

# INTERGENOTYPIC VARIATION AMONG ADVANCED

LINES OF *Brassica rapa*

BY

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A Thesis

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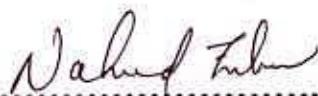
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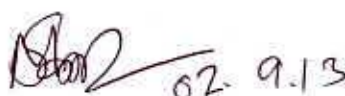
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## **CERTIFICATE**

This is to certify that thesis entitled, **"INTERGENOTYPIC VARIATION AMONG ADVANCED LINES OF Brassica rapa"** 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 bonafide research work carried out by **NAHID FARHANA**, **Registration No. 23883/00149** 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.

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**Place: Dhaka, Bangladesh**

  
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**REFERENCE ONLY**



**DEDICATED  
TO  
MY BELOVED  
CHILDREN**



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**December, 2012**

**SAU, Dhaka**

**The Author**

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## LIST OF ABBREVIATED TERMS

| FULL WORD                                  | ABBREVIATION  |
|--------------------------------------------|---------------|
| Agro-Ecological Zone                       | AEZ           |
| And others                                 | <i>et al.</i> |
| Bangladesh Agricultural Research Institute | BARI          |
| Bangladesh Bureau of Statistics            | BBS           |
| Centimeter                                 | cm            |
| Co-efficient of Variation                  | CV            |
| Etcetera                                   | <i>etc.</i>   |
| Figure                                     | Fig.          |
| Genotype                                   | G             |
| Genetic Advance                            | GA            |
| Genotypic Co-efficient of Variation        | GCV           |
| Genotypic Variance                         | $\delta^2_g$  |
| Gram                                       | g             |
| Heritability in broad sense                | $h^2_b$       |
| Journal                                    | j.            |
| Kilogram                                   | Kg            |
| Meter                                      | M             |
| Mean Sum of Square                         | MSS           |
| Millimeter                                 | Mm            |
| Muriate of Potash                          | MP            |
| Number                                     | No.           |
| Percent                                    | %             |
| Phenotypic Co-efficient of Variation       | PCV           |
| Phenotypic variance                        | $\delta^2_p$  |
| Randomized Complete Block Design           | RCBD          |
| Replication                                | R             |
| Research                                   | Res.          |
| Sher-e-Bangla Agricultural University      | SAU           |
| Standard Error                             | SE            |
| Square meter                               | $m^2$         |
| Triple Super Phosphate                     | TSP           |

# **INTERGENOTYPIC VARIATION AMONG ADVANCED LINES OF *Brassica rapa***

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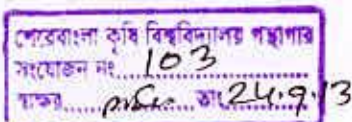
## **ABSTRACT**

A field experiment was conducted in the experimental field of Genetics and Plant Breeding field laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period of October 2010 to March 2011 to study the inter genotypic variation among advance lines of *Brassica rapa*. The experiment was carried out to study variability, heritability, genetic advance and genetic advance in percentage of mean, genetic diversity, character associations and direct and indirect effect of different traits on yield. Seeds are sown in the field in Randomized Complete Block Design (RCBD) with three replications. There was a great deal of significant variation for all the characters among the genotypes. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for no. of secondary branch, seed yield per plant and seed yield per hectare whereas low GCV was observed for length of siliqua and thousand seed weight. In all cases, phenotypic variances were higher than the genotypic variance. High heritability with high genetic advance in percent of mean was observed for yield per plant indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. The results obtained, showed that seed yield per hectare had highest significant positive correlation with yield per plant. Seed yield per plant had also significant positive correlation with seed per siliqua at genotypic level. Considering group distance and other agronomic performance the inter genotypic crosses between G16 and G18; G16 and G19; G16 and G22; G16 and G28 may be suggested for future hybridization program. So, these are found the important characters and could be used on direct selection for yield.



## CHAPTER I

### INTRODUCTION



*Brassica*, accounting for over 16% of the world's edible oil supply is an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. *Brassica* is cross pollinated oil crops belonging to the family Brassicaceae. *Brassica* have taproot system, with succulent, straight and cylindrical stem. The leaves are pinnati-divided. The inflorescence is racemose and flowering is indeterminate beginning at the lowest bud on the main raceme and blooming continues for two-three weeks. Stigma is receptive for about six days. The primary centre of origin for *Brassica campestris* is near the Himalayan region and the secondary centre of origin is located in the European -mediterranean area and Asia (Downey and Robelen, 1989). Major producing regions are China, the Indian subcontinent, Canada and Northern Europe (Ram and Hari, 1998).

*Brassica* have great economic and commercial value and play a major role in our daily diet. Fat and oils are vital components of the human diet because they are important sources of energy and act as a carrier of fat soluble vitamins. Poor intake of fat and oil reduce the availability of fat soluble vitamins and caused dietary imbalance and food wastage. In a balanced diet 20-25% of calories should come from fats and oils and the average need of fats and oils is about 37 g/day (Rahman, 1981). The seeds of *Brassica rapa* contain 42% oil and 25% protein (Khaleque, 1985).

According to FAO (2005), the oil yielding crop *Brassica* hold the second position in the world oil seed production. In Bangladesh rapeseed and mustard of *Brassica* are is the major source of edible oil and more than 183 thousand metric ton of rape and mustard produced from total 216.92

thousand hectares of cultivable land in the year 2005-2006 (BBS, 2006). Its average yield per hectare was only 733 kg in Bangladesh compared to the world average of 1575 kg (FAO, 2005).

Though Bangladesh is an agricultural country the country is facing increasing deficiency in oil seed production and consequently import cost is increasing. The causes are- low yield potential of the varieties, insufficient precipitation when the crops are cultivated under rain fed conditions, pressure of other crops and the primitive crop husbandry method. Moreover, area of oil seed crops including mustard and rapeseed is also decreasing. On the other hand; high population growth rate is also putting increased pressure on the per capita consumption of oils.

In Bangladesh there is limited scope to increase acreage due to pressure of other crops. And there is limited scope to increase yield because farmers usually cultivate the existing low yielding varieties with low input and management and almost all cultivars are brown seeded and smaller in size (2-2.5 g/1000 seeds). Short duration variety like Tori-7 of *B. rapa* is still popular in Bangladesh because it can fit well into the T.Aman - Mustard - Boro cropping pattern. There is no improved short duration variety of *B. rapa* is available to replace this short duration but low yielding variety.

The genus *Brassica* has generally been divided into three groups namely - rape seed, mustard and cole. The rape seed groups includes the diploid *Brassica rapa*, turnip rape (AA,  $2n=20$ ) and amphidiploid *Brassica napus* L, rape (AACC,  $2n=38$ ) while the mustard groups include species like *Brassica juncea* Czern and Coss; *Brassica nigra* Koch and *Brassica carinata* Braun. The genomic constitutions of the three elemental species of *Brassica* are as follows; "AA" for *Brassica campestris*, "BB" for *Brassica*



*nigra* and “CC” for *Brassica oleracea* having diploid chromosome number 20, 16 and 18 respectively. The species *Brassica juncea* (AABB,  $2n=36$ ) *Brassica carinata* (BBCC,  $2n=34$ ) and *Brassica napus* (AACC,  $2n=38$ ) are the amphidiploid and originated by combination of the diploid elemental species. All these species have many cultivated varieties suited to different Agro-climatic conditions. In the oleiferous *Brassica* group, a considerable variation of genetic nature exists among different species and varieties within each species in respect of different morphological characters (Malik *et al.* 1995; Kakroo and Kumar 1991).

Hybridization is one of the major tools for creating variability aiming at the improvement of a crop. Before hybridization genetic diversity of the existing materials or entries needs to be known. Information about genetic diversity in available germplasm is important for the optimal design of any breeding program. This helps to choose desirable parents for establishing new breeding population. Besides better knowledge on genetic diversity could help to sustain long term selection gain (Chowdhury *et al.* 2002).

Information on genetic variability is a prerequisite for initiating a successful breeding program aiming to develop high yielding varieties. Determination of correlation co-efficient between the characters has a considerable importance in selecting breeding materials. The path co-efficient analysis has been found to give more specific information on the direct and indirect influence of each of the component characters upon seed yield (Behl. *et al.* 1992).

According to Burton (1952), for the improvement of any character through breeding, it is essential to know the extent of variability present in that species, nature of association among the characters and the

contribution of different characters towards seed yield. The efficiency of a plant breeding program depends on the amount of genetic variability exist in nature or how much a plant breeder can create variability in the target population so as to perform effective selection.

Yield is the complex end product of many factors which jointly or singly influence the seed yield. *Brassica* yield is dependent on many important characters as well as on the environmental influence. For yield improvement it is essential to have knowledge on genetic variability of a biological population. It is an outcome of genetic constitution of the individuals making up that population in relation to prevailing environment. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme.

Conceiving the above idea the present study was undertaken-

- To estimate inter-genotypic variation among the advanced lines of *Brassica rapa*,
- To assess the association of different characters and their direct and indirect effect on yield and
- To determine the contribution of different traits towards divergence.



## 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, co-efficient analysis, heritability and genetic advance have been carried out in many countries of the world. Therefore, the review of the important research work relevant to the present study, are stated below

#### **2.1 Variability and character association**

The representative varieties used in many different studies under certain agro- ecological conditions of production have expressed different degrees of variation. Parts of these were genetic and part non-genetic. It is therefore, important to review the variabilities that have been found in different materials for some specific characters of interest.

Satyendra and Mishra (2007) used twenty-one genotypes of Indian mustard to work out genetic variability and heritability and genetic advance. The study revealed that the treatments differed highly significantly from each other for days to flowering and maturity, plant height, siliquae per branch and seed yield per plant, characters. The estimates of phenotypic variances were higher than their corresponding genotypic variances. Plant height, siliquae per branch and seed yield per plant had high heritability estimates along with high genetic advance.

