties of *Brassica rapa* during November 2007 to March 2008. Significant variation was observed among all genotypes for all the characters studied. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of secondary branches / plant, siliqua / plant, yield / plant whereas days to maturity showed very low GCV. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50 % flowering indicating that this trait was under additive gene control and selection improvement for this trait would be effective.

An experiment was carried out Mahmud (2008) with 58 genotypes of *Brassica rapa* to study inter genotypic variability. Significant variation was observed among all the

genotypes for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in percentage of mean were obtained for days to 50 % flowering, number of secondary branches per plant, seeds per siliqua and siliqua length.

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

Uddin (2008) conducted an experiment to study the variability among seven parental genotypes and their twenty one F_2 progenics of *Brassica rapa* .He found that the phenotypic variance were than more genotypic variance. High GCV was observed in secondary branches per plant. High heritability with high genetic advance was observed in the number of secondary branches per plant.

Aytac *et al.*, (2008) studied on six genotypes of spring rape seed and found highest genotypic and phenotypic variances in seed yield per plant. High heritability was found with range 87 % to 99 %. Plant height and siliqua length had high heritability and low genetic advance. Seed yield per plant, seed yield, siliqua per plant showed high heritability with high genetic advance.

Parveen (2007) conducted an experiment to study the variability in F_2 progenies of the inter-varietal crosses of seventeen genotypes of *Brassica rapa*. Significant variations among different genotypes were found. High heritability coupled with high genetic advance in percent of mean was observed in number of primary branches per plant and branches per plant.

Rashid (2007) studied variability of 40 oleiferous *Brassica* species. Result revealed that genotypes showed wider variation for morphological characteristics and thus were categorized under three cultivated species- *B. rapa, B. napus* and *B. juncea* considering genetic parameters. High GCV value was observed for days to 50 % flowering, days to maturity, plant height and number of siliqua / plant.

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

Niraj and Srivastava (2004) studied on variability and character association of twenty one genotypes of *Brassica juncea*. The highest PCV (phenotypic co-efficient of variation) was found in thousand seed weight. Days to 50% flowering, days to maturity and plant height showed high heritability.

Katiyar *et al.*, (2004) studied on variability for the seed yield in ninety intervarietal crosses of *Brassica campestris* . Existence of significant variation among parents and crosses indicated the presence of adequate genetic variance between parents which reflected in differential performance of individual cross combinations.

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

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

2.2 Correlation among different characters

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

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

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

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

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

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

Khayat *et al., (*2012) reported high positive correlation between plant height and yield per plant , siliqua per plant of *Brassica napus.*

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

Tahira *et al.,* (2011) conducted an experiment with ten wide genetic ranged varieties of *Brassica juncea* and the result revealed correlation among the different characters studied. The highest phenotypic correlation was found between plant height, branches per plant, siliqua length and seeds per siliqua. Seed yield was only significantly correlated with plant height and siliqua length. Plant height, branches per plant, siliqua length and thousand seed weight were genotypically correlated with yield per plant .A highly significant and strong positive genetic relation was observed between plant height and branches per plant, siliqua length and seed per siliqua.

Belele (2011) studied with different yield treating characters of *Brassica carinata* and observed that genotypic correlation coefficient of seed yield per area had direct positive correlation with seed per pod seed per plant.

Afrin *et al.,* (2011) studied on *Brassica napus* and found positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliqua per plant. Highest significant positive correlation was found between days to 50 % flowering and plant height.

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

Alam (2010) conducted an experiment by using twenty six F_4 populations of some inter-varietal crosses of *Brassica rapa* to study correlation and it revealed that yield per plant and significant positive association with plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua at both genotypic and phenotypic level.

Gangaper *et al.,* (2009) evaluated forty-six genotypes of Indian mustard (*Brassica juncea*) under controlled and uncontrolled (disease and pest) condition and studied correlation and the result revealed that seed yield per meter was highly and significantly correlated with seed yield per plant, number of siliqua per plant number

of primary and secondary branches per plant, yield per plant, thousand seed weight, number of seeds per siliqua at genotypic and phenotypic level under both protected and unprotected conditions.

Uddin (2008) conducted an experiment to study the correlation among seven parental genotypes and their twenty one F_2 progenies of *Brassica rapa* and found positive significant association in seed yield per plant with number of primary branches per plant , number of secondary branches per plant and number of siliqua per plant.

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

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

Parveen (2007) studied F_2 population of *Brassica rapa* and resulted non-significant positive correlation in yield per plant with plant height, number of secondary branches per plant, day to 50% flowering ,number of siliqua per plant, length of siliquaand number of seed per siliqua.

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

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

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

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

Zahan (2006) studied correlation and observed highly positive association in yield per plant with plant height, length of siliqua, siliquae per plant and seed per siliqua where insignificant negative association with days to 50 % flowering and days to maturity.

Afrose *et al.,(*2004) studied correlation and reported that seed yield per plant had positive significant with number of primary branches per plant and number of siliqua per plant.

Mahak *et al.,* (2004) conducted an experiment and studied correlation for 8 quantitative characters. Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000 seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard.

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

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.

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

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

Uddin *et al., (*2013) conducted an experiment with seven parental and twenty one F_2 progenies of *Brassica rapa* to study path coefficient and reported that days to 50 % flowering, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seed per siliqua and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association.

Tahira *et al.,* (2011) conducted an experiment with ten wide genetic ranged variety of *Brassica junce* to study relationship among the characters. The result reported that plant height and siliqua length had positive direct effect on seed yield per plant while positive indirect effect on seed yields per plant. Siliqua length contributed negative indirect effect through plant height, seed per siliqua and thousand grain weight.

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

Singh (2010) studied sixty two F_1 and twenty four parental lines of *Brassica juncea* and the path analysis revealed that highest positive direct effect was found in secondary branches per plant followed by plant height and seeds per siliqua on seed yield per plant while highest negative effect was in the plant height on seed yield per plant.

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

flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plants.

Gangapur *et al.*, (2009) evaluated forty-six genotypes of Indian mustard (*Brassica juncea*) under controlled (disease and pest) condition and studied path coefficient analysis. The number of siliqua per plant showed highest positive direct effect on seed yield in both protected and unprotected conditions.There were direct and indirect effect of number of primary branches per plant and plant height in both phenotypically and genotypically under both controlled and uncontrolled condition.

Uddin (2008) conducted an experiment to study the correlation among seven parental genotypes and their twenty one F_2 progenics of *Brassica rapa* and studied path co-efficient analysis. He observed that the seed yield per plant had positive direct effect on days to 50 % flowering, number of primary branches per plant, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seed per siliqua and thousand seed weight while days to maturity and plant height had direct negative effect on yield per plant.

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

Mahmud (2008) carried out an experiment with fifty eight genotypes of *Brassica rapa.* Path analysis showed highest direct effect of yield per plant was followed by number of primary branches per plant, number of siliqua per plant, number of secondary branches per plant and number of seed per siliqua.

Gangapur (2008) reported on his path analysis at *Brassica juncea* that days to maturity and secondary branch per plant had direct effect on seed yield.

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

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.

Parveen (2007) conducted an experiment 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.

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

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

2.4 Genetic diversity

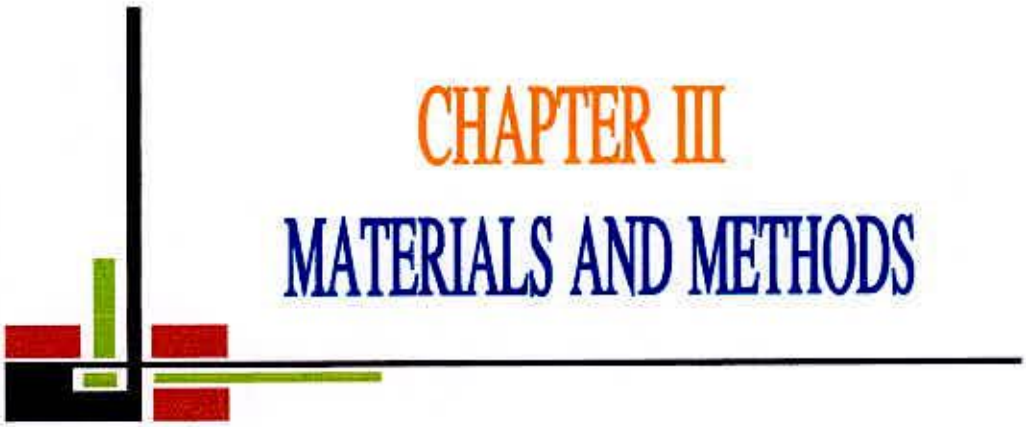
Zahan *et al.*, (2008) studied genetic divergence among 41 genopes of rapeseed and mustard by using D^2 analysis. In each case of three species *B. napus, B. rapa* and *B. juncea*, the genotypes under study fell into six cluster. The inter -cluster distances were larger than the intra-cluster distances in each species suggesting wide genetic diversity among the genotypes of each species. The characters days to maturity, plant height and number of siliqua per plant made the greatest contribution towards genetic divergence.

Islam *et al.*, (2007) conducted an experiment on analysis of genetic divergence for quality improvement in 22 rapeseed and mustard by using principal component analysis and non-hierarchical Euclidean cluster analysis. Twenty-two *Brassica* genotypes were grouped into four clusters. The highest inter-cluster distance was observed between the clusters I and III while the lowest value was between I and II. The highest intra-cluster distance was observed in clusters I and the lowest intra-cluster value was observed in cluster II. The role of oleic acid and erucie acid indicate the important components of genetic divergence in the present material.

Sial *et al.*, (2004) performed an analysis of genetic divergence for quality improvement in 144 toria (*Brassica rapa* L. sptoria). They grouped 144 toria into six clusters in respect of major fatty acids. The distribution pattern indicated that cluster I, III and IV contained eight and cluster II contained four genotypes. The two characters oleic acid and erucic acid contributed maximum to the divergence in *Brassica* species (*Brassica rapa* L. sp. *totia*). Divergence in the present material due to these two characters will offer a good scope for improvement of oil quality through rational selection of parents for producing heterotic hybrids.

Sen *et al.*, (2002) carried out an investigation to assess genetic divergence, morphological and quality attributes in 12 accessions of each of three *Brassica* species viz, *B. juncea, B. napus* and *B.carinata.* The inter species variation was higher than inter variety variability. The range of variation was the highest in *B. juncea* followed by *B. napus* and *B. carinata.*

Choudhary and Joshi (2001) studied genetic diversity among 88 entries including eighty F_4 derivatives i.e. 20 each selected from *Brassica* crosses viz, *B.juncea* × *B.napus,B.juncea*×*B.*rapavar.*toria,B.juncea*×*B.rapa*var. yellow sarson and *B.tournefortii* × *B.juncea* and eight parent genotypes were assessed through multivariate analysis and reported significant differences among the family groups as well as within the family were recorded for the trait that were studied. The multivariate (D^2) analysis revealed enormous diversity among inters specific cross derivatives. They also calculated genetic distances 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. They reported that derivatives selected from cross of diverse parents revealed greater diversity. 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. They also reported that the traits namely, plant height, secondary branches per plant, days to flowering and 1000 seed weight were contributed maximum towards genetic divergence.



CHAPTER III

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site

The present experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during November, 2012 to February, 2013. The location of the experimental site was situated at 23°74′N latitude and 90°35′E longitudes with an elevation of 8.6 meter from the sea level.

3.2 Soil and Climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agro-ecological 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 iii). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix iv).

3.3 Plant materials

A total number of 51 (fifty one) materials were used in this experiment where seven (7) were parents, forty four (44) were F_1 to F_{11} segregating generations. All the Materials were collected from Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The materials used in that experiment is shown in Table-1

Table 1: List of *Brassica rapa* genotypes used in the experiment

SL.No.	Designation	F_1 to F_{11} population
1	G-1	BARI 9×BARI6 F_{11}
2	G-2	BARI 9×BARI 6 Yellow F_{11}
3	G-3	BARI 9×F_6F_{11}
4	G-4	BARI 9×BARI 6 Special Early F_{11}
5	G-5	BARI 9
6	G-6	BARI 9×BAR I6 $F_{11}S_6$
7	G-7	BARI 9× F_3F_{11} Yellow S_3
8	G-8	BARI 9×BARI 6 F_{11} S_{18}(Brown)
9	G-9	BARI 9 F_{11} Selection
10	G-10	BARI 9×F_6 F_{11} Medium
11	G-11	TORI 7×BARI 9 F_{11}
12	G-12	TORI 7×BARI 6 F_3
13	G-13	TORI 7×SAU 1F_3
14	G-14	TORI 7×BARI 6 F_{11} S_{22}
15	G-15	TORI 7×SAU 1 F_{11}
16	G-16	TORI 7
17	G-17	TORI 7×BARI 6 F_{11} Early
18	G-18	TORI 7×BARI 6 F_{11}
19	G-19	BARI 6×SAU 2
20	G-20	BARI 6×TORI 7 F_{11}
21	G-21	BARI 6×SAU 3 F_3
22	G-22	BARI 6×SAU 2 F_3
23	G-23	BARI 6×TOR7 S_3 F_{11}
24	G-24	BARI 6×SAU 1 F_3
25	G-25	BARI 6
26	G-26	SAU 1×TORI 7 F_3
27	G-27	SAU 1×BARI 6 F_3
28	G-28	SAU 2×BAR6 F_3
29	G-29	SAU 3×SAU1 F_3 S_5

30	G-30	SAU 1×SAU 2 F_3
31	G-31	SAU1 F_3
32	G-32	SAU 1
33	G-33	SAU-2
34	G-34	SAU 3
35	G-35	SAU 1×SAU 2
36	G-36	SAU 1×BARI 6
37	G-37	SAU 3×SAU1 F_3
38	G-38	SAU2×BARI6 F_3 S_{17}
39	G-39	SS_{75}×TORI-7 F_{11}
40	G-40	BARI15×SS_{75} F_5
41	G-41	BARI15×SS_{75} F_3(Late)
42	G-42	BARI15×BARI6 F_3
43	G-43	BARI 15×SAU 2 F_3
44	G-44	BARI 15×SAU 2
45	G-45	BARI 15×SAU3 F_3
46	G-46	BARI15
47	G-47	BARI 15×SAU 1 F_3
48	G-48	BARI 15×TORI 7 F_3
49	G-49	BARI 15×BARI9 $F_{11}S_6$
50	G-50	F_6×BARI9 F_3
51	G-51	F_6×BARI9 S_4 F_3

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. The initial field view of the experiment is presented in plate 1.

Plate 1: The initial field view of the experiment

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tones of Cowdung, 250 kg Urea, 175 kg Triple Super Phosphate (TSP), 85 kg Muriate of Potash (MOP), 250 kg Gypsum, 3 kg Zinc oxide and Boron 1 kg per hectare. The half amount of urea, total amount of Cowdung, TSP, MOP, Gypsum, Zinc Oxide and Boron was applied during after 25 days of sowing.

3.4.3 Experimental design and layout

Field layout 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 37m × 11m = $407m^4$. Each replication size was 37m× 2.7m, and the distance between replication to replication was 1m. The spacing between lines to line was 30 cm. Seeds were sown in lines in the experimental plots on 15 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.

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 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 @ 2m / liter of water was applied. The insecticide was applied in the afternoon.

3.4.5 Crop harvesting

Harvesting was done from 4th to 15th 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 (10) plants were selected at random from of the parental line and F_{11} 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

3.4.6 Data collection

For studying different genetic parameters and inter-relationship ten characters were taken into consideration. The data were recorded on randomly ten selected plants for each of the parental line and F_1 to F_{11} progenies 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 from the base of the plant to the tip of the longest inflorescence. Data were taken after harvesting.

iv. Number of primary branches / 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/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 siliqua/plant: Total number of siliqua of each plant was counted and considered as the number of siliqua/ 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 siliqua.

viii.Number of seeds /siliqua: Well filled seeds were counted from ten representative siliqua which was considered as the number of seeds/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 weighted 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 (1959).

a.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 genotype

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,

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

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

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

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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{X}$ = Population mean

iii) Estimation of heritability:

Broad sence 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

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic 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).