Variability was studied in  $F_2$  progenies of the inter-variatal crosses of 17 *Brassica rapa* genotypes by Parveen (2007). The result revealed that there



were significant variations among the different genotypes used in the experiment. Number of primary branches/plant and secondary branches/plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage of mean.

Correlation co-efficient analysis revealed that yield/plant had non-significant positive association with plant height, number of secondary branches/plant, days to 50% flowering, length of siliqua, number of siliquae/plant and number of seeds/siliqua. Path coefficient analysis revealed that number of seeds/siliqua showed highest direct effect on yield/plant.

In an experiment, variability of 40 genotypes of oleiferous *Brassica* species was audied by Rashid (2007). 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 plant height, number of siliquae/plant, days to 50% flowering and days to maturity.

High heritability with low genetic advance was observed for the characters days to 50% flowering, days to maturity, primary branches/plant, 100-seed weight and yield/plant. Yield/plant confirmed highly significant positive association with plant height (0.503), length of siliqua (0.277), siliquae/plant (0.658) and seeds/siliqua (0.303) but insignificant negative association with days to 50% flowering (-0.058) and days to maturity (-0.092). Path analysis showed that siliquae/plant had positive direct effect (0.628) on yield/plant, while days to 50% flowering had negative direct effect (-0.184) on yield/plant [Zahan(2006)].

Inter genotypic variability, correlation and path analysis of quantitative characters of oleiferous *Brassica campestris* L. studied by Siddikee (2006). His study revealed all the characters were highly significant and variations among the genotypes were wide. In general, environmental influences were minimal on yield and its component. Heritability, genetic advance and genetic advance in percent of mean were high for almost all the characters. The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficient. Yield per plant had highest significant positive correlation with number of siliquae per plant followed by number of secondary branches per plant, seeds per siliqua, thousand seed weight, length of siliqua, number of primary branches per plant, plant height and days to first flowering and non significant positive correlation with days to maturity in both genotypic and phenotypic level. Path coefficient analysis revealed that thousand seed weight had the highest positive direct effect on seed yield per plant.

A study was conducted by Tusar *et al.* (2006) to assess the nature and extent of variability of 11 yield-related characters of 5 *Brassica spp.* genotypes. Phenotypic correlation studies indicated that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliquae per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Path coefficient analysis revealed that the number of siliquae per plant had the greatest direct contribution on seed yield, followed by the number of seeds per siliqua and 1000-seed weight, while indirectly via number of siliquae per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very



high positive direct effect on yield, but its correlation with yield was non-significant and negative.

Rai *et al.* (2005) was carried out study with Indian mustard involving 60 F<sub>1</sub>S derived from the crosses of 15 lines as females and 4 testers as males. Higher estimates of phenotypic coefficient of variation and genotypic coefficient of variation were recorded for 1000-seed weight, seed yield per plant, number of primary branches, seeds per siliqua and number of siliquae on main raceme. Genetic advance in absolute value ranged from 1.14 for number of primary branches to 17.25 for plant height. At phenotypic level, seed yield per plant had significant positive correlation with number of primary branches per plant (0.523) followed by plant height (0.455). All the characters, except for days to maturity, days to 50% flowering and oil content, demonstrated moderate to high estimates of GA% coupled with high heritability values. The direction of phenotypic and genotypic associations was the same for all the character pairs, except for days to maturity with 1000-seed weight. The correlation studies revealed that seed yield per plant was significantly and positively associated with plant height, number of primary branches per plant, days to 50% flowering and number of siliquae on main raceme.

Hoque (2006) studied gene action and combining ability in 8x8 diallel experiment on Indian mustard. His study revealed significant variations among the genotypes for all the characters studied. The components of variance for general combining ability (gca) and specific combining ability (sea) were highly significant for all traits indicating the role of both additive and nonadditive components in the genetic system on these characters. The inheritance of secondary branches per plant, length of siliqua, siliquae per plant and seed yield per plant was controlled by non-additive type of gene action.



Genetic variability, correlation and path analysis of 14 genotypes of mustard and rape were studied by Afroz *et al.* (2004). The highest genetic advance was observed in percent of pollen sterility. Seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliquae per plant. Path coefficient revealed maximum direct positive effects on plant height followed by number of siliquae per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant.

Mahak *et al.* (2004) conducted an experiment on genetic variability, heritability, genetic advance and correlation for 8 quantitative characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters. High heritability coupled with high genetic advance in percentage of mean was observed for days to flowering, followed by 1000- seed weight, days to maturity and plant height. 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.

Niraj and Srivastava (2004) associated an experiment on variability and character association studies in Indian mustard of 21 genotypes of *Brassica juncea*. RH-9704 and IGM-21 recorded the highest seed yield. Phenotypic coefficient of variation was high for oil yield per plant, seed yield per plant and seed weight. Heritability was high for test weight, days to flowering, days to maturity and plant height. Seed and oil yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

Katiyar *et al.* (2004) carried out a study 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. The variability, heritability, and genetic advance of 40 Indian mustard cultivars was studied in Ranchi, Bihar, India, during the 1995 rabi season by Poonam *et al.* (2003). The varietal differences were highly significant for plant height, days to 50% flowering, siliquae per plant, seeds per siliqua, days to maturity, 1000-seed weight and seed yield per plot. The coefficient of genotypic and phenotypic variations was highest for 1000-seed weight and was minimum for days to maturity. The highest genetic advance was obtained with 1000-seed weight (39.08), followed by seed yield per plot (20.18), days to 50% flowering (16.79), and siliquae per plant (16.49).

Mukesh *et al.* (2007) was conducted an experiment by studied in 25 genotypes of Indian mustard. Pooled analysis of variance revealed significant variation among the genotypes for all traits except pod length. The genotypes were classified into clusters I (6 genotypes), II (5 genotypes), III (3 genotypes), IV (4 genotypes), V (4 genotypes), VI (2 genotypes) and VII (one genotype). The intercluster distance was highest between clusters VI and VII. Cluster VII registered the highest seed yield per plant, 1000-seed weight, number of secondary branches, length of the main shoot, number of pods on the main shoot, and number of pods on secondary branches. Cluster VI showed the highest mean values for number of days to 50% flowering and maturity, seed filling period, number of secondary branches, length of the main shoot, and number of pods on primary branches.



Choudhary *et al.* (2003) variability studies in Indian mustard for 10 characters were during rabi season in India. A wide range of variability was observed for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua and 1000-seed weight. Genotypic and phenotypic coefficient of variability was recorded high for secondary branches per plant, seed yield per plant and number of siliquae per plant. High heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action.

Correlation studies and path coefficient analysis were conducted on 14 traits of Indian mustard genotypes done by Badsra and Chaudhary (2001). Seed yield was positively correlated with stem diameter, number of siliquae per plant and oil content, while oil content was positively correlated with harvest index only. Among the 3 characters positively correlated with seed yield, only number of siliquae per plant had a positive and high direct effect. Positive and direct effects on seed yield were also exhibited by test weight and number of seeds per siliqua.

Genetic variability for 9 traits was assessed by Pant and Singh. (2001) in 25 genotypes. Analysis of variance revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. All traits showed high heritability, with the highest value estimated for seed yield per plant. The estimates of genetic advance were comparatively low for oil content and days to flowering. The genotypic coefficient of variation and heritability estimates for oil content and days to flowering suggest that these traits

cannot be improved effectively merely by selection.

Genetic variability and association of yield components in Indian mustard among 12 yield components were studied for 36 genotypes selected from different geographical regions by Ghosh and Gulati (2001). The genotypic and phenotypic coefficients of variability (GCV and PCV respectively) were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied, coupled with high heritability except plant height, indicating the usefulness of phenotypic selection in improving these traits. High heritability, coupled with high genetic advance was observed for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per silique. This result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection. Seed yield exhibited significant positive association with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliquae on main shoot and oil content.

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

Khulbe *et al* (2000) conducted an experiment to estimates of variability, heritability and genetic advance for yield and its components in Indian mustard revealed maximum variability for seed yield. All the characters except oil content exhibited high heritability with high or moderate genetic advance, suggesting the role of additive gene action in conditioning the



traits. Nonadditive gene action appeared to influence the expression of days to maturity, while environment had a major influence on oil content. The use of pedigree selection or biparental mating in advanced generations was advocated to achieve substantial gains.

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

Masood *et al.* (1999) studied seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* to calculate genetic variability. The coefficient of variation was high for thousand seed weight, pod length and number of seeds per pod for both genotypic and phenotypic variability. The genotypic and phenotypic correlation coefficients showed that seed yield per plant were significantly positively correlated with plant height, number of siliquae per plant and number of seeds per siliqua. Path analysis of yield with the traits indicated that number of seeds per siliqua exerted the highest effect on seed yield.

Khulbe and Pant (1999) reported that number of siliquae/plant, siliqua

length, number of seeds/silique, 1000 seed weight were positively associated with seed yield. Kumar *et al.* (1999) studied 15 genotypes of *B. juncea*, 3 of *B. napus*, 4 of *B. rapa* and one of *B. chinensis*. For more character studied, genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic co-efficient. Seed yield was positively correlated with plant height, number of siliques/plant and 1000 seed weight.

Thakral *et al.* (1999) studied genotypic and phenotypic correlation co-efficient on seed yield and yield contributing characters in 8 Indian mustard (*Brassica juncea*) parents and their 28 F<sub>1</sub> hybrids grown at Hisar. The data indicated that higher seed yields could be obtained by selecting for increased plant height.

Patel *et al.* (1999) derived correlations from 12 yield related traits in the parents and 60 F<sub>1</sub> progeny of a 20 line x 3 tester cross of *Brassica juncea*. Based on path analysis, siliques per plant, primary branches per plant and plant height made in greatest contribution to seed yield.

Sheikh *et al.* (1999) assessed the direct and indirect influence of seven quantitative and developmental traits on seed yield in 24 diverse genotypes of toria under two environments at Khudwani, pooled analysis revealed highly positive direct effects of thousand seed weight and siliques per plant on seed yield. These characters can be used to maximize genetic gain for yield.