Genetic Advance inpercentage of mean $=\frac{GeneticAdvance}{\bar{X}}\times 100$

vi) Estimation of simple correlation co-efficient: Simple correlation (r) was estimated from the replicated data with the help of following formula (Singh and Chaudhary, 1985).

$$r=\frac{COV_{xy}}{\sqrt{Vx.Vy}}$$

Where,

COV_{xy} = Covariance of x and y traits

V_x = Variance of x traits

V_y =Variance of y traits

vii) Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) 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 and indirect effect of the correlated characters, say, xl, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yxl}=P_{yxl}+P_{yx2}r_{xlx2}+P_{yx3}\,r_{x1x3}$

$r_{yx2}= P_{yxl}r_{x1x2}+P_{yx2}+P_{YX3}\,r_{x2x3}$

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

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

Total correlation, say between x_1 and y is thus partitioned follows:

Pyxl = The direct effect of x1 via x_2 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x_2 on y.

$P_{yx3}r_{x1x}$ = The indirect effect of x1 via x_3 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):

$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots\ldots + r_{12.y}P_{12.y})$

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

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

$r_{1.y}$ = Correlation of the i^{th} character with yield y.

viii) Estimation of diversity:

A. Principle Component Analysis (PCA)

Principle Component Analysis (PCA), one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from sum of squares and product matrix for the characters. Therefore, principle component were computed from the correlation matrix and genotypes scores obtained from the first components (which has the property of accounting for the maximum variance) and succeeding components with latent roots greater than 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. Principle Coordinate Analysis (PCO)

Principal Coordinate Analysis (PCO) is equivalent to Principal Component Analysis (PCA) 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.Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering was done using non-hierarchical classification. Starting from the initial classification of the genotypes into required groups, the algorithm repeatedly transfer genotypes from one group to another so long as such transfers improve the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm swiches to a second stage which examines the effect of swapping two genotypes of different classes and so on.

D. Canonial Variate Analysis (CVA)

Using canonical vector analysis 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. Thus, in this analysis a series of orthogonal transformations sequentially maximizing the ratio of the among groups to the with group variations.

E. Computation of Average Intra-cluster Distances

When the cluster were formed, 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 genotypes included in the cluster. The square root of the average D^2 values represents the distances (D^2) within cluster.

F.Cluster Diagram

Cluster diagram was drawn using the intra and inter cluster distances. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among 51 materials of *Brassica rapa* genotypes and also to study the correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different characters such as days to 50 % flowering, days to 50 % maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, total number of siliqua / plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and yield per plant (g). The data were statistically analyzed and thus obtained results are described below under the following heads:

4.1. Variability study in *Brassica rapa*

4.1.1.Variability among the genotypes

Plant height (cm)

The highest plant height was observed in BARI 9 × BARI 6 $F_{11}S_6$ (120.0 cm) followed by BARI 6 × SAU 2 F_3 (119.20cm), BARI 6× SAU 1 F_3 (117.77cm) where as lowest plant height was observed in Tori×BARI6 F_3 (87.0 cm) (Table 2). Plant height showed phenotypic variance (55.45) and genotypic variance (41.00) with relatively high differences between them which indicating large genetic influence on this trait (Table 3). The higher PCV (7.13) than the GCV (6.13) from Table 3.gave an information that there were much variation among the genotypes in case of plant height. There was less environmental effect as the ECV (3.64) was lower than the GCV. Jahan (2008) found low GCV (5.73) and high PCV (8.19). Low PCV and GCV were found in Ghosh and Gulati (2001).

Number of primary branches per plant

Among the 51 genotypes the highest number of primary branches / plant was observed in Tori 7 × BARI 6 F_{11} (7.03) whereas the lowest number of primary branches / plant was observed in BARI 9× BARI 6 Special Early F_{11} (3.40). The number of primary branches / plant in BARI 9× BARI 6 F_{11}, BARI 15×SAU 2 F_3,

SAU 2× BARI 6 F_3, SAU 1× BARI 6 F_3 was observed 6.27, 6.03, 5.87 and 5.50 respectively (Table 2). Number of primary branches per plant showed low differences between phenotypic variance (0.60) and genotypic variances (0.48) indicating higher environmental influence on this character (Table 3).The PCV and GCV was 16.51 and 14.78 respectively which stated that the existence of inherent variability among the population with the possibility of high potential for selection. As high ECV (7.37) was presented indicated that there were high environmental influence the character (Table 3) .High PCV (20.28) and low GCV (4.92) was found by Aktar (2010).

Number of secondary branches per plant

The highest number of secondary branches/plant was observed in BARI 9 × BARI6 $F_{11}S_6$ (5.60) followed by BARI 9 × BARI6 F_{11} (5.43) and BARI 15× SS_{75} F_3 (Late) (5.27) whereas the lowest number of secondary branches / plant was observed in SAU 2 (0.0) and SAU 3 × SAU 1F_3S_5 (Table 2).).Number of secondary branches per plant showed low differences between phenotypic variance (1.83) and genotypic variances (1.62) indicating lower environmental influence on this character (Table 3). High PCV (71.20) than GCV (66.97) presented the existence of high inherent variations among the lines themselves as well as checks and also within the both. The ECV was much lower (24.18) than the GCV indicated that the genetic influence was much on the trait than the environment (Table 3). Low GCV (20.19) and high PCV (33.81) was found by Khan *et al.*, (2013)

Number of Siliqua per plant

In the present experiment the highest variation was found for this trait. The highest number of siliqua / plant was observed in BARI 15 (313.73) whereas the lowest number of siliqua / plant was observed in SAU 2 (67.85). The number of siliqua / plant of BARI 15× SS_{75} F_3(Late), BARI9 × BARI6 F_{11}, Tori 7×BARI6 F_{11} were 194.63, 192.50 and 192.30 respectively (Table 2). The highest phenotypic variance (1442.54) and genotypic variance (1331.54) was observed for number of siliqua per plant with large environmental influence (Table 3). High PCV (27.14) and low GCV (25.89) indicated that variation among the lines and checks was not only due to genotypes but also due to environment and low ECV (8.11) represented that the environmental effect was less considerable (Table 3). Roy *et al.* (2011) found this type of result i.e. high PCV (45.36) and low GCV (31.38) in *Brassica rapa*.

Number of seed per siliqua

The highest number of seeds per siliqua was observed in SAU 2 × BARI 6 F_3 (26.03) followed by SAU 1× SAU 2 (24.75) and BARI 15 × SAU 1 (24.33) where as the minimum number of seeds per siliqua was observed in BARI 15× SAU 2 (12.74) (Table 2). The phenotypic variances and genotypic variances for this trait were observed 7.91 and 7.22 respectively (Table 3). Low genetic variance among the genotypes were found due to low differences between the PCV (15.52) and GCV (14.84). There are moderate difference between the ECV (4.56) and GCV said that there were more genotypic influence than the environment on the trait (Table 3). Nasim *et al.* (2013) found 21.36 % PCV and 16.44 % GCV in *Brassica napus.* Naznin (2013) also found same result in *Brassica rapa.*

Siliqua length (cm)

The highest siliqua length was observed in SAU 1 (6.38 cm) followed by BARI 9 × BARI6 F_{11} (6.14cm), BARI 15 × SAU 1 F_3 (6.11 cm), SAU1 × SAU 2 (6.07 cm) where as the lowest siliqua length was observed in SS_{75} × BARI 6 F_3 S_{17} (4.16 cm) (Table 2). Siliqua length showed phenotypic variance (0.37) and genotypic variance (0.18) with minimum difference between them indicating that they were more responsive to environmental factor for their phenotypic expression (Table 3). Moderate genetic variance among the genotypes were found due to moderate differences between the PCV (11.72) and GCV (8.20).There are lower difference between the ECV (8.37) and GCV said that there were more environmental influence than the genotype on the trait (Table 3). Nasim *et al.* (2013) found 21.36 % PCV and 16.44% GCV in *Brassica napus* . Naznin (2013) also found same result in *B. rapa.*

Table 2: Mean performance of 51 genotypes of *Brassica rapa*

Sl No.	Genotypes	PH	NPB	NSB	NSP	NSS	SL	D50%F	D50%M	TSW	YPP
1	BARI9×BARI6F_{11}	100.33	6.27	5.43	192.50	21.63	6.14	52.00	107.67	3.33	13.83
2	BARI9×BARI6Yellow F_{11}	95.13	4.53	0.60	119.47	19.33	5.27	45.00	105.33	3.43	7.91
3	BARI9×F_6F_{11}	120.00	3.60	1.37	117.40	17.41	5.14	51.00	104.00	2.32	4.73
4	BARI9×BARI6Special Early F_{11}	98.63	3.40	1.20	142.40	17.99	4.40	53.00	108.33	2.60	6.66
5	BARI9	108.97	4.63	1.90	145.37	16.54	5.20	51.67	109.33	2.84	6.83
6	BARI9×BARI6$F_{11}S_6$	102.17	5.03	5.60	165.13	21.25	6.07	50.00	101.00	2.82	9.91
7	BARI9×F_3 F_{11} Yellow S_3	100.10	5.73	3.23	165.80	21.88	5.62	43.67	103.33	2.95	10.71
8	BARI9×BARI6 F_{11} S_{18}(Brown)	99.70	4.83	1.73	142.33	16.88	4.51	50.00	102.67	2.57	6.17
9	BARI9 F_{11} Selection	103.20	4.23	0.60	125.90	17.87	5.82	54.00	106.33	2.77	6.21
10	BARI9×F_6F_{11} Medium	105.23	3.60	2.50	144.77	18.99	5.34	48.00	101.00	3.08	8.47
11	TORI7×BARI9 F_{11}	107.73	3.83	0.20	133.93	15.50	5.13	44.33	104.00	2.55	5.34
12	TORI7×BARI6 F_3	87.00	4.27	1.60	99.03	17.94	5.20	48.33	106.33	2.67	4.74
13	TORI7×SAU 1F_3	108.13	4.37	1.93	126.63	15.43	4.88	48.00	105.33	2.69	5.26
14	TORI 7×BARI 6 F_{11} S_{22}	107.53	4.73	0.00	132.77	16.85	4.99	49.00	107.00	2.69	6.01
15	TORI 7×SAU 1 F_{11}	103.90	4.33	0.90	117.50	15.41	5.01	48.00	100.00	2.60	4.70
16	TORI 7	108.57	5.37	1.50	93.47	19.39	4.81	50.00	108.67	2.80	5.07
17	TORI 7×BARI 6 F_{11} Early	100.77	3.90	2.00	122.87	15.48	4.97	49.00	108.33	2.69	5.12
18	TORI 7×BARI 6 F_{11}	102.53	7.03	2.20	192.30	16.23	5.22	50.00	102.67	2.97	9.24
19	BARI6×SAU 2	102.27	4.27	1.67	124.87	18.37	5.33	46.00	102.00	2.83	6.49

20	BARI 6×TORI7 F_{11}	109.60	5.23	2.33	175.07	18.27	5.31	49.00	104.00	3.18	10.16
21	BARI 6×SAU-3 F_3	98.17	4.43	1.53	122.73	17.73	4.45	45.67	101.33	3.27	7.10
22	BAR I6×SAU2 F_3	119.20	4.50	3.07	119.33	17.41	5.76	45.33	108.33	2.34	4.85
23	BARI 6×TORI7 S_3F_{11}	102.57	5.23	2.03	156.43	18.10	5.09	52.00	110.00	2.23	6.32
24	BARI 6×SAU 1 F_3	117.77	4.33	2.40	141.97	19.15	5.25	55.67	110.67	2.78	7.57
25	BARI 6	104.67	5.20	1.20	125.07	14.74	5.73	52.00	108.33	2.15	3.97
26	SAU 1×TORI 7 F_3	99.97	4.63	3.40	170.10	18.87	5.52	51.00	100.33	2.72	8.76
27	SAU 1×BARI 6 F_3	116.97	5.50	2.73	113.03	15.33	5.20	46.00	108.00	2.73	4.72
28	SAU 2×BAR6 F_3	109.73	5.87	2.10	118.37	26.03	5.59	50.00	100.33	2.26	6.96
29	SAU 3×SAU1 F_3S_5	104.03	4.87	0.00	102.17	17.79	5.33	53.00	111.33	3.03	5.50
30	SAU 1×SAU 2 F_3	108.20	4.90	1.00	136.20	19.85	5.70	48.00	101.67	2.42	6.54
31	SAU 1 F_3	108.50	5.07	1.37	157.47	21.42	5.19	51.67	101.00	2.25	7.59
32	SAU 1	103.20	4.33	1.10	150.57	22.65	6.38	51.00	109.00	3.36	11.42
33	SAU 2	88.10	3.57	0.00	67.85	17.14	4.69	46.00	104.00	2.45	2.85
34	SAU 3	109.40	4.63	0.90	143.27	18.97	5.71	51.00	113.67	2.74	7.44
35	SAU 1×SAU 2	103.67	4.97	0.60	108.40	24.75	6.07	46.00	103.00	2.91	7.81
36	SAU 1×BARI 6	99.80	4.23	1.53	140.53	16.78	4.73	47.00	106.67	2.89	6.78
37	SAU 3×SAU1 F_3	109.30	4.57	1.73	104.10	17.00	5.21	54.00	110.00	3.18	5.62
38	SAU2×BARI6 F_3 S_{17}	96.50	3.70	1.93	123.97	16.79	4.98	54.33	106.00	2.54	5.27
39	SS_{75}×TORI 7 F_{11}	95.97	5.07	1.43	149.73	15.69	4.16	48.00	105.67	2.73	6.44
40	BARI15×SS_{75} F_5	109.17	5.03	4.10	159.67	16.25	5.36	49.33	110.67	3.23	8.38
41	BARI15×SS_{75} F_3(Late)	102.87	5.20	5.27	194.63	17.06	5.14	47.33	104.67	2.24	7.45
42	BARI15×BARI6 F_3	103.20	4.50	2.77	140.00	13.71	4.85	45.00	102.67	2.14	4.08

43	BARI 15×SAU 2 F_3	101.83	6.03	1.97	133.13	21.10	5.58	48.00	101.33	2.54	7.10
44	BARI 15×SAU 2	100.97	4.57	1.53	115.40	12.74	5.01	45.67	106.00	2.76	4.05
45	BARI 15×SAU3 F_3	107.13	4.97	2.07	150.40	20.23	5.21	45.00	102.33	2.33	7.15
46	BARI 15	106.33	4.10	0.40	313.73	15.74	4.40	52.00	100.33	2.84	14.01
47	BARI 15×SAU 1 F_3	117.33	4.17	0.00	107.33	24.33	6.11	50.00	101.67	2.85	7.44
48	BARI 15×TORI 7 F_3	101.20	3.90	2.67	121.40	17.84	5.07	47.00	104.00	2.74	5.95
49	BARI 15×BARI9 $F_{11}S_6$	109.20	4.27	2.20	152.03	15.47	5.15	47.33	101.67	3.30	7.77
50	F_6×BARI9 F_3	100.53	5.17	1.73	162.00	17.13	5.30	48.33	101.00	2.77	7.75
51	F_6×BARI9 S_4 F_3	100.00	4.57	3.60	157.67	17.32	4.17	51.33	106.00	3.04	8.32
	Mean	**104.45**	**4.69**	**1.90**	**139.96**	**18.11**	**5.22**	**49.10**	**105.08**	**2.75**	**6.99**
	Min	**87.00**	**3.40**	**0.00**	**67.85**	**12.74**	**4.16**	**43.67**	**100.00**	**2.14**	**3.97**
	Max	**120.00**	**7.03**	**5.60**	**313.73**	**26.03**	**6.38**	**55.67**	**113.67**	**3.43**	**14.01**

PH= Plant height (cm), NPB = No. of primary branches per plant, NSB = No. of secondary branches per plant, NSP = No. ofsiliqua per plant, NSS= no. of seed persiliqua , SL=Siliqua Length of pod (cm), D50%F = day to 50% flowering, D50%M = day to 50% maturity, TSW = 1000 seed weight (g), SPP = Yield per plant (g).

Table 3 .Mean, Range and CV(%) of seed and yield contributing characters 51 genotypes of *Brassica rapa*

Parameters	Range	Mean	MS	CV (%)	SE
PH	87.00-120.00	104.45	137.44**	3.64	3.10
NPB	3.40-7.03	4.69	1.56**	7.37	0.28
NSP	0.00-5.60	1.90	5.06**	24.18	0.378
NSP	67.85-313.73	139.96	3,844.82**	7.14	8.16
NSS	12.74-26.03	18.11	22.35**	4.56	0.67
SL	4.16-6.38	5.22	0.74**	8.37	0.35
D50%F	43.67-55.67	49.10	25.35**	2.35	0.94
D50%M	100.00-113.67	105.08	36.64**	2.34	2.00
TSW	2.14-3.43	2.75	0.32**	7.59	0.17
YPP	2.85-14.01	6.99	15.57**	11.50	0.08

PH = plant height (cm), NPB = No. of primary branches per plant, NSB = No. of secondary branches per plant, NSP = No. of siliqua per plant, NSS = No. of seed per silique, SL= Siliqua Length (cm), D50%F = day to 50% flowering, D50%M = day to 50% maturity, TSW = 1000 seed weight (g), YPP= Yield per plant (g), MS = Mean sum of square and CV (%) = Coefficient of variation.

Table 4 .Estimation of some genetic parameters in respect of 51 genotypes in *Brassica rapa*

Parameters	σ^2 p	σ^2g	σ^2 e	PCV	GCV	ECV	Heritability (%)	Genetic advance (5%)	Genetic advance (% mean)
PH	55.45	41.00	14.45	7.13	6.13	3.64	73.93	11.34	10.86
NPB	0.60	0.48	0.12	16.51	14.78	7.37	80.10	1.28	27.25
NSB	1.83	1.62	0.21	71.20	66.97	24.18	88.47	2.46	129.72
NSP	1442.54	1313.54	129.00	27.14	25.89	8.11	91.06	71.24	50.90
NSS	7.91	7.22	0.68	15.52	14.84	4.56	91.38	5.29	29.23
SL	0.37	0.18	0.19	11.72	8.20	8.37	48.95	0.62	11.82
D50%F	9.34	8.01	1.33	6.22	5.76	2.35	85.72	5.40	10.99
D50%M	16.23	10.21	6.03	3.83	3.04	2.34	62.88	5.22	4.97
TSW	0.14	0.10	0.04	13.56	11.23	7.59	68.63	0.53	19.15
YPP	5.62	4.97	0.64	33.91	31.90	11.49	88.51	4.32	61.85

PH = Plant height (cm), NPB = No. of primary branches per plant, NSB = No. of secondary branches per plant, NSP = No. of siliqua per plant, SPS = no. of seed per pod, SL = Length of pod (cm), D50%F = day to 50% flowering, D50%M = day to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield perplant (g), MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2 e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation.

Days to 50 % flowering

Out of the 32 genotypes the lowest days to flowering was taken by BARI 9 × F_3 F_{11}Yellow S_3 (43.67 days) followed by Tori 7 × BARI 6 F_3 (44.33 days). The highest days to flowering was taken by BARI 6 × SAU 1 F_3 (55.67 days) which close with SAU 2 × BARI $6F_3S_{17}$ (54.33 days) (Table 2). The phenotypic and genotypic variances for this trait were 9.34 and 8.01 respectively. Comparatively low difference between PCV (6.22) and GCV (5.76) stated that there was low variation among the genotypes (Table 3) .There was low environmental influence on the trait. Naznin (2013) also found low difference between PCV (22.15) and GCV (19.74) in *Brassica rapa*. A pictorial view of 50 % flowering field as presented in plate 2.

Days to 50% maturity

The lowest days to maturity was taken by Tori 7 × SAU 1 F_3 (100 days) followed by SAU 2 × BARI 6 F_3 (100.33 days). The highest days to maturity was taken in BARI 15 (113.67 days) followed by BARI 6 × SAU 1 F_3 (110.67 days) and SAU3 × SAU $1F_3$ S_5 (111.33 days) (Table 2). The phenotypic and genotypic variance for days to maturity was observed 16.23 and 10.21 respectively (Table 3) which indicated that the trait expression is highly controlled by phenotypic parameters .Comparatively low difference between PCV (3.83) and GCV (3.04) stated that there was low variation among the genotypes (Table 3) .There was low environmental influence on the trait. Naznin (2013) also found low difference between PCV (22.15) and GCV (19.74) in *Brassica rapa.* A pictorial view of 50 % maturity field as presented in plate 3.

Thousand seed weight (g)

Thousand seed weight was found maximum in BARI 9× BARI 6 Yellow F_{11} (3.43 g) followed by SAU 1 (3.36 g) where as the minimum thousand seed weight was found in BARI 15 × BARI 6 F_3 (2.14 g) (Table 2). The phenotypic and genotypic variances for this were 0.14 and 0.10 respectively. (Table 3). Comparatively low difference between PCV (13.56) and GCV (11.23) stated that there was low variation among the genotypes (Table 3) .There was low environmental influence on the trait. Naznin (2013) also found low difference between PCV (22.15) and GCV (19.74) in *Brassica rapa.*

Plate 2 : Field view of 50 % flowering of the concerned treatments in a block

Plate 3 : Field view of 50 % maturity of the concerned treatments in a block

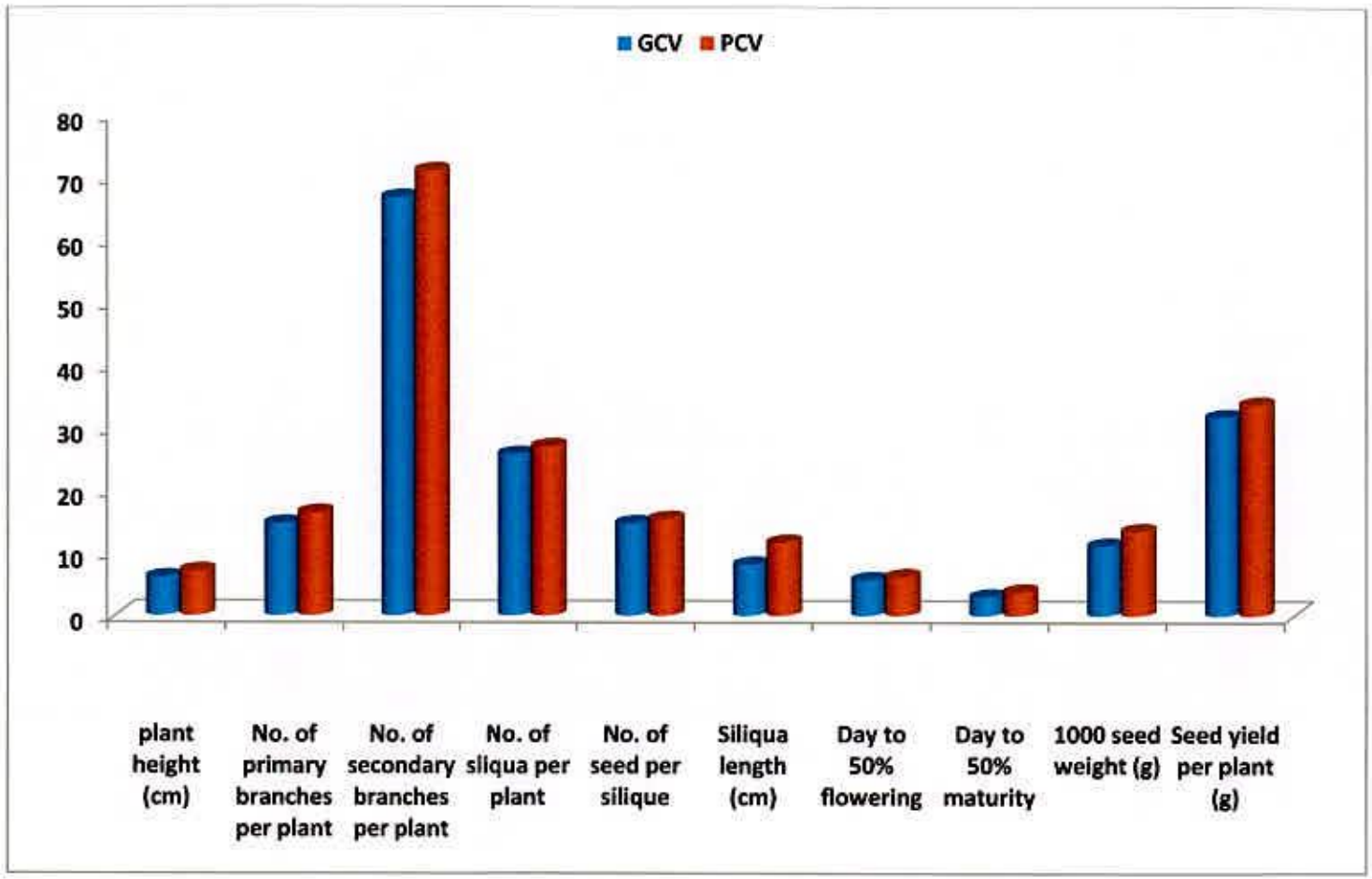


Fig 1 Genotypic and phenotypic variability in 51 genotypes of *Brassica rapa.*

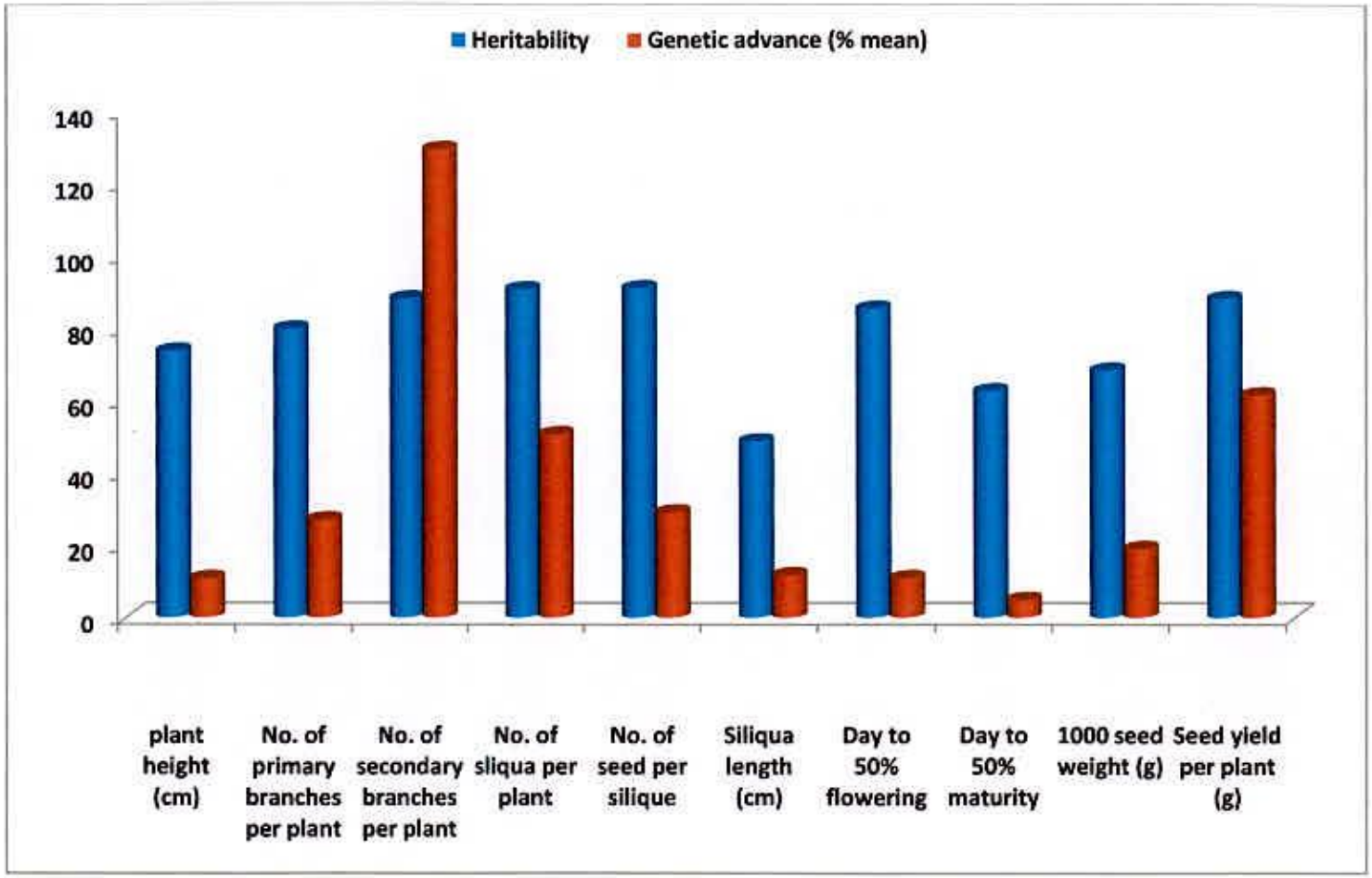


Fig 2 Heritability and genetic advance over mean in *Brassica rapa*

Yield per plant (g)

The highest amount of yield per plant was observed in BARI 15 (14.01 g) followed by BARI 9 × BARI 6 F_{11} (13.83 g) followed by SAU 1(11.42 g), BARI 9 × F_3 F_{11} Yellow S_3 (10.71 g) and BARI 6 × SAU 3 F_3 (10.16 g) where as the minimum yield per plant was observed in BARI 6 (3.97 g) (Table 2). The phenotypic variance and genotypic variance were 5.62 and 4.97 respectively (Table 3).The PCV and GCV was 33.91 and 31.90 respectively which stated that the existence of inherent variability among the population with the possibility of high potential for selection. As low ECV (11.49) was presented indicated that there were low environmental influence the character (Table 3) . High PCV (20.28) and low GCV (4.92) was found by Aktar (2010).

4.1.2.Heritability,genetic advance and selection

Days to 50 % flowering

Very high heritability (85.72%) and low genetic advance (5.40%) and low genetic advance in percent of mean (10.99) was found in days to 50 % flowering which revealed that the character was governed by non-additive genes and high heritability was being exhibited due to favorable environment rather than genotypes and selection for this trait may not be rewarding. Saifullah (2010) also found high heritability (88.86%) and low genetic advance (2.06). Aktar (2010) and Khan *et al.*, (2012) supported the result.

Days to 50% maturity

Moderate heritability (62.88 %) with low GA (5.22%) and low GA in percent of mean (4.97) was found days to 50 % maturity characters (Table 4 that indicated that environmental effect was more than the genotypical effect and due to non-additive gene action, selection for further improvement of trait might not be rewarding. Saifullah (2010) found similar result.

Plant height(cm)

The magnitude of heritability in broad sense (h^2 b) of this trait was high heritability (73.93 %) with low genetic advance (11.34 %) and low genetic advance in percent of mean (10.86). The result presented that due to presence of non-additive gene effect and environment was mainly responsible for high heritability where selection in that case might not be fruitful. Nazim (2013) found high heritability (89.14 %) with moderate genetic advance (8.69 %) and Saifullah (2010) found it with low genetic advance.