Gurdial and Hardip (1998) conducted a field trial during the rabi season of 1988-89 and 1989-90 in a loamy sand irrigated soil with gobhi sarson (*Brassica nigra*) cv. GSLs to study the relationships among different growth parameters and seed yield. Results indicated positive correlations of



number of branches per plant, number of siliquae per plant, siliqua length , seed yield , harvest index (HI), LAI, chlorophyll content, DM, photo synthetically active radiation (PAR) interception and seed yield were positively correlated among themselves. However, Plant height was negatively correlated with LAI, chlorophyll content, dry matter, yield components and seed yield. Thus dwarf plant gave higher yields.

Phenotypic correlation between yield and its components were estimated by Zajac *et al.* (1998). The range of yield and its component values indicated a great variability within them. The strong positive correlation occurred between seeds per siliqua and actual yield. Positive, though a weaker correlation was observed between seed yield and siliquae per plant. However, correcting actual yield, seeds per siliqua had the greatest influence and stand density and siliquae per plant had the smallest effect on yield.

Das *et al.* (1998) studied 8 genotypes of Indian mustard (*Brassica juncea*) they reported the presence of high positive genotypic correlations by siliqua length and seeds per siliqua with seed yield per plant.

In a study, Zhou *et al.* (1998) found significant variation in plant height in M<sub>2</sub> generation. Plant height was reported to be responsive to gamma rays, which decreased plant height substantially. Significant genetic variability was observed by many workers like Kumar *et al.* (1996), Malik *et al.* (1995), Yadava *et al.* (1993), Lebowitz (1989), Chauhan and Singh (1985), Sharma (1984) and many others among different genotypes of *B. napus*, *B. rapa* and *B. juncea*.

Lekh *et al.* (1998) reported that secondary branches showed highest

genotypic co-efficient of variation. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering in the same study. He found early flowering genotype will mature early and vice versa.

High genetic variation was found for this character by Yin (1989) working with cultivars of *B. napus*. The highest genotypic co-efficient of variation were calculated for secondary branches. High heritability estimates were observed for all the characters under all environments except harvest index and biological yield. Highest genetic advance and high genotypic and phenotypic co- efficient of variation was recorded for days to 50% flowering.

Benna *et al.* (1998) studied variability in mustard. Information was tabulated on mean, range, genotypic and phenotypic co-efficient of variation and heritability for 6 yield related traits in 22 mustard (*Brassica juncea*) genotypes grown at Nagpur during the rabi season of 1997-1998.

Yadava *et al.* (1996) studied 8x8 diallel analysis (excluding reciprocals). They found that both additive and dominance genetic component were important for seed yield and yield components in *B. rapa* var. toria. They reported higher heritability for days to maturity and 1000 seed weight. He also evaluated correlations from path coefficient analysis of 6 yield components of 25 diverse varieties of Indian mustard. He observed that number of siliquae per plant had the highest positive direct effect on seed yield per plant.

In general, high number of seeds per siliqua is desirable. Kumar *et al.*



(1996) reported the presence of significant variability in the genotypes of *Brassica napus*, *B. rapa* and *Brassica juncea*. Similar significant variability in number of seeds per siliqua in oleiferous *Brassica* materials of diverse genetic base have also been observed by Kudla (1993).

Character association and path coefficient analysis were used to determine relationships between growth and yield parameters in 28 lines of yellow and brown sarson (*B. rapa*) by Saini and Sharma, (1995). Results revealed that seeds/siliqua and 1000 seed weight had direct positive effect on yield.

Working with different strains of *B. napus* Malik *et al.* (1995) observed very high broad sense heritability ( $h^2_b > 90\%$ ) for number of primary branches per plant, days to 50% flowering and oil content and low heritability ( $h^2_b < 50\%$ ) for number of siliquae/plant, number of seeds/siliqua, plant height and seed yield. But Singh *et al.* (1991) found high heritability for all these character studied with *B. napus*.

Li *et al.* (1989) also observed similar results in studied with *B. napus*. 1000 seed weight was positively and significantly correlated with seed yield/plant and number of siliquae/plant but negatively and significantly correlated with siliqua length and number of seeds/siliqua in *B. rapa* (Nasim *et al.* 1994).

Diwakar and Singh (1993) studied heritability and genetic advance in segregating populations of yellow seeded Indian mustard (*Brassica juncea* L. Czern and Coss.). They used data on yield and 5 component traits in 8 cultivars and their 28  $F_3$  hybrids. They observed a wide range of phenotypic variation for most of the measured traits. They also reported that narrow sense heritability and genetic advance were high for days to flowering and plant height.

Working with several strains of *B. juncea* Kakroo and Kumar (1991), found



that 1000 seed weight had positive direct effect, but days to 50% flowering and primary branches had negative indirect effect via seeds/siliquea on seed yield. But Chauhan and Singh (1985), observed high positive direct effect of days to 50% flowering, plant height, primary branching, number of siliquae/plant, number of seeds/siliquea on yield. Again, Han (1990), working with *B. napus*, observed negative direct effect of number of siliquae/plant, siliquea length and positive direct effect on number of seeds/siliquea and plant height on yield.

Singh *et al.* (1991) studied different morpho-physiological characters of 29 genotypes of *B. napus* and *B. campestris*. They found significant genetic variability in days to 50% flowering. Siliquea length might have been influenced for the development of fruits in rape seed and mustard. Siliquea length varies due to difference in genotypes. High genetic variability was observed by Olsson (1990) in these characters. Lebowitz (1989) studied *B. rapa* population for siliquea length and found similar results.

The results of several experiments conducted by Das and Rahman (1989) in *B. rapa*, Ghosh and Chatarzee (1998) in *B. juncea*, Mishra *et al.* (1987) in *B. rapa*, Singh *et al.* (1987) in *B. juncea*, Chen *et al.* (1983) in *B. napus*, Srivastava *et al.* (1983) in *B. juncea*, revealed that plant height, days to maturity, 1000 seed weight, siliquae/plant and seeds/siliquea had positive direct effect and indirect effect on yield. But Varshney (1986), working with several strains of *B. rapa* found the negative direct effect of plant height, siliquae/plant, seeds/siliquea and 1000 seed weight on yield.

Significant genetic variation for number of primary branches/plant was recorded by several researchers. Singh *et al.* (1989) studied this character under normal and stress conditions in 29 genotypes of *B. napus* and *B. rapa* and found significant variation among the genotypes. Similar result was



reported earlier by Kakroo and Kumar (1991), Yin (1989), Jain *et al.* (1988), Labana *et al.* (1987), Gupta *et al.* (1987).

Selection for increased siliqua length is an effective strategy for yield improvement through raising seed weight/siliqua that was reported by Thurling (1998).

Dominance gene action was important in the expression of days to flowering observed by Jain *et al.* (1988) and partial dominance was observed by Kumar *et al.* (1999). It is obvious from all these results that sufficient genetic variation exists for days to 50% flowering.

According to Yin (1989), in *B. rapa*, in brown mustard, Kudla (1993) in sewede rape and Kumar and Singh (1994) in *Brassica juncea* reported different degrees of significant variations of 1000 seed weight due to variable genotypes.

Labana *et al.* (1987) studied 39 strains of Ethiopian mustard and found low genetic variation in plant height. But working with a number of strains of *B. napus*, *B. rapa* and *B. juncea*, Varshney *et al.* (1986) found high variability in plant height. Verma and Rai (1980) reported that gamma rays had inhibitory effect on plant height.

In *B. rapa* Singh *et al.* (1987), in *B. juncea*, Lebowitz (1989) reported that the siliqua length was positively correlated with both 1000 seed weight and number of seeds/siliqua. Chay and Thurling (1989) reported the inheritance of siliqua length among several lines of *B. napus* and suggested that lines with the longest siliqua generally gave significantly higher yield than those with short siliqua.

Gupta *et al.* (1987) studied with 51 *Brassica juncea* genotypes of diverse

origin and observed that harvest index, oil percentage and seed yield were positively correlated with oil yield both at the genotypic and phenotypic levels. The genotypic correlations being generally higher than phenotypic ones. Seed yield and oil percentage had the highest direct effect on oil yield. Singh (1986) studied 22 genotypes of *B. napus*, *B. rapa* and *B. juncea*. He observed high heritability and genetic advance in seed yield, 1000 seed weight and number of seeds/silique.

Vershney *et al.* (1986) found high heritability and high genetic advance for plant height in all three species; but high heritability and genetic advance were found for number of siliquae/plant only in *B. rapa* and in *B. juncea*. He reported high heritability and genetic advance in seed yield, 1000 seed weight and number of seeds/silique in *B. napus*.

Days to maturity are the most important character for oil seed crop, mustard and rapeseed in particular. The character is influenced by genotypes and various environmental factors. Working with 46 genotypes of *B. juncea* Sharma (1984) found low GCV and PCV values.

In a study of 46 genotypes of *B. juncea*, Sharma *et al.* (1995) observed high heritability for plant height, days to flowering and low heritability for days to maturity. He also found low genetic advance for days to maturity and high genetic advance for yield/plant. In another study of 179 genotypes of Indian mustard Singh *et al.* (1987) observed high heritability for yield/plant and low heritability for number of primary branches/plant.

Dhillon *et al.* (1997) observed negative indirect effect of days to flowering via plant height and silique length on yield in *B. juncea*. Singh *et al.* (1987);



also found negative direct effect of these traits, but Dhillon *et al.* (1997) observed highest positive direct effect of plant height on seed yield/plant. found, days to 50% flowering and plant height contributed to plant yield indirectly. Shabana *et al.* (1990); found the highest direct effect of number of siliquae/plant on seed yield/plant.