Number of primary branches per plant

Number of primary branches per plant exhibited high heritability (80.10 %) and low genetic advance (1.28 %) and genetic advance in percent of mean (27.25) that determined the presence of non-additive gene effect on the character and for this reason, improvement through selection might not be so wise. Environment was responsible for high heritability. Kahrizi and Alaahvarand found high heritability (93.18 %) and low genetic advance (14.08 %) in 2012 that was similar to the result.

Number of secondary branches per plant

Number of secondary branches per plant exhibited high heritability (88.47 %) and high percent of mean (129.72%) revealed that there were additive gene action in the trait. The environment influence was low on the trait. Saifullah (2010) found similar result.

Plate 3:BARI-9×BAR-I6F_{11}

Plate 4: BAR-I9×BARI-6

Plate 5:BARI-9×F_6F_{11}

Plate 6: BAR-I9×BARI-6 Special Early F_{11}

Plate 7:BARI 9

Plate 8:BARI 9×BARI6 $F_{11}S_6$

Plate 9:BARI 9× F_3F_{11} Yellow S_3

Plate 10:BARI 9×BARI 6 F_{11} S_{18}(Brown)

Plate 11:BARI 9 F_{11} Selection Medium

Plate 12:BARI 9×F_6 F_{11}

Plate 13:TORI 7×BARI 9 F_{11}

Plate14:TORI 7×BARI 6 F_3

Plate 15:TORI 7×SAU 1F_3

Plate 16: TORI 7×BARI 6 F_{11} S_{22}

Plate 17:TORI 7×SAU 1 F_{11}

Plate 18:TORI 7

Plate 19:TORI 7×BARI 6 F_{11} Early

Plate 20:TORI 7×BARI 6 F_{11}

Plate 21:BARI 6×SAU 2

Plate 22:BARI 6×TORI7 F_{11}

Plate 23:BARI 6×SAU 3 F3

Plate 24:BARI 6×SAU 2 F_3

Plate 25:BARI 6×TORI 7 S_3 F_{11}

Plate 26:BARI 6×SAU 1 F_3

Plate 27:BARI 6

Plate 28:SAU 1×TORI 7 F_3

Plate 29:SAU 1×BARI 6 F_3

Plate 30: SAU 2×BAR6 F_3

Plate 31:SAU 3×SAU1 F_3 S_5

Plate 32: SAU 1×SAU 2 F_3

Plate 33:SAU 1 F3

Plate 34:SAU 1

Plate 36: SAU 2

Plate 37:SAU 3

Plate 38:SAU 1×SAU 2

Plate 39:SAU 1×BARI 6

Plate 40:SAU 3×SAU1 F_3

Plate 41:SAU2×BARI6 F_3 S_{17}

Plate 42:SS_{75}×TORI 7 F11

Plate 43: BARI15×SS_{75} F_5

Plate 44:BARI15×$SS_{75}F_3$(Late)

Plate 45:BARI15×BARI6 F_3

Plate 46:BARI 15×SAU 2 F_3

Plate 47: BARI 15×SAU 2

Plate 48:BARI-15×SAU3 F_3

Plate 49: BARI 15

Plate 50:BARI 15×SAU 1 F_3

Plate 51:BARI 15×TORI 7 F_3

Plate 52:BARI 15×BARI9 $F_{11}S_6$

Plate 53:F_6×BARI9 F_3

Plate 54:F_6×BARI9 S_4 F_3

Number of siliqua per plant

Number of siliqua per plant exhibited high heritability (91.06 %) with genetic advance (71.24 %) and genetic advance in percentage of mean (50.90) (Table 4) indicated low influence of genotypic materials and additive gene effect was presented. Selection for this trait might be wise. Khan *et al.*, .(2012) found high heritability (60.17 %) and high genetic advance (17.89 %) for the trait.Malik *et al.*, (1995) reported high heritability (h2b≥ 90 %) for this trait.

Number of seed per siliqua

Number of seed per siliqua showed high heritability (91.38 %) with low genetic advance (5.29 %) and genetic advance in percent of mean (29.23) (Table 4) revealed higher possibility of selecting genotypes. The character was governed by non-additive genes and high heritability was being exhibited due to favorable environment rather than genotypes and selection for this trait may not be rewarding. Saifullah (2010) also found high heritability (88.86 %) and low genetic advance (2.06). Aktar (2010) and Khan *et al.*, (2012) supported the result.

Siliqua length (cm)

Siliqua length showed exhibited moderate heritability (48.95 %) with low genetic advance(0.62 %) and genetic advance in percent of mean (11.82) (Table 4). that indicated that environmental effect was more than the genotypical effect and due to non-additive gene action, selection for further improvement of trait might not be rewarding. Saifullah (2010) found similar result.

Thousand seed weight (g)

1000 seed weight exhibited moderate heritability (68.63 %) with low genetic advance (0.53 %) and genetic advance in percent of mean (19.15) that indicated that environmental effect was more than the genotypical effect and due to non-additive gene action, selection for further improvement of trait might not be rewarding. Saifullah (2010) found similar result.

Yield per plant

High heritability (88.51 %) coupled with low genetic advance (4.32 %) and genetic advance in percent of mean (61.85) indicated that low influence of genotypic materials and additive gene effect was presented (Table 3). Selection for this trait might be wise. Khan *et al.*,(2012) found high heritability (60.17 %) and high genetic advance (17.89 %) for the trait .Malik *et al.*, (1995) reported high heritability (h2b≥ 90%) for this trait. Johnson *et al.*, (1955) reported that heritability estimates along with genetic gain were more useful in prediction selection of the best individual.

4.1.3 Correlation co-efficient

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. Breeder always look for genetic variation among traits to select desirable type. Correlation co-efficient between pair of trait for F_1 to F_{11} combination of materials of *B. rapa* are shown in (Table 4.1 to Table 4.2).

Plant height (cm)

Plant height showed positive interaction with number of primary branches per plant (G = 0.057, P = 0.060) followed by positive interaction with no. of siliqua per plant (G = 0.042, P = 0.030), no. of seeds per pod (G = 0.119 , P = 0.083), day to 50 % flowering (G = 0.171 , P = 0.126), day to 50 % maturity (G = 0.171 and P = 0.090) ,seed yield per plant (G = 0.004 ,P = 0.009) and positive highly significant interaction with length of siliqua (G = 0.363, P = 0.210).Where as negative interaction with secondary branches per plant (G = -0.008 , P = -0.007) followed by thousand seed weight (G = -0.149 ,P =- 0.058), (Table 4.1 to Table 4.2). These finding are close resemblance to suports of Chowdhury *et al.* (1987) and Yadava *et al.*, (1978). Naznin (2013) showed similar positive correlation but these was positive correlation with the secondary branch per plant also.

Table 5a. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype *of Brassica rapa.*

Characters	NPB	NSB	NSP	NSS	SL	D50%F	D50%M	TSW	YPP
PH	0.057	-0.008	0.042	0.119	0.363**	0.171*	0.171*	-0.149	0.004
NPB		0.376**	0.254**	0.280**	0.300**	-0.035	-0.056	0.060	0.350**
NSB			0.324**	0.046	0.135	-0.042	-0.042	0.063	0.348**
NSP				-0.053	-0.125	0.178*	-0.252**	0.136	0.783**
NSS					0.690**	0.086	-0.238**	0.112	0.430**
SL						0.074	0.009	0.149	0.307**
D50%F							0.399**	0.043	0.184*
D50%M								0.168*	-0.210**
TSW									0.533**

** = Significant at 1%.

* = Significant at 5%.

PH = Plant height (cm), NPB = No. of primary branches per plant, NSB = No. of secondary branches per plant, NSP = No. of siliqua per plant, NSS= No. of seeds per siliqua , SL =Siliqua length (cm), D50%F = day to 50% flowering, D50%M = day to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).

Table 5b. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica rapa.*

Characters	NPB	NSB	NSP	NSS	SL	D50%F	D 50%M	TSW	YPP
PH	0.060	-0.007	0.030	0.083	0.210**	0.126	0.090	-0.058	0.009
NPB		0.335**	0.245**	0.241**	0.271**	-0.018	-0.024	0.002	0.307**
NSB			0.323**	0.040	0.155	-0.003	-0.004	0.061	0.340**
NSP				-0.054	-0.027	0.166*	-0.176**	0.104	0.767**
NSS					0.483**	0.086	-0.158	0.098	0.430**
SL						0.046	0.068	0.074	0.263**
D50%F							0.377**	0.018	0.168*
D50%M								0.095	-0.136
TSW									0.527**

** = Significant at 1%.

* = Significant at 5% level. PH = Plant height (cm), NPB = No. of primary branches per plant, NSB= No. of secondary branches per plant, NSP = No. of siliqua per plant, NSS = No. of seed per siliqua , SL =Siliqua Length (cm), D50%F = day to 50% flowering, D50%M = day to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).

Number of primary branches per plant

Positive and significant correlation of number of primary branches per plant was observed with secondary branches per plant (G = 0.376,P = 0.335) ,number of siliqua per plant (G = 0.254, P = 0.245), number of seeds per siliqua (G = 0.280, P = 0.241), length of siliqua (G = 0.300,P = 0.271) , seed yield per plant (G = 0.350, P = 0.307) and positive interaction with thousand seed weight (G = 0.060, P = 0.002). Where as negative interaction with days to 50% flowering (G=-0.035 ,P=-0.018) and days to 50 % maturity (G = -0.056, P = -0.024). Nazim (2013) found positive significant relation with yield while Akter (2010) found negative correlation with the yield .

Number of secondary branches per plant

Positive significant correlation was found in number of siliqua per plant (G = 324,P = 0.323), seed yield per plant (G = 0.348, P = 0.340) and positive correlation with number of siliqua per plant (G = 0.046, P = 0.040), length of siliqua (G = 0.135, P = 0.155), thousand seed weight (G = 0.063 and P = 0.061). Where as negative correlation with days to 50 % flowering (G = -0.042, P = -0.003) and days to 50 % maturity (G = -0.042, P = -0.004). Saifullah (2010) reported positive significant correlation of the trait with yield.

Number of siliqua per plant

Positive significant correlation was observed in seed yield per plant (G = 0.783 ,P = 0.767) and positive correlation with days to 50 % flowering (G = 0.178, P = 0.166) and thousand seed weight (G = 0.136 , P = 0.104). Where as negative significant correlation with days to 50 % maturity (G = -0.252, P = -0.176) and negative correlation with number of seeds per plant (G = -0.053, P = -0.054) and siliqua length (G = -0.125, P = -0.027). Hossain (2008) reported negative correlation with siliqua length and thousand seed weight.

Number of seed per siliqua

Positive significant correlation with siliqua length (G = 0.690, P = 0.483) , seed yield per plant (G = 0.430, P = 0.430**) and significant correlation with days to 50 % flowering (G = 0.086, P = 0.086) and thousand seed weight (G = 0.112, P =

0.098).Where as negative correlation with days to 50 % maturity (G = -0.238, P = -0.158). Nazim (2013) found negative significant correlation with yield.

Siliqua length (cm)

Siliqua length showed significant positive correlation with seed yield per plant (G = 0.307, P = 0.263) and positive correlation with days to 50 % fl0wering (G = 0.074,P = 0.046) , days to 50% maturity (G = 0.009, P = 0.068) and thousand seed weight (G = 0.149, P = 0.074). Saifullah (2010) reported positive significant correlation of the trait with yield.

Days to 50% flowering

Days of flowering showed positive significant correlation with days to 50 % maturity (G = 0.399, P = 0.377) and positive correlation with thousand seed weight (G = 0.043,P = 0.018) and seed yield per plant (G = 0.184 ,P = 0.168). Saifullah (2010) reported positive significant correlation of the trait with yield.

Days to 50 % maturity

Days to 50 % maturity showed negative significant correlation with seed yield per plant (G = -0.210, P = -0.136) and positive correlation with thousand seed weight (G = 0.168, P = 0.095). Akter (2010) found positive correlation with number of siliqua per plant, length of siliqua and yield per plant also.

Thousand seed weight (g)

Thousand seed weight showed showed positive significant correlation with seed yield per plant (G = 0.533, P = 0.527). Alam (2007) found no significant positive correlation of the trait with yield. Akter (2010) found positive significant correlation with yield per hectare at genotypic level but negative correlation at phenotypic level while Saifullah (2010) found positive significant correlation at both level.

4.1.4 Path co-efficient analysis

Association of character determined by correlation co-efficient may not be provide an exact picture of the relative importance of direct and indirect influence of each of yield components on seed yield per plant.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 50 % maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length , 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 rapa* is presented in (Table 5).

The cause and effect relationship between seed yield per plant and yield contributing traits have been presented diagrammatically in Figure 1. Residual effects of their independent variables, which have influenced on yield to a medium extent, have been denoted as 'R' in the diagram. The results are discussed briefly as follows:

Path co-efficient analysis revealed that, plant height had negative direct effect (-0.064) on yield per plant (Table 5).The character had positive indirect effect on yield per plant through siliqua length (0.044) followed by number of seeds per (0.043), number of siliqua per plant (0.032), days to 50 % maturity (0.004) and secondary branches per plant (0.000). Negative indirect effect through primary branches per plant (-0.001), days to 50 % flowering (-0.001) and thousand seed weight (-0.053). Dilek Basalma (2008) found direct negative effect of plant height (-0.28) on seed yield.

Table 6: Path coefficient analysis showing direct and indirect effects of different characters on yield of *Brassica rapa*

Characters	Direct effect	PH	NPB	NSB	NSP	NSS	SL	D50%F	D50%M	TSW	Genetic Correlation with yield
PH	-0.064	-	-0.001	0.000	0.032	0.043	0.044	-0.001	0.004	-0.053	0.004
NPB	-0.018	-0.004	-	0.019	0.195	0.102	0.036	0.000	-0.001	0.021	0.350**
NSB	0.051	0.001	-0.007	-	0.249	0.017	0.016	0.000	-0.001	0.022	0.348**
NSP	0.767	-0.003	-0.005	0.017	-	-0.019	-0.015	-0.001	-0.006	0.048	0.783**
NSS	0.364	-0.008	-0.005	0.002	-0.041	-	0.083	0.000	-0.006	0.040	0.430**
SL	0.121	-0.023	-0.005	0.007	-0.096	0.251	-	0.000	0.000	0.053	0.307**
D50%F	-0.005	-0.011	0.001	-0.002	0.137	0.031	0.009	-	0.010	0.015	0.184*
D50%M	0.024	-0.011	0.001	-0.002	-0.193	-0.087	0.001	-0.002	-	0.059	-0.210**
TSW	0.354	0.010	-0.001	0.003	0.104	0.041	0.018	0.000	0.004	-	0.533**

Residual effect: **0.0119**

* = Significant at 5%.

** = Significant at 1%.

PH = Plant height (cm), NPB = No. of primary branches per plant,NSB = No. of secondary branches per plant, NSP = No. of siliqua per plant, NSS = No. of seed per siliqua, SL = Siliqua Length (cm), D50%F = day to 50% flowering, D50%M = day to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).

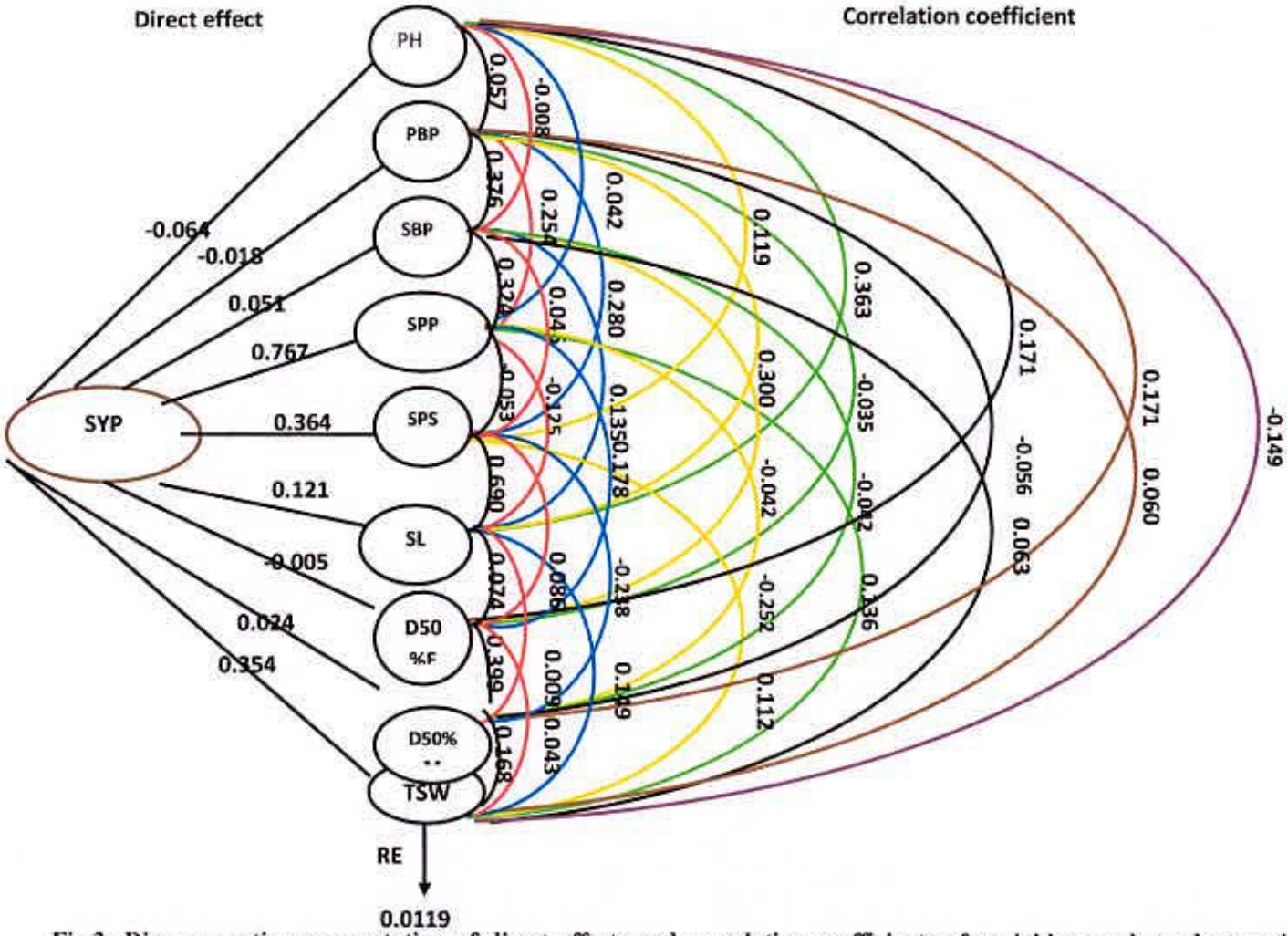


Fig.3: Diagrammatic representation of direct effects and correlation coefficients of variables on dependent variable in *Brassica rapa* genotype

Number of primary branches per plant had negative direct effect (-0.018) on yield per plant and positive indirect effect was seen on secondary branches per plant (0.019), number of siliqua per plant (0.195), number of seeds per siliqua (0.102), siliqua length (0.036) , days to 50 % flowering (0.000) and thousand seed weight (0.021). It had negative indirect effect on days to 50 % maturity (-0.001). In 1990 positive direct effect of plant height (0.32) was observed by Han that supported the findings.

Number of secondary branches per plant had positive direct effect (0.051) on yield per plant and positive indirect effect on yield per plant through plant height (0.001), number of per siliqua plant (0.249), number of seed per siliqua (0.017), siliqua length (0.016), days to 50 % flowering (0.000) and thousand seed weight (0.022).Where as negative indirect effect on yield through number of primary branches per plant (-0.007) and days to 50 % maturity (-0.001). Path analysis done Dilek Basalma (2008) indicated that branches per plant had positive effect (0.077) on seed yield.

Number of siliqua per plant had positive direct effect (0.767) on yield per plant and positive indirect effect through number of secondary branches per plant (0.017) and thousand seed weight (0.048). It had negative indirect effect through plant height (-0.03), primary branches per plant (-0.005), number of seeds per siliqua (-0.019), siliqua length (-0.015), days to 50 % flowering (-0.001) and days to 50 % maturity (-0.006). Han (1990) worked with *Brassica napus* and found negative direct effect of number of siliqua per plant (0.808) that is agreeable to the mentioned result. Marjanovic-Jeromela *et al.*, (2008) worked on *Brassica napus* and found positive direct effect (0.26) on yield.

Number of seeds per siliqua had direct effect (0.364) on yield per plant and positive indirect effect through secondary branches per plant (0.002), siliqua length (0.083) , days to 50 % flowering (0.000) and thousand seed weight (0.040). It had indirect negative effect through plant height (-0.008), primary branches per plant (-0.005), number of siliqua per plant (-0.041) and days to 50 % maturity (-0.006). Han (1990) worked with *Brassica napus* and found that number of seeds per siliqua had positive direct effect (10.449) on yield that was disagreement with the findings. Tusar-Patral *et al.*, (2006) concluded that the number of seeds per siliqua had strongest direct effect on yield.

Siliqua length had direct positive effect (0.121) on yield per plant and also indirect positive effect through number of secondary branches per plant (0.007), number of seeds per siliqua (0.251), days to 50 % flowering (0.000), days to 50 % maturity (0.00) and thousand seed weight (0.053). It had indirect negative effect through plant height (-0.023), primary branches per plant (-0.005) and number of siliqua per plant (-0.096). Ejaz-UI-Hasan *et al.*, (2014) observed that siliqua length had direct positive effect (0.241) on yield.

Days to 50 % flowering had direct negative effect (-0.005) on seed yield per plant and indirect positive effect through primary branches per plant (0.001), number of siliqua per plant (0.137), number of seeds per siliqua (0.031), siliqua length (0.009), days to 50 % maturity (0.010) and thousand seed weight (0.015). It had indirect negative effect through plant height (-0.011) and secondary branches per plant (-0.002). Zahan (2006) reported that days to 50% flowering had negative direct effect on yield.

Days to 50 % maturity had direct positive effect (0.024) on seed yield per plant and indirect positive effect through primary branches per plant (0.001), siliqua length (0.001) and thousand seed weight (0.059). Where as indirect negative effect through plant height (-0.011), secondary branches per plant (-0.002), number of siliqua per plant (-0.193), number of seeds per siliqua (-0.087) and days to 50 % flowering (-0.002).Negative direct effects on plant yield were exhibited by days to maturity (-0.015) was observed byNaazar Ali *et al.*, (2003).

Thousand seed weight showed direct positive effect (0.354) on yield per plant. It had positive indirect effect through plant height (0.010), secondary branches per plant (0.003), number of siliqua per plant (0.104), number of seed per siliqua (0.041) , siliqua length (0.018), days to 50 % flowering (0.000) and days to 50 % maturity (0.004). It had only indirect negative effect on seed yield per plant through primary branches per plant (-0.001). Kakroo and Kumar (1991) found that thousand seed weight had positive direct effect (0.784) and negative indirect effect (-0.129) via number of seeds per siliqua on seed yield.

Through path analysis the residual effect was observed. The residual effect R was 0.0119, which indicating the character under study contributed 98.81 of the seed yield per plant (Table 6). It is suggested that there were some others factors those

contributed 1.19% to the seed yield per plant not included in the present study may exert significant effect on seed yield.

4.2 DIVERSITY ANALYSIS

4.2.1 Principal component analysis (PCA)

Principal component analysis was carried out with 51 genotypes of *Brassica*. First three Eigen values for three principal coordination axes of genotypes accounted for 58.08 % variation (Table 7). A two dimensional scattered diagram (Fig. 5) was developed on the basis of the principal component score, Z_1 and Z_2 score of two principal coordinates axes I and II of Fig. 4.

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between SAU 2 and BARI 15 (246.89) followed by Tori 7 and BARI 15 (220.56), Tori 7 × BARI 15(215.82), SAU1 × SAU 2 and BARI 15 (211.88) and SAU3 × SAU 1 F_3 and BARI 15 (209.91) (Table 6). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 51 genotypes of *Brassica*. The highest intra-cluster was recorded in cluster V (10.43) containing four genotypes BARI 9×BAR I6F_{11}, Tori 7×BARI 6 F_{11}, BAR I15×SS_{75} F_3 (Late), BARI 15 (Table 8). The lowest intra-cluster was recorded in cluster I (0.0) having two genotypes Toril 7 × BARI 6 F_3, SAU 2. It favored to decide that intra-group diversity was the highest in cluster V and cluster I. Cluster II having nine genotypes BARI 9 × F_6F_{11}, Tori 7, BAR-6 × SAU-2 F_3, SAU 1 × BARI 6 F_3, SAU 2 × BAR6 F_3, SAU 3 × SAU 1 F_3 S_5, SAU 1 × SAU 2 , SAU 3 × SAU 1 F_3 ,BARI15 × SAU1 F_3. Cluster III having nineteen genotypes BARI9 × BARI6 Special Early F_{11}, BARI9, BARI9 × BARI6$F_{11}S_6$, BARI9 × F_3 F_{11} Yellow S_3, BARI9 × BARI6 F_{11} S_{18}(Brown), BARI9 × F_6 F_{11} (Medium), BARI6 × Tori7 F_{11}, BARI 6 × Tori 7 S_3 F_{11}, BARI 6 × SAU 1 F_3, SAU1 × Tori 7 F_3, SAU 1 F_3, SAU 1, SAU 3, SS_{75} × Tori 7 F_{11}, $BARI_{15}$ × SS_{75} F_5, BARI 15 × SAU 3 F_3, BARI 15 × BARI 9 $F_{11}S_6$, F_6 × BARI 9 F_3, F_6 × BARI 9 S_4 F_3.Cluster IV having 17 genotypes BARI 9 × BARI6Yellow F_{11}, BARI 9 F_{11} Selection, Tori 7 × BARI9 F_{11},Tori 7 × SAU1F_3, Tori 7 × BARI 6 F_{11} S_{22}, Tori 7 × SAU 1 F_{11}, Tori 7 × BARI 6 $_{F11}$ Early, BARI6 × SAU 2, BARI 6 × SAU 3 F_3, BARI 6, SAU 1 × SAU 2 F_3, SAU 1 × BARI 6 , SAU 2 × BARI

6 F_3 S_{17}, BARI 15 × BARI 6 F_3, BARI 15 × SAU 2 F_3, BARI15 × SAU 2 , BARI 15 × Tori 7 F_3 (Table 11).

Table 7: Ten highest and ten lowest inter genotypic distance among the 51 genotypes of *Brassica rapa*

Highest distance				Lowest distance			
Sl. No.	**Genotype**		**Distance**	**Sl. No.**	**Genotype**		**Distance**
01	G33	G46	246.89	01	G4	G8	0.15
02	G16	G46	220.56	02	G21	G38	1.24
03	G12	G46	215.82	03	G11	G14	1.27
04	G29	G46	211.88	04	G1	G18	1.28
05	G37	G46	209.91	05	G17	G48	1.36
06	G46	G47	206.78	06	G9	G25	1.68
07	G35	G46	205.49	07	G8	G36	1.92
08	G27	G46	201.32	08	G4	G36	1.93
09	G44	G46	198.76	09	G3	G22	1.96
10	G3	G46	197.04	10	G18	G41	2.22

Table 8: Eigen values and yield percent contribution of 10 characters of 51 genotypes of *Brassica* rapa

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
plant height (cm)	2.696	26.96	**26.96**
No. of primary branches per plant	1.643	16.43	**43.39**
No. of secondary branches per plant	1.469	14.69	**58.08**
No. of sliqua per plant	1.170	11.70	**69.78**
No. of seed per sliqua	0.979	9.79	**79.57**
Siliqua length (cm)	0.776	7.76	**87.33**
Day to 50% flowering	0.591	5.91	**93.24**
Day to 50% maturity	0.372	3.72	**96.96**
1000 seed weight (g)	0.295	2.95	**99.91**
Yield per plant (g)	**0.008**	**0.09**	**100.00**

Table 9:Intra (Bold) and inter cluster distances (D^2) for 51 genotypes of *Brassica rapa*

Cluster	I	II	III	IV	V
I	**0.01**	6.69	6.55	4.47	10.43
II		**0.045**	3.82	3.39	8.26
III			**0.007**	2.63	4.86
IV				**0.009**	6.98
V					**0.459**

Table 10:The nearest and farthest clusters from each cluster between D^2 values in *Brassica rapa*

Sl.No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	IV (4.47)	V (10.43)
2	II	IV (3.39)	V (8.26)
3	III	I (2.63)	I (6.55)
4	IV	III (2.63)	V(6.98)
5	V	III (4.86)	I (10.43)

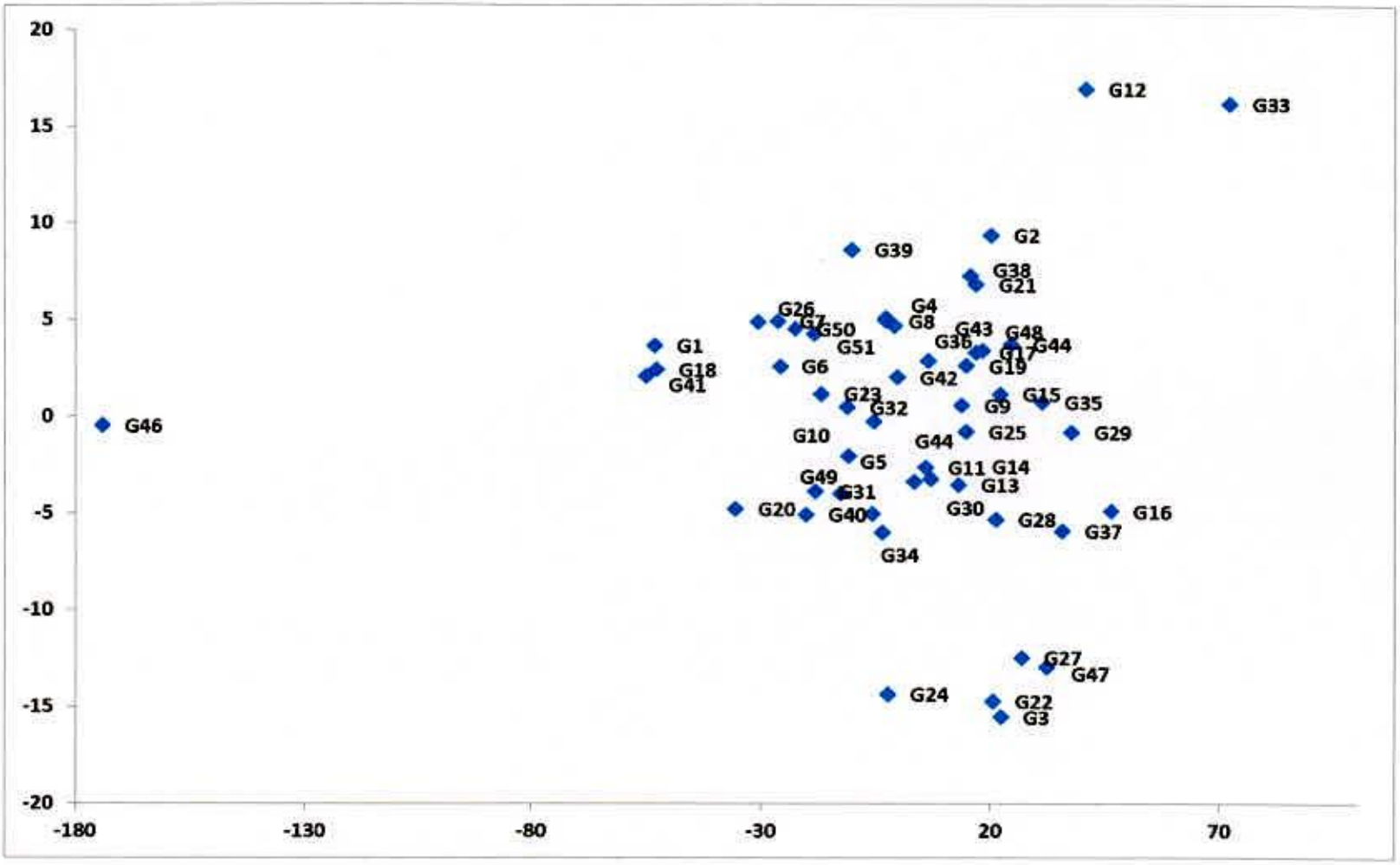


Figure 4:Scatter distribution of 51 *Brassica rapa* genotypes based on their principal component scores.