High heritability and genetic advance for flowering time, number of primary branches/plant and plant height was observed by Wan and Hu (1983). Low heritability of yield was reported by many researches like Malik *et al.* (1995), Yadava *et al.* (1985), Li *et al.* (1989), Chen *et al.* (1983) etc. But Singh (1986) found high heritability for this trait. Low to medium heritability of siliqua length was observed by Kakroo and Kumar (1991), Sharma (1997) and Yadava *et al.* (1996).

In *B. juncea* seed yield showed significant positive association with number of primary branches, number of secondary branches, plant height and days to maturity both at the genotypic and phenotypic levels (Srivastava *et al.* 1983).

Working with 104 mutants of Indian mustard in *B. juncea* (Linn.) Czern and Coss Labana *et al.* (1980) found that plant height and number of seeds/siliqua were highly heritable where as siliqua length, number of primary branches/plant and seed yield per plant were less heritable. The yield variation is thus principally pouring to the environmental influence, for which selection would not be more practicable for plant height and number of seeds/siliqua. In the same experiment the GA (expressed as percentage of mean) was highest for plant height followed by number of seeds/siliqua and seed yield/plant. Plant height found negative correlation with siliqua length and number of seeds/siliqua by him. Positive correlation

of plant height with number of seeds/siliquea, number of siliquae/plant and negative correlation with 1000 seed weight were reported.

1000 seed weight was found to positively associate with days to 50% flowering and days to 80% maturity by Yadava *et al.* (1978) in *B. juncea* but Shivahare *et al.* (1975) and Singh *et al.* (1987) found negative correlation. Negative correlation of 1000 seed weight with plant height, number of primary branches/plant and number of siliquae/plant was also reported by Yadava *et al.* (1978). Positive correlation with flowering time, days to maturity and 1000 seed weight was observed by Yadava *et al.* (1978) and Singh *et al.* (1987).

Working with 30 varieties of *B. rapa* Chandola *et al.* (1977) found high genetic advance for plant height. Paul *et al.* (1976) observed in his study that a good genetic advance was expected from a selection index comprising seed yield, number of seeds/siliquea, number of siliquae/plant and number of primary branches/plant.

Working on genetic variability, heritability and genetic advance of seed yield and its components in Indian mustard Katiyar *et al.* (1974) reported that high genetic co-efficients of variation were observed for seed yield/plant, days to first flowering and plant height, whereas low values were observed for other characters like days to maturity and number of primary branches.

GCV for yield was found to be 48.76 by Yadava (1973) among 29 strains of *B. juncea*, but Bhardwaj and Singh (1969) found the value as 96.99 among different strains of brown sarson. Again, Tak and Patnaik (1977) found GCV of 18.96 and PCV of 82.4 in yellow sarson. Singh *et al.* (1987)



observed GCV and PCV values of 44.04 and 46.9; while the same values were only 9.6 and 19.47 among different genotypes of *B. juncea* (Labana *et al.* 1987).

Significant correlation was found between number of siliquae/plant and numbers of seeds/siliquea in yellow sarson (Banerjee, 1968). But Tak and Patnaik (1977) found negative genotypic correlation between number of siliquae/plant and numbers of seeds/siliquea in brown sarson and toria varieties of *B. rapa*. On the contrary, Das *et al.* (1984) reported number of siliquae/plant showed significant and positive correlation with number of seeds/siliquea and 1000 seed weight.

## **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:

A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten F<sub>3</sub> progenies including reciprocals. He found yield per plant showed highest significant and positive correlation with days to maturity followed by number of seeds per siliquea, number of secondary branches per plant, length of siliquea and number of siliquae 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 siliquae per plant.

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica species* to estimate correlation and observed that, highly significant positive

association of yield per plant with number of primary branches per plant , number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

Portocarrero *et al.* (2006) studied effects of different pre-freezing blanching procedures on the physicochemical properties of *Brassica rapa* leaves (Turnip Greens, Grelos). The result revealed that the blanching, the grelos were stored for up to 120 days at -18 degrees C, with sampling at two-weekly intervals for analysis of physicochemical properties (ash weight, vitamin C content, pH, acid value, moisture content and CIEL\*a\*b\* colour variables). In almost all respects steam blanching gave the best results: notably, vitamin C losses were markedly lower, while moisture content and colour remained closer to those of the fresh product.

Parveen (2007) conducted an experiment with F<sub>2</sub> population of *Brassica rapa* to study the correlation and observed that yield per plant had non-significant positive association with plant height, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant, days to 50% flowering and length of siliqua.

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

Tusar *et al.* (2006) studied phenotypic correlation and observed that seed yield per plant was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliquae per



plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield.

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

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

Mahak *et al.* (2004) conducted an experiment and studied correlation for 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 Srivastava (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.

Pankaj *et al.* (2002) studied four parental cultivars and the 174 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the

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majority of the characters. The number of siliquae per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliqua and test weight at both levels. The number seeds per siliqua were positively associated with siliqua length and yield per plant at both levels.

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

Badsra and Chaudhary (2001) studied correlation on 14 traits of 16 Indian mustard genotypes. Seed yield was positively correlated with stem diameter, number of siliquae per plant and oil content, while oil content was positively correlated with harvest index only. Among the characters only 3 characters positively correlated with seed yield.

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

Days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. The number of branches per plant and number of siliquae per plant showed significant negative correlation with



number of seeds per siliqua and 1000 seed weight was reported by Malek *et al.* (2000), while studied correlation analysis.

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

In a study of correlations in 8 Indian mustard (*Brassica juncea*) parents and their 28 F<sub>1</sub> hybrids Khulbe and Pant (1999) revealed that the number of siliquae per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and harvest index were positively associated with seed yield.

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

Kumar *et al.* (1999) reported that genotypic correlation co-efficient were higher in magnitude than corresponding phenotypic correlation co-efficient for most characters. The plant height, siliquae on main shoot, siliquae per plant and thousand seed weight were positively correlated with seed yield.

Das *et al.* (1998) carried out an experiment with 8 genotypes of Indian mustard (*B. juncea*) and reported that the length of siliqua, seeds per siliqua had high positive genotypic correlated with seed yield per plant.

Zajac *et al.* (1998) studied phenotypic correlation between yield and its component and reported that strong positive correlation occurred between seeds per siliqua and actual yield. The number of seeds per siliqua had the

greatest influence and siliquae number per plant had the smallest effect on yield.

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

Plant height, siliquae per plant, siliqua length, seed weight, and seeds per siliqua had positive and significant effects on seed yield per plant was observed by Tyagi *et al.* (1996) while carried out an experiment with 6 yield components in 3 cultivars of mustard.

Gill and Narang (1995) studied correlation in gobhi sarson (*B. campestris* var. sarson) and observed that seed yield was positively correlated with number of primary branches and secondary branches per plant, number of siliquae per plant and thousand seed weight.

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

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

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



correlated with siliqua length and number of seeds per siliqua.

Siliqua length, number of siliquae per plant, number of seeds per siliqua and seed weight per siliqua was positively and linearly associated with seed yield per plant was observed by Ahmed (1993) while working with 8 cultivars of *B. campestris* and *B. juncea* for study of nature and degree of interrelationship among yield components.

Chaudhury *et al.* (1993) observed seed yield was positively correlated with siliqua length when evaluated 7 of *B. juncea*, 2 of *B. carinata* cultivars and 1 cultivar each of *B. campestris* and *B. tournefortii*.

The number of seeds per siliqua negatively correlated with siliquae per plant was reported by Zaman *et al.* (1992) when they studied several yield contributing traits of Swedish advanced rape lines.

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

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

In F<sub>3</sub> population of brown sarson Das *et al.* (1984) observed 1000 seed weight had highly significant genotypic and phenotypic correlation with seed yield per plant.

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

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

Increasing the number of branches is a means of increasing yield, since the number of primary and secondary branches have a significant positive correlation with seed yield (Singh *et al.* 1969; Katiyar and Singh, 1974).

Banerjee, (1968) found significant correlation between number of siliqua/plant and numbers of seeds/siliqua in yellow sarson. But Tak and Patnaik (1977) found negative genotypic correlation between number of siliqua/plant and numbers of seeds/in brown sarson and toria varieties of *B. rapa*. On the contrary, Das *et al.* (1984) reported number of siliquae/plant showed significant and positive correlation with number of seeds/siliqua and 1000 seed weight. Chay and Thurling (1989) studied the inheritance of siliqua length among several lines of *B. napus* and reported that the siliqua length when increased there was an increase in the number of seeds per siliqua and thousand seed weight. The siliqua length was positively correlated with both number of seeds per siliqua and thousand seed weight was observed by Singh *et al.* (1987) in *B. rapa*, Chowdhury *et al.* (1987), Lebowitz (1989) and Lodhi *et al.* (1979) in *B. juncea*.

### **2.3 Genetic Divergence**

Genetic divergence means the nature and degree of variability existing among the genotypes under studies, which is measured by range, mean, standard deviation, variance, standard error, coefficient of variation etc.



Genetic diversity analysis is mainly based on multivariate techniques. During last decades different multivariate techniques have been developed through the development of computer program. However, literature related to efficient multivariate techniques for diversity analysis is reviewed in the following paragraphs.

Kadir *et al.* (2007) were studied genetic diversity among 25 genotypes of *Brassica napus* L. the results revealed that, among the 4 clusters, cluster IV contained the maximum no of genotypes while cluster I contained lowest. The highest intra-cluster distance was found for cluster I and the lowest in cluster

The highest inter cluster distance was found between the cluster I & II, where as lowest between the cluster II & IV. 1000 seed weight, no. of seeds/silique, no. of branches/plant, contribute maximum towards divergence.

Diversity of 40 oleiferous *Brassica* species was studied by Rashid (2007) and estimated by cluster distance genotypes were grouped into six clusters. Cluster

II had the maximum 10 and cluster I and III had the minimum 5 number of genotypes. The highest intra-cluster distance was observed in cluster V where as inter-cluster distance highest in between cluster I and VI. The lowest inter cluster distance was in between the cluster III and V.

Zahan (2006) studied genetic diversity among 41 genotypes of oleiferous *Breassicca* species. Her study revealed the genotypes showed greater diversity. The genotypes were classified in 6 different Cluster. Cluster III and V was the largest cluster comprising of 10 genotypes and Cluster I and

II with 3 genotypes each. Cluster II had the highest intra-cluster distance (0.813) cluster IV had the lowest intra Cluster distance (0.378). Inter cluster distance was maximum (0.902) between clusters II and VI. The results revealed that genotypes chosen for hybridization from clusters with highest distances would give high heterotic  $F_1$  and broad spectrum of variability in segregation generations.

Patel and Patel (2006) conducted an experiment on the title of genetic divergence in *Brassica juncea*. The 40 strains were grouped into 4 clusters. Cluster I was the largest, consisting of 28 strains, while group IV comprised only one strain, suggesting that genotype Zem 2 diverged most from others. The intra-cluster distance was maximum in cluster II (102.7) and minimum in cluster IV (0.00), therefore, the 8 strains in cluster II indicated to be the most heterogeneous. As regards inter-cluster distance, the maximum statistical distance appeared between cluster III and cluster IV (594.1) followed by cluster I and cluster IV (415.5), suggesting wide diversity between them. An examination of cluster mean value showed that the importance of cluster IV for number of primary and secondary branches per plant, number of siliquae per plant, seeds per siliqua and seed yield and that of cluster III for early flowering, dwarf plant type, high oil content and high harvest index became obvious. The crosses involving parents belonging to the most divergent clusters are expected to manifest maximum heterosis. The clusters comprising only one genotype with specific traits could also be used in hybridization program. Thus, the crosses between the genotypes of cluster III (SKM, TM 24 and TM 9) with that of cluster IV (Zem 2) would produce high heterosis and is also likely to exhibit new recombination with desired traits.

Genetic divergence was found not to be related with the geographical



divergence carried out with 100 rape seed and mustard genotypes by Kamal (2006). His study revealed genotypes were grouped in to eight clusters. Cluster VII included the maximum (30) and cluster IV the minimum (3) number of genotypes. The highest inter-cluster distance was observed between clusters I and VI and the lowest between clusters I and II. Siliqua length and harvest index contributed maximum towards divergence.

Padilla *et al.* (2005) conducted an experiment to determine the genetic diversity and morphological resemblances among the *B. rapa* and evaluate their agronomic characteristics, considering the three potential products that can be harvested. A collection of 120 landraces was evaluated for 34 morphological and agronomical traits by an augmented design at two locations. Two landraces were the most promising for turnips production (MBG-BRS0183 and MBG- BRS0256), two showed the best characteristics for turnip greens (MBG- BRS0082 and MBG-BRS0184), and three were the most appropriate landraces for turnip tops production (MBG-BRS0143, MBG-BRS0173 and MBG- BRS0401). Landraces were classified into five clusters (A-E) using the Ward- MLM (Modified Location Model) strategy. As conclusion, landraces evaluated in this work displayed enough variability to differentiate among appropriate populations for each one of the distinct crops. Their classification, using the Ward-MLM strategy, grouped accessions with similar characteristics into homogeneous categories.

Ashwini *et al.* (2004) conducted an experiment on genetic divergence using Mahalanobis  $D_2$  statistics was studied in 33 genetically diverse genotypes of Indian mustard. Five characters, number of siliquae plant<sup>-1</sup>, plant height, days to 50% flowering, days to maturity and seed yield plant<sup>-1</sup>, were

important sources of variation as observed from both canonical, cluster mean and variance analysis. The genotypes were grouped into eight different clusters. The cluster-III was the biggest with 11 genotypes followed by cluster-I with 9 genotypes. Cluster-V and VI consisted of 4 and 3 genotypes respectively. Cluster II and VII both included two genotypes each and similarly cluster-IV and VIII included one genotype each.

Genetic divergence of 14 genotypes in mustard and rape were analyzed by Afroz *et al.* (2004). The genotypes were grouped into six clusters. Cluster VI contained the maximum (4) and cluster I and II had only (1) genotype. The maximum intra cluster distance was found in cluster V, the highest inter cluster distance was observed between III and IV and lowest between III and VI. Yield and yield contributing characters such as number of primary branches per plant, 1000- seed weight and days to 50% flowering and seed yield per plant contributed more towards genetic divergence considering diversity pattern.

Verma and Sachan (2000) in 64 genotypically diverse genotypes of Indian mustard for days to flower initiation, 50% flowering and maturity, number of primary and secondary branches per plant, plant height, length of main shoot, number of siliquae on main shoot, number of siliquae per plant, average number of seeds per siliqua, 1000 seed weight (g) and oil content (%). The genotypes were grouped into 12 clusters. No parallelism was observed between geographic diversity and genetic diversity.

Srivastav and Singh (2000) analyzed 26 cultivars of Indian mustard for the characters: plant height, length of main raceme, number of primary branches, number of secondary branches, days to 50% flowering, reproductive phase, days to maturity, oil percentage, 1000-grain weight and



seed yield per plant. The cultivars were grouped into 6 clusters using  $D^2$  statistics. Based on average cluster means for the studied characters, cultivars in cluster III had the highest number of primary (6) and secondary branches (22), oil percentage (40.79%) and highest mean seed yield per plant (33.32 g/plant). Cultivars in cluster V were early maturing (118 days) with 1000-grain weight of 5.70 gm.

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

The clustering and ordination methods used often cannot deal explicitly with the computational consequences of large data sets with incomplete information. However, it is shown that the ordination technique of principal component analysis and the mixture maximum likelihood method of clustering can be employed to achieve such analysis (Harch *et al.* 1999). Genotypes within the cluster are having a smaller  $D^2$  value among themselves than those from group belonging to two different clusters. On the other hand, the inter-cluster distance is the criterion used for selecting genotypes as parent for hybridization. The genotypes those in clusters with maximum inter cluster distance are genetically more divergent. Variation within the cluster is measured by inter-cluster distance.

Forty four genotypes of toria were evaluated by Mitra and Saini (1998) collected from different eco-geographical areas for yield and various components during rabi 1991-92. On the basis of  $D^2$  analysis, the 43 genotypes were grouped into 7 clusters. No evidence was obtained for any

correlation between genetic divergence and geographical diversity. Silique in the main shoot and seeds per silique were the major contributors to genetic divergence.

Genetic divergence was studied for seed yield and six important yield component of mustard (*Brassica juncea* Czern and Coss) by Dhillon *et al.* (1997). They grouped mustard genotypes into eight diverse clusters. Clustering of population followed their geographic or location distribution. Seed yield per plant showed maximum divergence followed by number of siliques on main shoot and minimum by number of branches per plant.

Nineteen genotypes (crosses and parents) of Indian mustard (*B. juncea*) grown at Ranchi during the winter season under rainfed conditions. Genotypes were grouped into 3 cluster based on  $D^2$  analysis was studied by Mahto (1996).

Islam (1995) studied genetic divergence among 90 genotypes of groundnut using  $D^2$  and principal components analysis and grouped the varieties into 5 clusters. The inter-cluster distances were larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups.

Uddin (1994) reported from an experiment on genetic divergence among 34 genotypes of mustard were estimated using D and principal component analysis. The genotypes were divided into four clusters. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups.

Gupta *et al.* (1991) performed preliminary multiple regression analysis on



118 geographically diverse lines and selected 48 lines for further study. They recorded data on nine morphological traits and analyzed them using the  $D^2$  statistic. They also suggested that selection of parents for breeding should be based on diversity estimates. Based on seed yield and components, the lines were grouped into five clusters, with no correlation between geographical and genetic diversity.

Nineteen genotypes of rape mustard (*B. rapa*) were studied by Jagadev *et al.* (1991) which were grown during the winter season. They studied different characters and analyzed the variance using the  $D^2$  statistic. Genotypes were grouped into 5 clusters. Seed weight, days to maturity and seed yield were the largest contributors to  $D^2$  values.

Rabbani *et al.* (1989) conducted an experiment on the title of genetic diversity and the relationships among a collection of mustard (*B. juncea*) germplasm, including 41 accessions. Cluster analysis based on these genetic similarities placed most of the collected germplasm and oilseed cultivars/lines close to each other, showing a low level of polymorphism between the oilseed accessions collected in Pakistan. However, the clusters formed by the oilseed collections and cultivars were distinct from those formed by the vegetable cultivars. A low level of genetic variability of oilseed mustard in Pakistan was attributed to the selection for similar traits and horticultural uses. The farmers' preference for more remunerative crops and perhaps the close parentage of these accessions further contributed towards their low diversity. The study demonstrated that the RAPD is a simple and fast technique for comparing genetic relationships and the patterns of variation among accessions of this crop.

Degby *et al.* (1989) reported that the co-ordinates obtained from the PCA is

used as input of PCO analysis to calculate distances among the points. Thus, PCA is used for graphical representation of the points while PCO is used to calculate the minimum distance in a straight line between each pair of points. They have also suggested that both the analyses should be used to represent the distances of points.

The hierarchical nature of the grouping into various number of classes can impose undue constraints and the statistical properties of the resulting groups are not at all clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. Also the squared distance between means are Mahalanobis's  $D^2$  statistics when all the dimensions are used can be computed using principal co-ordinate analysis (PCO). It was also recommended the canonical Vector Analysis (CVA) for discriminatory purposes (Payne *et al.* 1989).

Godshalk and Timothy (1988) compared of index selections with principal factor analysis, maximum likelihood factor analysis and principal component analysis. Multivariate analysis was performed on both simple and genotypic correlation matrices for three sets of traits (five traits per set) in switch grass (*Panicum virgatum*). Among the multivariate analysis methods, PCA had the highest correlation with the index selection. They also suggested that PCA is more economic than the other analysis.