4.2.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among 51 genotypes of *Brassica* and grouped them into six clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So, the results obtained through PCA were confirmed by non hierarchical clustering (Table 11) represents the clusters occupied by 51 genotypes of *Brassica*. It explains that's cluster III contained the highest number of genotypes 19, cluster IV contains 17 genotypes, cluster II constitute by 9 genotypes, cluster V constitute by 4 genotypes and cluster I constitute by 2 genotypes. Cluster III composed of (BARI9 × BARI6 Special Early F_{11}, BARI9, BARI9 × BARI6$F_{11}S_6$, BARI9 × F_3 F_{11} Yellow S_3, BARI9 × BARI6 F_{11} S_{18}(Brown), BARI9 × F_6 F_{11} (Medium), BARI6 × Tori7 F_{11}, BARI 6 × Tori 7 S_3 F_{11}, BARI 6 × SAU 1 F_3, SAU1 × Tori 7 F_3, SAU 1 F_3, SAU 1, SAU 3, SS_{75} × Tori 7 F_{11}, $BARI_{15}$ × SS_{75} F_5, BARI 15 × SAU 3 F_3, BARI 15 × BARI 9 $F_{11}S_6$, F_6 × BARI 9 F_3, F_6×BARI 9 S_4 F_3) . Intra cluster mean for 10 traits are presented in (Table 9). These clusters were unable to lead in respect of the highest cluster. Cluster 1 was formed by two genotypes viz. Tori 7 × BARI 6 F_3, SAU 2.

Table 11:Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G12, G33	2	TorilI7×BARI6 F_3, SAU 2,
II	G3,G16, G22, G27, G28, G29, G35, G37, G47	9	BARI9×F_6F_{11}, Tori 7, BAR-6×SAU-2 F_3, SAU 1×BARI 6 F_3, SAU 2×BAR6 F_3, SAU 3×SAU1 F_3 S_5, SAU 1×SAU 2 , SAU 3×SAU1 F_3 , BARI15×SAU1 F_3
III	G4, G5, G6, G7, G8, G10, G20, G23, G24, G26, G31, G32, G34, G39, G40, G45, G49, G50, G51	19	BARI9×BARI6 Special Early F_{11}, BARI9, BARI9×BARI6$F_{11}S_6$, BARI9×F_3 F_{11} Yellow S_3, BARI9×BARI6 F_{11} S_{18}(Brown), BARI9×F_6F_{11}(Medium), BARI6×Tori7 F_{11}, BARI 6×Tori 7 S_3 F_{11}, BARI 6×SAU 1 F_3, SAU1×Tori 7 F_3, SAU 1 F_3, SAU 1, SAU 3, SS_{75}×Tori 7 F_{11}, $BARI_{15}$×SS_{75} F_5, BARI 15×SAU3 F_3, BARI 15×BARI9 $F_{11}S_6$, F_6×BARI9 F_3, F_6×BARI9 S_4F_3
IV	G2, G9, G11, G13, G14, G15, G17,G 19,G21, G25, G30, G36, G38, G42, G43, G44, G48	17	BARI 9×BARI6Yellow F_{11}, BARI9 F_{11}Selection, Tori 7×BARI9 F_{11}, Tori 7×SAU1F_3, Tori 7×BARI 6 F_{11} S_{22}, TorilI 7×SAU 1 F_{11}, Tori 7×BARI 6 $_{F11}$ Early, BARI6×SAU 2, BARI 6×SAU 3 F_3, BARI 6, SAU 1×SAU 2 F_3, SAU 1×BARI 6 , SAU2×BARI 6 F_3 S_{17}, BARI15×BARI6 F_3, BARI 15×SAU 2 F_3, BARI15×SAU 2 , BARI 15×Tori 7 F_3
V	G1, G18, G41, G46	4	BARI9×BARI6F_{11}, Tori 7×BARI 6 F_{11}, BARI15×SS_{75} F_3(Late), BARI 15

Table 12: Cluster mean values of 10 different characters of 51 genotypes of *Brassica rapa*

Characters	I	II	III	IV	V
plant height (cm)	87.55	**112.09**	104.62	102.54	**103.01**
Number of primary branches per plant	3.92	4.82	4.72	4.45	5.65
Number of secondary branches per plant	0.80	1.46	2.36	1.41	3.32
Number of sliqua per plant	83.44	109.29	154.33	127.20	223.29
Number of seed per siliqua	17.54	**19.94**	18.58	16.80	**17.66**
Siliqua length (cm)	4.94	**5.47**	5.21	5.15	**5.22**
Days to 50 % flowering	47.17	49.48	49.84	48.00	50.33
Days to 50 % maturity	105.17	**106.15**	105.35	104.49	**103.84**
1000 seed weight (g)	2.56	2.71	2.82	2.69	2.85
Yield per plant (g)	**3.79**	**5.86**	**8.10**	**5.76**	11.13

Plate 55: Siliqua view of different *Brassica rapa* genotypes of Cluster-I

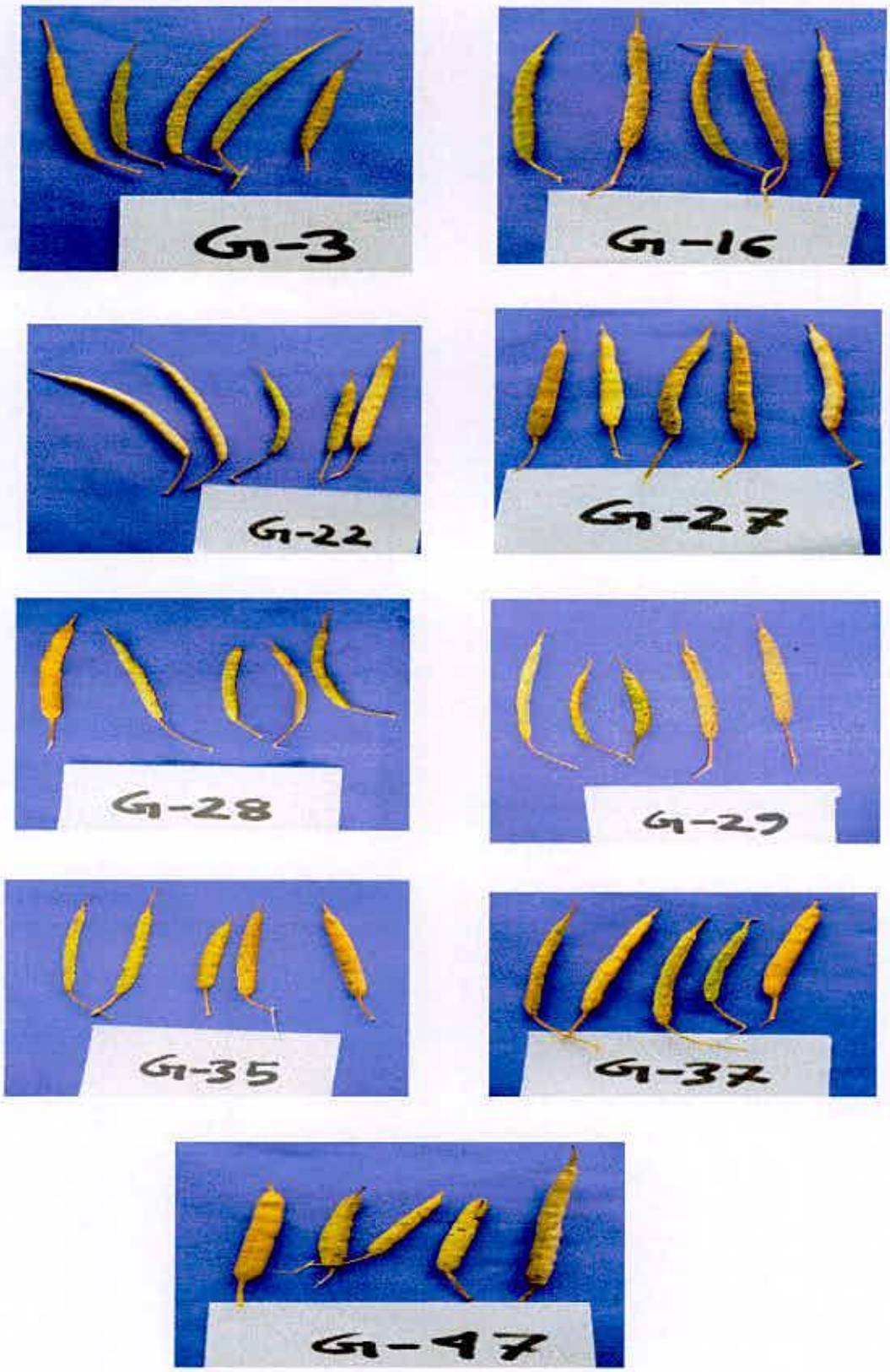


Plate 56: Siliqua view of different *Brassica rapa* genotypes of Cluster-II

Plate 57: Siliqua view of different *Brassica rapa* genotypes of Cluster-III

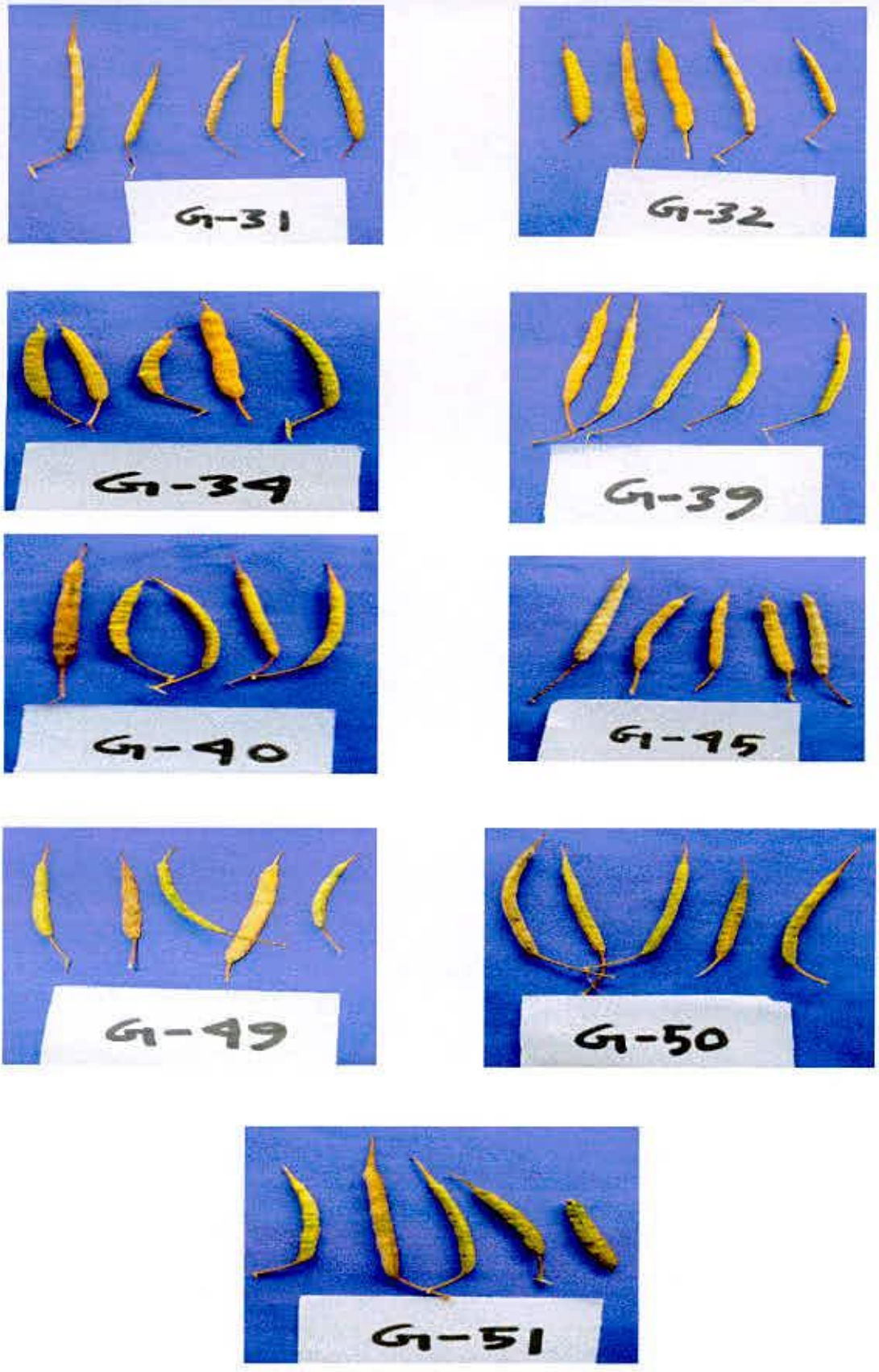


Plate 58: Siliqua view of different *Brassica rapa* genotypes of Cluster-III

Plate 59: Siliqua view of different *Brassica rapa* genotypes of Cluster-IV

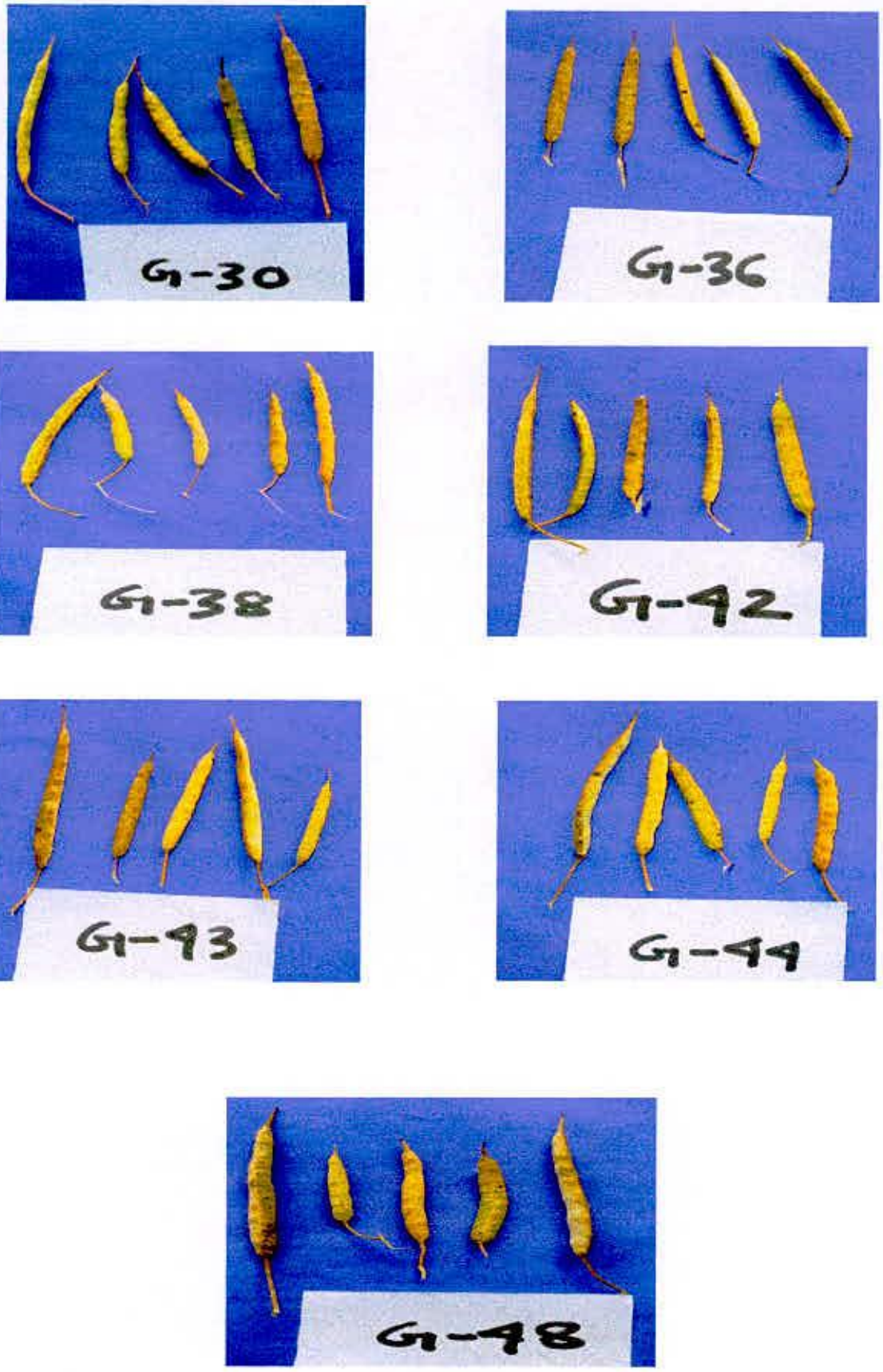


Plate 60: Siliqua view of different *Brassica rapa* genotypes of Cluster-IV

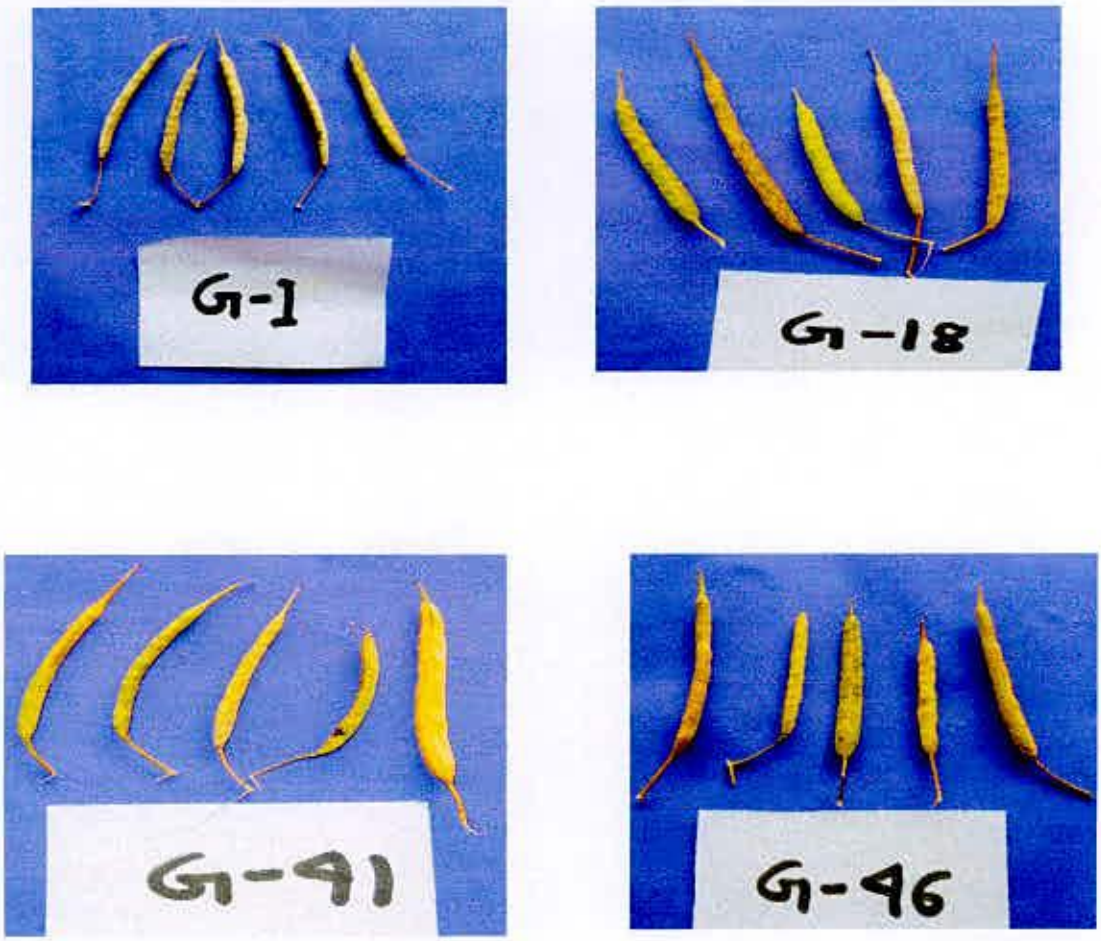


Plate 61: Siliqua view of different *Brassica rapa* genotypes of Cluster-V

These cluster were able to lead in respect of the highest cluster mean for maximum characters. Among 10 characters this cluster stood first for five characters viz. plant height (112.09), number of sliqua per plant (223.29), number of seed per siliqua (19.94), days to 50 % flowering (50.33), days to 50 % maturity (106.15), and seed yield per plant (11.13). Cluster 1 has two genotypes named Tori 7 × BARI 6 F_3, SAU 2. The highest cluster mean value was achieved for three characters viz. for plant height (112.09), number of sliqua per plant (223.29) and days to 50 % maturity (106.15). (Table12). The genotype BARI 9 × F_6 F_{11}, Tori 7, BAR 6×SAU 2 F_3, SAU 1× BARI 6 F_3, SAU 2 × BAR6 F_3, SAU 3 × SAU 1 F_3 S_5, SAU 1 × SAU 2, SAU 3 × SAU 1 F_3, BARI15 × SAU1 F_3 established cluster II.

4.2.4 Canonical variate analysis(CVA)

The highest inter-cluster distance was observed (Table 9) between I and V (10.43). The intra cluster distance was the highest (0.459) in cluster V. The lowest inter-cluster distance was observed between cluster III and cluster IV (2.63). Moderate or intermediate distance was found between cluster II and III (6.55), cluster I and II (6.69) and cluster IV and V (6.98). The inter cluster distance were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups.

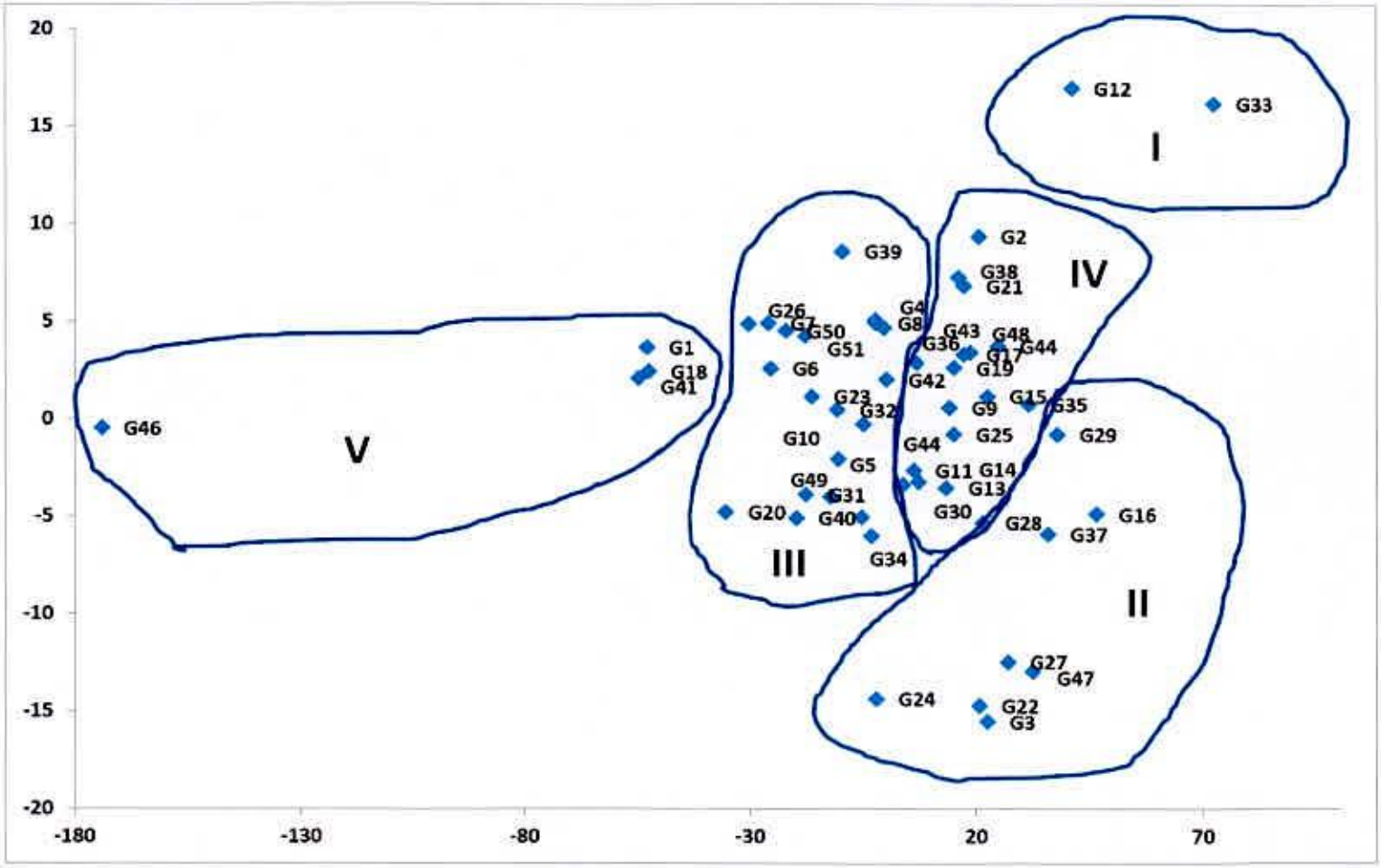


Fig 5:Scatter distribution of 51 *Brassica rapa* genotypes based on their principle Component scores superimposed with clustering.

Table 13:Relative contributions of the ten characters of 51 varieties to the total divergence

Characters	Vector-1	Vector-2
plant height (cm)	-0.0850	-0.4109
Number of primary branches per plant	-0.3526	-0.0414
Number of secondary branches per plant	-0.3192	0.1675
Number of sliqua per plant	-0.3897	0.4287
Number of seed per sliqua	-0.3430	-0.3917
Siliqua length (cm)	-0.3163	-0.5271
Day to 50 % flowering	0.1067	0.2230
Day to 50 % maturity	0.1058	-0.3124
1000 seed weight (g)	-0.2532	0.0799
Yield per plant (g)	0.5571	0.1806

Table14: Principal component scores (Z_1-Z_2 values) for 51 *Brassica rapa* genotypes.

Genotypes	Designation	Z_1	Z_2
G-1	BARI 9×BARI6 F_{11}	-52.78	3.69
G-2	BAR I9×BARI 6 Yellow F_{11}	20.57	9.39
G-3	BARI 9×F_6F_{11}	22.49	-15.53
G-4	BARI 9×BARI 6 Special Early F_{11}	-2.34	5.11
G-5	BARI 9	-5.37	-5.04
G-6	BARI 9×BAR I6 $F_{11}S_6$	-25.39	2.60
G-7	BARI 9× F_3F_{11} Yellow S_3	-25.91	4.94
G-8	BARI 9×BARI 6 F_{11} S_{18}(Brown)	-2.36	4.96
G-9	BARI 9 F_{11} Selection	14.06	0.59
G-10	BARI 9×F_6 F_{11} Medium	-4.95	-0.25
G-11	TORI 7×BARI 9 F_{11}	6.14	-2.63
G-12	TORI 7×BARI 6 F_3	41.15	16.96
G-13	TORI 7×SAU 1F_3	13.38	-3.52
G-14	TORI 7×BARI 6 F_{11} S_{22}	7.27	-3.22
G-15	TORI 7×SAU 1 F_{11}	22.45	1.17

G-16	TORI 7	46.55	-4.86
G-17	TORI 7×BARI 6 F_{11} Early	17.25	3.33
G-18	TORI 7×BARI 6 F_{11}	-52.43	2.46
G-19	BARI 6×SAU 2	15.09	2.65
G-20	BARI 6×TORI 7 F_{11}	-35.27	-4.77
G-21	BARI 6×SAU 3 F_3	17.22	6.85
G-22	BARI 6×SAU 2 F_3	20.71	-14.71
G-23	BARI 6×TORI 7 S_3F_{11}	-16.33	1.17
G-24	BARI 6×SAU 1 F_3	-2.10	-14.37
G-25	BARI 6	15.04	-0.77
G-26	SAU 1×TORI 7 F_3	-30.28	4.90
G-27	SAU 1×BARI 6 F_3	26.99	-12.46
G-28	SAU 2×BAR6 F_3	21.43	-5.31
G-29	SAU 3×SAU1 F_3 S_5	37.91	-0.79
G-30	SAU 1×SAU 2 F_3	3.71	-3.37
G-31	SAU 1 F_3	-17.64	-3.86
G-32	SAU 1	-10.71	0.50
G-33	SAU 2	72.36	16.19
G-34	SAU 3	-3.18	-6.00

G-35	SAU 1×SAU 2	31.52	0.76
G-36	SAU 1×BARI 6	-0.46	4.69
G-37	SAU 3×SAU1 F_3	35.87	-5.90
G-38	SAU2×BARI6 F_3 S_{17}	16.06	7.28
G-39	SS_{75}×TORI 7 F_{11}	-9.64	8.61
G-40	BARI15×SS_{75} F_5	-19.69	-5.08
G-41	BARI15×SS_{75} F_3(Late)	-54.62	2.12
G-42	BARI15×BARI6 F_3	0.10	2.05
G-43	BARI 15×SAU 2 F_3	6.78	2.89
G-44	BARI 15×SAU 2	24.75	3.75
G-45	BARI 15×SAU3 F_3	-10.44	-2.04
G-46	BARI 15	-173.97	-0.46
G-47	BARI 15×SAU 1 F_3	32.43	-12.95
G-48	BARI 15×TORI 7 F_3	18.61	3.42
G-49	BARI 15×BARI9 $F_{11}S_6$	-12.18	-3.98
G-50	F_6×BARI9 F_3	-22.09	4.55
G-51	F_6×BARI9 S_4 F_3	-17.75	4.28

No parallel relationship was found between genetic and geographic divergence, which may be due to continuous exchange of germplasm from one place to another. Differently originated genotypes found in same cluster or genotypes from same origin were dispersed in different clusters. It was observed that group I formed with ten genotypes originated in Bangladesh and group II occupied by four genotypes originated from Bangladesh and Thailand origin and group III occupied by four genotypes originated from Bangladesh and Thailand group IV occupied by two genotypes originated from Bangladesh origin. Genotypes from Thailand and Bangladesh being in different clusters, indicating the broad genetic variability. There was evidence from Shanmugan and Rangasamy (1982) showed that materials from same origin distributed in different clusters are an indication of broad genetic base of the genotypes belonging to that origin.