48 lines among 118 geographically diverse lines of mustard was selected by Gupta *et al.* (1987) following preliminary multiple regression analysis. Based on seed yield and components, the lines were grown into 5 clusters, with no correlation between geographical and genetic diversity.

Analyzing the data on pod/seed yield and 12 related traits, Reddy *et al.* (1987)



found that 20 germplasms of groundnut, investigated for two years divided into six clusters in both the years. They also observed that genetic diversity was not related to geographical distribution.

Multivariate analysis using Mahalanobis  $D^2$  statistic to group 83 genotypes on the basis of yield/plant and six other agronomic characters of bunch groundnut by Nadaf *et al.* (1986). They found nine clusters, which were not related to the grouping formed by geographical origin. They also observed that variation in pod yield accounted for 88% of the total variation between clusters but number of developed pods, days to 50% flowering and 1000 seed weight were important in accounting for divergence with clusters.

Shanmugam and Rangasamy (1982) observed that the characters yield per plant and pod per plant contributed considerably towards diversity in black gram. Again the same authors in 1982 assigned 45 genotypes of black gram of ten clusters by analyzing data on yield and nine yield components using Mahalanobis's  $D^2$  statistic and stated that geographical diversity was not the only factor for determining genetic diversity. The clustering pattern more or less confirmed the canonical (vector) analysis. They found that yield per plant contributed most too genetic divergence. Furthermore, investigated diversity in 20 strains of black gram from different agro-ecological zones of India using Mahalanobis's  $D^2$  statistic. They observed no parallelism between geographical and genetic diversity.

## **CHAPTER III**

### **MATERIALS AND METHODS**

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period of October 2010 to March 2011 to study the inter genotypic variation among advance lines of *Brassica rapa*. The materials and methods of this experiment are presented in this chapter under the following headings

#### **3.1 Experimental site**

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during October 2010-March 2011. The location of the site was 23° 74' N latitude and 90° 35' E longitude with an elevation of 8.2 meter from sea level (Appendix I).

#### **3.2 Climate and Soil**

The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agro-ecological regions of “Madhupur Tract” (AEZ No. 28). Its top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 4.47 to 5.63 and organic carbon content is 0.82%. The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II).

#### **3.3 Materials**

To study the inter-genotypic variability a total of 30 genotypes were used for this research work. The name of the genotypes is mentioned in Table 1.



**Table 1. List of 30 *Brassica rapa* genotypes used in the experiment**

| <b>List</b> | <b>Symbol</b>         | <b>Genotype</b>                                          |
|-------------|-----------------------|----------------------------------------------------------|
| <b>1</b>    | <b>G<sub>1</sub></b>  | <b>BARI 6 × Tori 7 S<sub>3</sub></b>                     |
| <b>2</b>    | <b>G<sub>2</sub></b>  | <b>Tori 7 × F<sub>6</sub> S<sub>5</sub></b>              |
| <b>3</b>    | <b>G<sub>3</sub></b>  | <b>BARI 6 × Tori 7 S<sub>7</sub></b>                     |
| <b>4</b>    | <b>G<sub>4</sub></b>  | <b>BARI 9 × F<sub>6</sub>P<sub>4</sub> S<sub>4</sub></b> |
| <b>5</b>    | <b>G<sub>5</sub></b>  | <b>BARI 9 × F<sub>6</sub>P<sub>7</sub> S<sub>7</sub></b> |
| <b>6</b>    | <b>G<sub>6</sub></b>  | <b>F<sub>6</sub> × BARI 9</b>                            |
| <b>7</b>    | <b>G<sub>7</sub></b>  | <b>Tori 7 S<sub>8</sub></b>                              |
| <b>8</b>    | <b>G<sub>8</sub></b>  | <b>BARI 9 × BARI 6 S<sub>13</sub></b>                    |
| <b>9</b>    | <b>G<sub>9</sub></b>  | <b>BARI 6 × Tori 7 S<sub>10</sub></b>                    |
| <b>10</b>   | <b>G<sub>10</sub></b> | <b>BARI 9 × BARI 6 S<sub>17</sub></b>                    |
| <b>11</b>   | <b>G<sub>11</sub></b> | <b>BARI 6 × R.Tori 7 S<sub>15</sub></b>                  |
| <b>12</b>   | <b>G<sub>12</sub></b> | <b>Tori 7 × F<sub>6</sub> S<sub>10</sub></b>             |
| <b>13</b>   | <b>G<sub>13</sub></b> | <b>Tori 7</b>                                            |
| <b>14</b>   | <b>G<sub>14</sub></b> | <b>BARI 9 × BARI 6 S<sub>21</sub></b>                    |
| <b>15</b>   | <b>G<sub>15</sub></b> | <b>SS-75 × Tori 7</b>                                    |
| <b>16</b>   | <b>G<sub>16</sub></b> | <b>BARI 6 × Tori 7 S<sub>27</sub></b>                    |
| <b>17</b>   | <b>G<sub>17</sub></b> | <b>BARI 6 × Tori 7 S<sub>31</sub></b>                    |
| <b>18</b>   | <b>G<sub>18</sub></b> | <b>F<sub>6</sub> × BARI 9 S<sub>18</sub></b>             |
| <b>19</b>   | <b>G<sub>19</sub></b> | <b>BARI6 × F<sub>6</sub> S<sub>15</sub></b>              |
| <b>20</b>   | <b>G<sub>20</sub></b> | <b>BARI 6 × Tori 7 S<sub>32</sub></b>                    |
| <b>21</b>   | <b>G<sub>21</sub></b> | <b>BARI 6 × R.Tori 7 S<sub>35</sub></b>                  |
| <b>22</b>   | <b>G<sub>22</sub></b> | <b>F<sub>6</sub> × BARI 9 S<sub>31</sub></b>             |
| <b>23</b>   | <b>G<sub>23</sub></b> | <b>Tori 7 × F<sub>6</sub> S<sub>18</sub></b>             |
| <b>24</b>   | <b>G<sub>24</sub></b> | <b>BARI 9 × F<sub>6</sub> S<sub>11</sub></b>             |
| <b>25</b>   | <b>G<sub>25</sub></b> | <b>BARI 9 × F<sub>6</sub> S<sub>23</sub></b>             |
| <b>26</b>   | <b>G<sub>26</sub></b> | <b>BARI 6 × Tori 7 S<sub>42</sub></b>                    |
| <b>27</b>   | <b>G<sub>27</sub></b> | <b>SAU Sharisha 1</b>                                    |
| <b>28</b>   | <b>G<sub>28</sub></b> | <b>BARI 6 × Tori 7 S<sub>45</sub></b>                    |
| <b>29</b>   | <b>G<sub>29</sub></b> | <b>BARI 9 × BARI 6 S<sub>38</sub></b>                    |
| <b>30</b>   | <b>G<sub>30</sub></b> | <b>BARI 6 × Tori 7 S<sub>52</sub></b>                    |

### **3.4 Methods**

The following 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 power tiller and country plough to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

#### **3.4.2 Fertilizer application**

Fertilizers such as Urea, Triple Super Phosphate (TSP), Muriate of Potash (MP), Gypsum and Boron were applied at the rate of 250, 170, 85, 150 kg per hectare and 1-1.5 kg per hectare respectively. Urea was applied by two installments. Total amount of TSP, MP, gypsum, borax and boron along with half of the urea were applied at the time of final land preparation as a basal dose. The second half of the urea was top-dressed at the time of flower initiation.

#### **3.4.3 Experimental design**

Field lay out was done after final land preparation. The materials were laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 13 m x 55 m. A distance of 1 m from block to block, 30 cm from row to row and 10 cm from plant to plant was maintained. The seeds were placed at about 1.5 cm depth in the soil (Plate 1).





Plate I: Field view and replication wise close field view of the experimental site.



#### **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 by sprinkler 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; simultaneously 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. The crop was protected from the attack of aphids by spraying Malathion-57 EC@ 2 ml/litre of water. The genotypes differed widely for days to flowering. The insecticide was applied for the first time approximately before one week of flower initiation and it was applied for another two times at an interval of 15 days. To protect the crop from the *Alternaria* leaf spot disease, Rovral-50 WP was sprayed at the rate of 2g/l water at 50% flowering stage for the first time and it was again applied for two times at an interval of 15 days. Both the insecticide and fungicide were applied in the evening.

#### **3.4.5 Harvesting**

Harvesting was done from 3<sup>rd</sup> to 23<sup>rd</sup> February, 2011 depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw colour of siliquae, leaves, stem and desirable seed colour in the matured siliquae, the crop was assessed to attain maturity. At maturity, ten plants were selected at random from all lines in each plot. The sample plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.



### 3.4.6 Methods of data collection

- i. **Plant height (cm):** It was measured in centimeter (cm) from the base of the plant to the tip of the longest inflorescence. Data were taken after harvesting.
- ii. **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.
- iii. **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.
- iv. **Number of siliquae/plant:** Total number of siliquae of each plant was counted and considered as the number of siliquae/plant.
- v. **Siliqua length (cm):** This measurement was taken in centimeter (cm) from the base to the tip of a siliqua without beak of the ten representative siliquae.
- vi. **Number of seeds/siliqua:** Well filled seeds were counted from ten representative siliquae, which was considered as the number of seeds/siliqua.
- vii. **1000 seed weight (g):** Weight in grams of randomly counted thousand seeds of each entry was recorded.
- viii. **Seed yield/plant (g):** All the seeds produced by a representative plant was weighed in g and considered as the seed yield/plant.
- ix. **Seed yield ( $\text{t ha}^{-1}$ )**

Seed yield was recorded on the basis of total harvested seeds  $\text{plot}^{-1}$  and was expressed in terms of yield ( $\text{t ha}^{-1}$ ). Seed yield was adjusted to 12% moisture content.

### 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).

### 3.4.8 Estimation of genotypic and phenotypic variances:

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

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

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

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

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

$\delta^2e$  = Environmental variance = Mean sum of 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).



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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

$\delta_g$  = Genotypic standard deviation

$\delta_p$  = Phenotypic standard deviation

$\bar{x}$  = Population mean

### iii) Estimation of heritability:

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

$$h^2_b(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

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

$\delta_g^2$  = Genotypic variance

$\delta_p^2$  = Phenotypic variance

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

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

**v) Estimation of simple correlation co-efficient:** Simple correlation co-efficients (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

$$r = \frac{\frac{\sum x \cdot \sum y}{N} - \frac{(\sum x)^2}{N} \cdot \frac{(\sum y)^2}{N}}{\left[ \left\{ \frac{\sum x^2}{N} - \frac{(\sum x)^2}{N} \right\} \left\{ \frac{\sum y^2}{N} - \frac{(\sum y)^2}{N} \right\} \right]^{1/2}}$$

Where,  $\sum$  = Summation

x and y are the two variables correlated

N = Number of observations

### 3.4.9 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's general distance ( $D^2$ ) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's  $D^2$  statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao suggested that the



quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

#### **3.4.9.1 Principal Component analysis (PCA)**

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

#### **3.4.9.2 Principal Coordinate analysis (PCO)**

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

#### **3.4.9.3 Cluster analysis (CA)**

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values

of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

#### **3.4.9.4 Canonical Vector analysis (CVA)**

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

#### **3.4.9.5 Calculation of $D^2$ values**

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

$$D^2 = \sum_i d_i^2 = \sum_i (Y_i^j - Y_i^k) \quad (j \neq k)$$

Where,

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

to x

x = Number of characters.

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



#### **3.4.9.6 Computation of average intra-cluster distances**

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

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

Where,

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

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

#### **3.4.9.9 Selection of varieties for future hybridization programme**

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance ( $D^2$ ) express the maximum divergence among the genotypes included into these different clusters. Variety(s) or line(s) were selected for efficient hybridization programme according to Singh and Chowdhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

- Choice of cluster from which genotypes are selected for use as parent (s)
- Selection of particular genotype(s) from the selected cluster(s)
- Relative contribution of the characters to the total divergence

## **Chapter IV**

### **RESULTS AND DISCUSSION**

This chapter comprises the presentation and discussion of the findings obtained from the study with the help of suitable genetic parameters like genetic coefficient of variation under selection etc. Nine characters such as plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, length of siliqua, thousand seed weight and seed yield per plant, yield per ha were studied in respect of 30 genotypes. Results of different studies are described in separate section on character basis.

Variability and other biometrical studies

**(1) Variability**

**(2) Correlation co-efficient**

**(3) Multivariate analysis**

#### **4.1 GENETIC PARAMETERS**

The analysis of variance indicated the existence of highly significant variability for all the characters studied. The mean sum of square, mean, range, variance components, coefficients of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 2). The results are discussed character wise as follows:



#### **4.1.1 Plant height**

Mean sum of square for plant height was highly significant (Table 2) indicating existence of considerable difference for this trait. The maximum plant height was found 124.00 cm and the minimum was recorded 81.20 cm with mean value 93.52 cm (Appendix III). The genotypic variance (44.53), phenotypic variance (115.74), genotypic co-efficient of variation (7.09) and phenotypic co-efficient of variation (11.42) were close to each other indicating less environmental influence in case of plant height. Heritability (38.00) estimates for this trait were moderate together with considerable moderately high genetic advance in percent of mean (9.03) indicated that selection for this character would be more effective. Tyagi *et al.* (2001) observed the highest variation in plant height among parents and their hybrid.

#### **4.1.2 Number of primary branches per plant**

Mean sum of square for number of primary branches per plant was highly significant (Table 2) indicating existence of considerable variability for this trait. The maximum number of primary branches per plant was found 8.00 and the minimum was recorded 5.30 with mean value 6.627 (Appendix III). The genotypic variance (0.41), phenotypic variance (1.95), genotypic co-efficient of variation (9.48) and phenotypic co-efficient of variation (20.68) were close to each other indicating less environmental influence in case of number of primary branches per plant. Heritability (21.03) estimates for this trait was very high genetic advance in percent mean (19.64) were also found high, indicated that selection for this character would be more effective. Chowdhary *et al.* (1987) found significant differences for number of primary branches per plant.

#### **4.1.3 Number of secondary branches per plant**

Mean sum of square for number of secondary branches per plant was highly significant (Table 2) indicating existence of considerable variability for this trait. The maximum number of secondary branches per plant was found 10.90 and the minimum was recorded 1.80 with mean value 5.477 (Appendix III). The genotypic variance (0.90), phenotypic variance (8.97), genotypic co-efficient of variation (17.21) and phenotypic co-efficient of variation (54.34) were close to each other indicating less environmental influence in case of number of primary branches per plant. Heritability (10.03) estimates for this trait was very high genetic advance in percent mean (11.41) were also found high, indicated that selection for this character would be more effective Chowdhury *et al.* (1987) found significant differences for number of primary branches per plant.

#### **4.1.4 Number of siliqua per plant**

Mean sum of square for number of siliqua per plant was highly significant in Brassica rapa (Table 2) indicating existence of considerable variability for this trait. The maximum number of siliqua per plant was found 239.7 and the minimum was recorded 81.70 with mean value 137.3 (Appendix III). The genotypic variance (497.90), phenotypic variance (1576.88), genotypic co-efficient of variation (16.02) and phenotypic co-efficient of variation (28.51) were close to each other indicating less environmental influence in case of no. of siliqua per plant. Heritability (31.58) estimates for this trait was found moderate and genetic advance in percent of mean (18.53) was found moderately high, indicated that selection for this character would be effective. Higher genotypic variances indicate the better transmissibility of a character from parent to the offspring (Ushakumari *et al.* 1991).



#### **4.1.5 Number of seed per siliqua (g)**

Mean sum of square for number of seed per siliqua was significant in *Brassica rapa* (Table 2) indicating existence of considerable difference for this trait. The maximum number of seed per siliqua was found 19.30 and the minimum was recorded 12.10 with mean value 15.47 (Appendix III). The genotypic variance (1.74), phenotypic variance (4.87), genotypic co-efficient of variation (8.49) and phenotypic co-efficient of variation (14.21) were close to each other indicating less environmental influence in case of number of seed per siliqua. Heritability (35.73) estimates for this trait was low together with considerable genetic advance in percent of mean (4.73) indicated that selection for this character would be more effective. Lebowitz (1989) studied *Brassica campestris* population for pod length and observed high genetic variation on this trait. Olsson (1990) found high genetic variability for this trait.

**Table 2. Genetic parameters of nine yield contributing characters of thirty *Brassica rapa* genotypes**

| Character                 | GM     | MSS    | Error  | $\sigma^2_g$ | $\sigma^2_p$ | $\sigma^2_e$ | GCV   | PCV   | $h^2_b$ | GA%<br>mean | CV<br>(%) |
|---------------------------|--------|--------|--------|--------------|--------------|--------------|-------|-------|---------|-------------|-----------|
| Plant height (cm)         | 94.17  | 204.79 | 71.21  | 44.53        | 115.74       | 71.21        | 7.09  | 11.42 | 38.00   | 9.03        | 8.96      |
| No. of primary branches   | 6.75   | 2.77   | 1.55   | 0.41         | 1.95         | 1.55         | 9.48  | 20.68 | 21.03   | 19.64       | 18.42     |
| No. of secondary branches | 5.51   | 10.77  | 8.06   | 0.90         | 8.97         | 8.06         | 17.21 | 54.34 | 10.03   | 11.41       | 51.51     |
| no. of<br>silique/plant   | 139.28 | 252.67 | 108.98 | 497.90       | 1576.88      | 1078.99      | 16.02 | 28.51 | 31.58   | 18.53       | 23.58     |
| No. of<br>seed/silique    | 15.530 | 8.35   | 3.12   | 1.74         | 4.87         | 3.12         | 8.49  | 14.21 | 35.73   | 4.73        | 11.38     |
| Silique length<br>(cm)    | 5.18   | 0.44   | 0.24   | 0.07         | 0.30         | 0.24         | 5.11  | 10.58 | 23.33   | 5.08        | 9.37      |
| 1000 seed weight<br>(g)   | 0.32   | 0.006  | 0.005  | 0.001        | 0.005        | 0.005        | 5.40  | 22.03 | 6.00    | 2.72        | 21.05     |
| Yield/plant (g)           | 4.488  | 3.68   | 2.098  | 0.53         | 2.63         | 2.10         | 16.22 | 36.13 | 38.02   | 15.18       | 32.27     |
| Yield/ha                  | 1.483  | 0.40   | 0.227  | 0.06         | 0.29         | 0.28         | 16.52 | 36.32 | 20.68   | 30.62       | 23.22     |

Here, GM= grand mean MSS= Mean sum of squares 30 genotypes, CV= Co-efficient of Variation,  $\sigma^2_g$ = Genotypic variance,  $\sigma^2_p$  = phenotypic variance,  $\sigma^2_e$  = Environmental variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation,  $h^2_b$ = Heritability, GA%M= Genetic advance in percent of mean



#### **4.1.6 Siliqua length (cm)**

Mean sum of square for siliqua length was highly significant in *Brassica rapa* (Table 2) indicating existence of considerable difference for this trait. The maximum siliqua length was found 6.00 cm and the minimum was recorded 4.40 cm with mean value 5.153 (Appendix III). The genotypic variance (0.07), phenotypic variance (0.30), genotypic co-efficient of variation (5.11) and phenotypic co-efficient of variation (10.58) were close to each other indicating less environmental influence in case of siliqua length. Heritability (23.33) estimates for this trait was genotypic advance in percent of mean (5.08), indicated that selection for this character would be effective (plate3). Labowitz (1989) studied *Brassica campestris* population for pod length and observed high genetic variation on this trait. Olson (1990) found high genetic variability for this trait.