4.2.5 Contribution of characters towards divergence of the genotypes

The values of vector I and vector II are presented in Table 13 . Vector I obtain from PCA express days to 50 % maturity (0.1058) was major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II number of secondary branches per plant (0.1675), number of siliqua per plant (0.4287), 1000 seed weight (0.0799) and seed yield per plant (0.1806) (Table13) showed their important role toward genetic divergence. Number of siliqua per plant indicating the highest contribution of these traits towards the divergence The value of vector I and vector II revealed that both vectors and positive values for days to 50 % flowering and seed yield per plant among 51 genotypes of *Brassica* contribute towards the total divergence.

4.2.6.Selection of genotypes as parent for hybridization programme

Among the inter cluster distance, distance I and V (10.43) were the highest and other cluster were more or less intermediate distance. Inter mediate diverse parents have the more chance to contribute heterosis in the subsequent generations. To select cluster to obtain more heterotic genotype five pairs of clusters to be considered for this purpose, they are I and V (10.43), II and V (8.26), IV and V (6.98), I and II (6.69) and I and III (6.55). Cluster V had the highest cluster mean for number of primary branches per plant (5.65), number of secondary branches plant (3.52), number of siliqua per plant (223.29), days to 50 % flowering (50.33), thousand seed weight (2.85) and seed yield per plant (11.13) (Table12) were the most important yield contributing character with the BARI 9 × BAR I6F_{11}, Tori 7 × BARI 6 F_{11}, BAR I15 × SS_{75} F_3 (Late), BARI 15. On the other hand the cluster II comprised the highest cluster mean for plant height (112.09), number of seeds per siliqua (19.94), length of siliqua (5.47) and days to 50 % maturity (106.15) and with the genotype BARI 9 × F_6F_{11}, Tori 7, BAR 6 × SAU 2 F_3, SAU 1 × BARI 6 F_3, SAU 2 × BAR6 F_3, SAU 3× SAU 1 F_3 S_5, SAU 1 × SAU 2 , SAU 3 × SAU 1 F_3 ,BARI15 × SAU1 F_3 .Hybridization between the genotypes of cluster V and cluster II may will manifest maximum heterosis and creates wide genetic variability.

Genetically distant parents are usually able to produce highest heterosis. Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance the genotype G-1, G-18, G-41.and G-46 from cluster V and G-3, G-16, G-22, G-27, G-28, G-29, G-35, G-37 and G-47 would be suitable for highest yield per for future hybridization programme.

It assumed that highest heterosis would be manifest in cross combination involving the genotypes belonging to divergent clusters. However for a practical plant breeder, the objective was not only high heterosis but also to achieve high level of production. Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between between G-1 and G-3, G-1 and G-16, G-1 and G-22, G-1 and G-27, G-1 and G-28, G-1 and G-29, G-1 and G-35, G-1 and G-37, G-1 and G-47,

G-18 and G-3, G-18 and G-18 and G-16, G-18 and G-22, G-18 and G-27, G-18 and G-28, G-18 and G-29, G-18 and G-35, G-18 and G-37, G-18 and G-47, G-41 and G-3, G-41 and G-16, G-41 and G-22, G-41 and G-27, G-41 and G-28, G-41 and G-29, G-41 and G-35, G-41 and G-37 , G-41 and G-47, G-46 and G-3, G-46 and G-16, G-46 and G -22, G-46 and G-27, G-46 and G-28, G-46 and G-29, G-46 and G-35, G-46 and G-37 and G-46 and G-47 might be suitable choice for future hybridization programme.

CHAPTER V

SUMMARY AND CONCLUSION

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In order to study the inter genotypic variability and genetic diversity of *Brassica rapa*, the present experiment was carried out during the period of November , 2012 to February 2013, at the experimental farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka. It was involved with 51 genotypes of *Brassica rapa* of different origin / sources. The experiment was conducted to study inter genotypic variability considering ten important yield and yield contributing characters, viz, days to 50 % flowering, days to 50 % maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua, thousand seed weight, yield per plant. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replication. The results of the present study are summarized as follows:

Highly significant variation was observed among the genotypes for all the characters except hundred seed weight. From the mean value, G-7 and G-46 was early flowering and early maturing respectively while G-24 was flowering and G-34 late maturing respectively. G-3 was the tallest type plant, whereas G-12 was the shortest. G-18 produced highest number of primary branches per plant and G-4 produced lowest. Highest number of secondary branches per plant was observed in G-6 while G-14 produced lowest. G-46 showed highest number of siliqua per plant and G-33 showed lowest.The length of siliqua was highest and lowest in G-32 and G-39 respectively. G-28 produced highest number of seeds per siliqua while G-44 produced lowest. Highest 1000 seed weight was recorded in G-2 while lowest in G-42. G-46 produced highest yield per plant where as lowest was produced by G-25.

Most of the characters showed wide range of variation. The phenotypic variation was higher than the corresponding genotypic variance for all the characters. Among the characters, primary branches per plant, secondary branches per plant, thousand seed weight and seed yield per plant showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of those characters. Amongest the characters the highest genotypic and phenotypic co-efficient

of variationwas recorded for secondary branches per plant (GCV = 66.97, PCV =71.20), seed yield per plant (GCV = 31.90, PCV = 33.91), number of siliqua per plant (GCV = 25.89,PCV = 27.14) and primary branches per plant (GCV = 14.78, PCV = 16.51) and number of seed per siliqua (GCV = 14.84, PCV = 15.52). Amongest the characters the lowest genotypic and phenotypic co-efficient of variation was recorded for days to 50 % flowering (GCV = 5.76, PCV = 6.22), days to 50 % maturity (GCV = 3.04, PCV = 3.83), plant height (GCV = 6.13, PCV = 7.13), siliqua length (GCV = 8.20, PCV = 11.72) and thousand seed weight (GCV = 11.23, PCV = 13.56).

Among the ten characters highest estimated heritability was 91.38 % for number of seeds per siliqua and lowest for the siliqua length 48.95 %. The highest genetic advance was found in number of siliqua per plant (71.24 %) and the lowest genetic advance was found in thousand seed weight (0.53 %). The highest genetic advance in percent of mean was observed for secondary branches per plant (129.72 %) and the lowest was days to 50 % maturity (4.97%). Number of seeds per siliqua was showed high heritability (91.38 %) but low genetic advance in percent of mean (5.29 %) indicated non-additive gene action for the expression of the characters. In such case, high heritability was exhibited due to favorable environment rather than genotype

Correlation revealed that highly significant positive association of seed yield per plant was observed with number of siliqua per plant, thousand seed weight,number of seed per siliqua, number of primary branches per plant (both genotypic and phenotypic level). Path analysis showed that, yield per plant had the highest direct effect on number of siliqua per plant, number of seed per siliqua and thousand seed weight.

As per PCA , D^2 and cluster analysis, the genotypes were grouped into five different clusters. These cluster were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. Cluster III had maximum (19) and Cluster I had minimum (2) number of genotypes.The highest inter-cluster distance was observed between cluster I and cluster V (10.43). The highest intra cluster distance was cluster V (0.459). The lowest intra cluster distance was cluster I (0.01). Moderate or intermediate inter cluster distance was found between cluster I and cluster IV (4.47) and cluster III and cluster V (4.86). The inter cluster distances were higher than the intra cluster distance suggesting wider genetic diversity among the genotypes of different groups.

To select cluster to obtain more heterotic genotype five pairs of clusters to be considered for this purpose, they are I and V (10.43), II and V (8.26) , IV and V (6.98) , I and II (6.69) and I and III (6.55). Cluster V had the highest cluster mean for no. of primary branches per plant (5.65), number of secondary branches plant (3.52), number of siliqua per plant (223.29), days to 50 % flowering (50.33), thousand seed weight (2.85) and seed yield per plant (11.13) (Table 9) were the most important yield contributing character with the BARI 9 × BAR I6 F_{11}, Tori 7 × BARI 6 F_{11}, BAR I15 × SS_{75} F_3(Late) and BARI 15 . On the other hand the cluster II comprised the highest cluster mean for plant height (112.09), number of seeds per siliqua (19.94), siliqua length (5.47) and days to 50 % maturity (106.15) and with the genotype BARI 9 × F_6F_{11}, Tori 7, BAR-6 × SAU 2 F_3, SAU 1 × BARI 6 F_3, SAU 2 × BAR6 F_3, SAU 3 × SAU 1 F_3 S_5, SAU 1 × SAU 2, SAU 3 × SAU 1 F_3 ,BARI15 × SAU1 F_3 . Hybridization between the genotypes of cluster V and cluster II may will manifest maximum heterosis and create wide genetic variability.

Considering group distance and agronomic performance , the inter genotypic crosses between between G-1 and G-3, G-1 and G-16, G-1 and G-22, G-1 and G-27, G-1 and G-28, G-1 and G-29, G-1 and G-35, G-1 and G-37, G-1 and G-47, G-18 and G-3, G-18 and G-18 and G-16, G-18 and G-22, G-18 and G-27, G-18 and G-28, G-18 and G-29, G-18 and G-35, G-18 and G-37, G-18 and G-47, G-41 and G-3, G-41 and G-16, G-41 and G-22, G-41 and G-27, G-41 and G-28, G-41 and G-29, G-41 and G-35, G-41 and G-37 , G-41 and G-47, G-46 and G-3, G-46 and G-16, G-46 and G -22, G-46 and G-27, G-46 and G-28, G-46 and G-29, G-46 and G-35, G-46 and G-37 and G-46 and G-47 might be suitable choice for future hybridization programme.

Considering the magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster mean for different characters and field performance the genotypes G-35 and G-47 from cluster III and G-I, G-18, G-41 and G-46 from cluster V would be suitable for highest yield per plant for future hybridization programme. Involvement of such diverse genotypes in crossing program produces desirable segregants. So, divergent genotypes are recommended to use as parenent in hybridization program.

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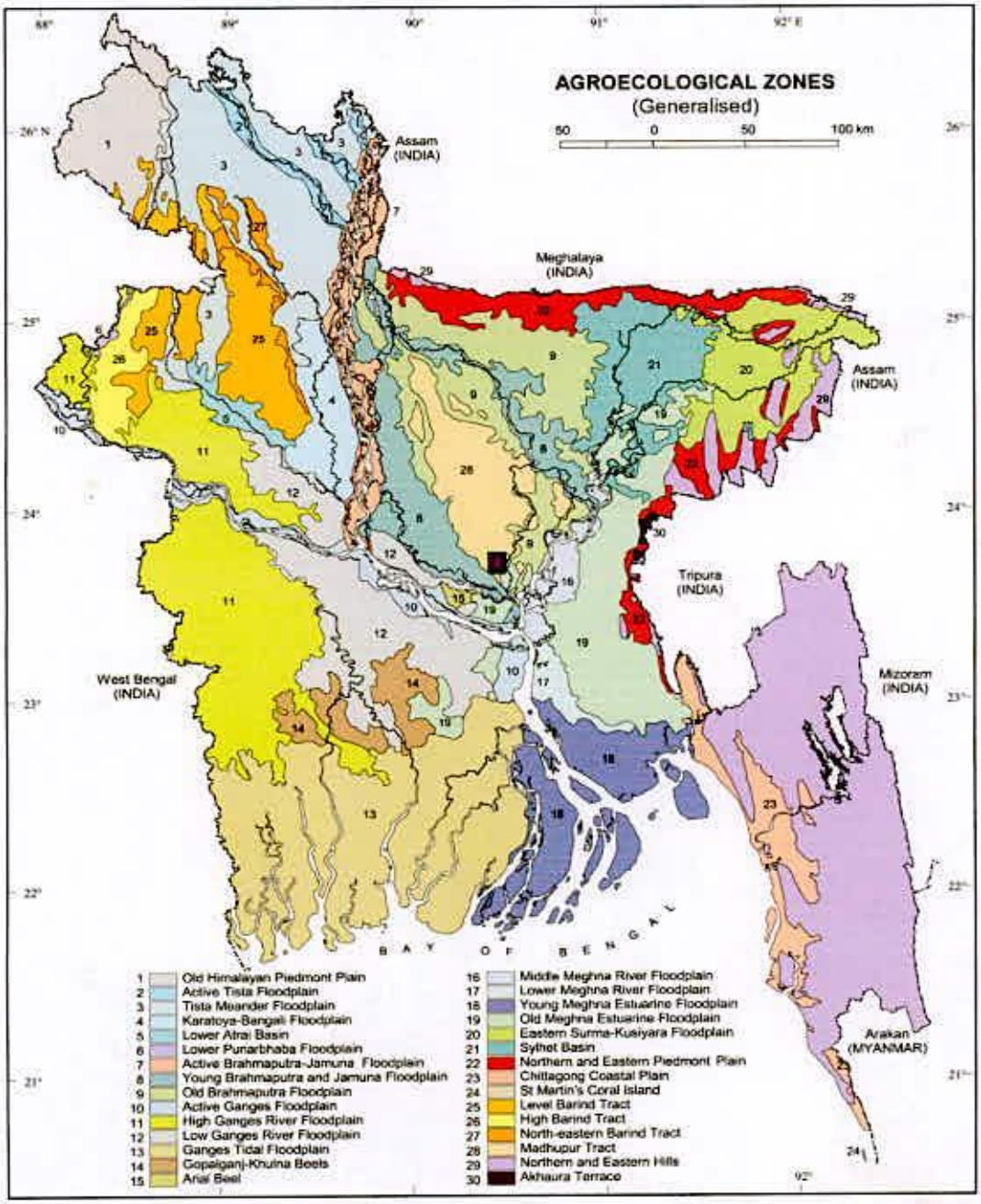
APPENDICES

Appendix I:

Map showing the experimental site under study



Appendix II

ANOVA Table

Source	Df	MS									
		PH	PBP	SBP	SPP	SPS	SL	D50%F	D50%M	TSW	SYP
REP	2	18.70	0.57	0.24	45.91	0.30	0.26	0.31	21.07	0.01	0.20
G	50	137.44**	1.56**	5.06**	3,844.82**	22.35**	0.74**	25.35**	36.64**	0.32**	15.57**
Error	100	14.45	0.11	0.21	99.92	0.68	0.19	1.33	6.02	0.04	0.64

AppendixIII. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from October, 2012 to April, 2013

Month	Air temperature		Relative Humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
October, 2013	33.1	18	77	227	5.4
November, 2013	32	15	67	0	7.8
December, 2013	28.2	13.5	79	0	3.5
January, 2014	24.5	11.5	72	1	5.7
February, 2014	33.1	12.9	55	1	8.1
March, 2014	33.6	15.3	63	43	7.5
April, 2014	36	21.2	65	86	9.5

Source: Bangladesh Metrological Department (Climate division),

Agargaon, Dhaka-1212

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

A. Physical composition of the soil

Soil separates	%	Metdods 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
01.	Organic carbon (%)	0.82	Walkley and Black, 1947
02	Total N (kg / ha)	1790.00	Bremmer and Mulvaney,1965
03	Total S (ppm)	225.00	Bardsley and Lanester,1965
04	Total P (ppm)	840.00	Olsen and Sommers, 1982
05	Available N (kg / ha)	54.00	Bremner, 1965
06	Available P (kg / ha)	69.00	Olsen and Dean ,1965
07	Exchangeable K (kg / ha)	89.00	Pratt, 1965
08	Available S (ppm)	16.00	Hunter,1984
09	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-1207