#### **4.1.7 Thousand Seed Weight (g)**

Mean sum of square for thousand seed weight was highly significant in *Brassica rapa* (Table 2) indicating existence of considerable difference for this trait. The maximum thousand seed weight was found 0.40g and the minimum was recorded 0.30g with mean value 0.32 (Appendix III). The genotypic variance (0.0003), phenotypic variance (0.005), genotypic co-efficient of variation (5.40) and phenotypic co-efficient of variation (22.03) were close to each other indicating less environmental influence in case of thousand seed weight. Heritability (6.00) estimates for this trait was low together with considerable genetic advance in percent of mean (2.72) indicated that selection for this character would be less effective.

#### **4.1.8 Yield per plant (g)**

Mean sum of square for yield per plant (kg) was highly significant in *Brassica rapa* (Table 2) indicating existence of considerable difference for this trait. The maximum yield per plant was found 7.10g and the minimum was recorded 2.80g with mean value 4.44 (Appendix III). The genotypic variance (0.53), phenotypic variance (2.63), genotypic co-efficient of variation (16.22) and phenotypic co-efficient of variation (36.13) were close to each other indicating less environmental influence in case of yield per plant. The heritability value (38.02) as well as genetic advance in percent of mean (15.18) was observed very high. The very high heritability with moderate genetic advance in percentage of mean was provided opportunity for selecting high valued genotypes for breeding programme.

#### **4.1.9 Yield per plant (t/ha)**

Mean sum of square for yield (t/ha) was highly significant in *Brassica rapa* (Table 2) indicating existence of considerable difference for this trait. The maximum yield per hectare was found 2.30 ton and the minimum was recorded 0.90 ton with mean value 1.469 (Appendix III). The genotypic variance (0.06), phenotypic variance (0.29), genotypic co-efficient of variation (16.52) and phenotypic co-efficient of variation (36.32) were close to each other indicating less environmental influence in case of yield per plant. The heritability value (20.68) as well as genetic advance in percent of mean (30.62) was observed very high. The very high heritability with moderate genetic advance in percentage of mean was provided opportunity for selecting high valued genotypes for breeding programme.



## **4.2 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. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for 30 materials of *B. rapa* are shown in Table 3.

### **4.2.1 Plant height (cm)**

Plant height showed positive significant interaction with Number of primary branches (0.229), Number of secondary branches (0.024), number of Siliqua per plant (0.0738), seed per siliqua (0.098), thousand seed weight (0.017), yeild per plant(0.077) and yield per hecter (0.086) whereas negative interaction were found in length of siliqua (0.095) (Table 3). These findings are close resemblance to the reports of Chowdhury *et al.* (1987) and Yadava *et al.* (1978).

### **4.2.2 Number of primary branches per plant**

Number of primary branches per plant showed positive significant interaction with to number of secondary branch (0.366), umber of Siliqua per plant (0.444), seed per siliqua (0.069), length of siliqua (0.012), thousand seed weight (0.160), yield per plant(0.463) and yield per hectare (0.462) (Table 3). Similar results were obtained by Afroz *et al.* (2004), Rashid (2007), Siddikee (2006), Kumar *et al.* (1996), and Shabana *et al.* (1990).

#### **4.2.3 Number of secondary branches per plant**

Number of secondary branch showed positive significant interaction with number of Siliqua per plant (0.680), yield per plant(0.494), yield per hecter (0.496) Whereas negative interaction were found number of seed per siliqua (-0.030), siliqua length (0.066), Thousand seed weight (-0.203) (Table 3). These findings are closing similar to the reports of Chowdhary *et al.* (1987) and Mahmud (2008)



Table : 3 Correlations co-efficient among different characters of *Brassica rapa*:

|                         | Plant height | No. of primary branch | No. of secondary branch | No. of Siliqua /plant | No. of Seed/ Siliqua | Siliqua length | Thousand seed weight | Yield/plant | Yield/ha |
|-------------------------|--------------|-----------------------|-------------------------|-----------------------|----------------------|----------------|----------------------|-------------|----------|
| Plant height            |              |                       |                         |                       |                      |                |                      |             |          |
| No. of primary branch   | 0.229*       |                       |                         |                       |                      |                |                      |             |          |
| No. of secondary branch | 0.024*       | 0.361*                |                         |                       |                      |                |                      |             |          |
| No. of Siliqua /plant   | 0.073*       | 0.444*                | 0.680*                  |                       |                      |                |                      |             |          |
| No. o Seed/ Siliqua     | 0.098*       | 0.069*                | -0.030                  | -0.048                |                      |                |                      |             |          |
| Siliqua length          | -0.095       | 0.012*                | -0.066                  | 0.023*                | 0.507*               |                |                      |             |          |
| Thousand seed weight    | 0.017*       | 0.160*                | -0.203                  | -0.192*               | -0.152*              | -0.073         |                      |             |          |
| Yield/plant             | 0.086*       | 0.463                 | 0.494*                  | 0.568*                | 0.183*               | 0.066*         | 0.349*               |             |          |
| Yield/ha                | 0.086*       | 0.462                 | 0.496*                  | 0.568*                | 0.185*               | 0.065*         | 0.350*               | 0.999*      |          |

\* Significant at the 5% level of probability

#### **4.2.4 Number of Siliqua per plant**

Siliquea per plant showed positive significant interaction with siliquea length (0.02391), yield per plant (0.568715) and yield per hectare (0.568889), Whereas the negative interaction was found in number of seed per siliquea (0.04824) and thousand seed weight (0.19212) (Table 3). Dileep *et al.* (1997) reported that number of siliquae per plant, were positively correlated with seed yield. Tyagi *et al.* (1996) reported that no. of seeds per siliquea had positive and significant effects on seed yield per plant.

#### **4.2.5 Number of Seeds per Siliqua**

Seeds per Siliquea showed positive interaction with siliquea length (0.507222) and yield per plant (0.183042), yield per hector (0.185838) and negative interaction with thousand seed weight (-0.15235) (Table 3). Dileep *et al.* (1997) reported that number of siliquae per plant, thousand seed weight were positively correlated with seed yield. Tyagi *et al.* (1996) reported that no. of seeds per siliquea had positive and significant effects on seed yield per plant.

#### **4.2.6 Length of Siliqua (cm)**

Length of Siliquea showed positive significant interaction with yield per plant (0.066458), yield per hectare (0.06571) and showed negative interaction with thousand seed weight (-0.07392) (Table 3). Das *et al.* (1998) reported that seed yield per plant positively correlated with length of siliquea and seeds per siliquea.



#### **4.2.7 Thousand seed weight**

Thousand seed weight showed negative interaction with yield per plant (-0.34957) and yield per hectare (-0.35014) (Table 3). Saini and Sharma (1995), Kakroo and Kumar (1991) and Olsson (1990) found positive association which support the results.

### **4.3 MULTIVARIATE ANALYSIS**

#### **4. 3.1 Principal coordinates analysis (PCO)**

The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 30 genotypes of *Brassica rapa*. The highest intra-cluster distance was recorded in cluster IV (0.632) containing four genotypes G<sub>4</sub>, G<sub>5</sub>, G<sub>18</sub> and G<sub>29</sub>. The lowest intra-cluster distance was observed in cluster I (0.00) having one genotype G<sub>16</sub>. It favored to decide that intra-group diversity was the highest in cluster IV and the lowest in cluster I. The cluster II consisted thirteen genotypes viz. G<sub>2</sub>, G<sub>3</sub>, G<sub>6</sub>, G<sub>9</sub>, G<sub>10</sub>, G<sub>11</sub>, G<sub>14</sub>, G<sub>15</sub>, G<sub>23</sub>, G<sub>24</sub>, G<sub>25</sub>, G<sub>27</sub>, G<sub>28</sub> and had an intra-cluster distance 0.440. Cluster III having five genotypes viz. G<sub>1</sub>, G<sub>8</sub>, G<sub>12</sub>, G<sub>13</sub>, and G<sub>30</sub> and had an intra-cluster distance 0.482. Cluster V having seven genotypes and had an intra-cluster distance 0.323 (Table 4 and 5).

**Table 4. Distribution of thirty *Brassica rapa* genotypes in five clusters**

| Cluster | Number of genotypes | Genotype                                                    |
|---------|---------------------|-------------------------------------------------------------|
| I       | 1                   | G16                                                         |
| II      | 13                  | G2, G3, G6, G9, G10, G11, G14, G15, G23, G24, G25, G27, G28 |
| III     | 5                   | G1, G8, G12, G13, G30                                       |
| IV      | 4                   | G4, G5, G18, G29                                            |
| V       | 7                   | G7, G17, G19, G20, G21, G22, G26                            |

**Table 5. Average Inter and intra cluster distance of 30 *Brassica rapa* genotypes**

| Cluster | I      | II    | III    | IV    | V     |
|---------|--------|-------|--------|-------|-------|
| I       | 0.00   |       |        |       |       |
| II      | 18.858 | 0.440 |        |       |       |
| III     | 23.584 | 5.019 | 0.482  |       |       |
| IV      | 13.455 | 6.115 | 10.461 | 0.632 |       |
| V       | 15.960 | 3.310 | 7.937  | 3.915 | 0.323 |



### 4.3.2 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among thirty genotypes of *Brassica rapa* and grouped them into five 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 4 represents the clusters occupied by thirty genotypes of *Brassica rapa*. Cluster I contained the highest number of genotypes one, cluster II constitute by thirteen genotypes, cluster III constitute by five genotypes, cluster IV constitute by four genotypes, cluster V constitute by seven genotypes. Cluster I was composed of G16. The genotypes of cluster I was collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 9 traits are presented in (Table 6). Cluster II was formed by four genotypes viz. G4, G5, G18 and G29. They were collected from Plant Genetic Resource Centre, BARI, Gazipur. These clusters were unable to lead in respect of the highest cluster mean value for maximum characters.

Among nine characters cluster I produced the maximum cluster mean for the five characters viz. number of primary branch (7.90), number of secondary branch (10.90), number of siliqua per plant (239.70), yield/plant (6.70) and yield per hectare (2.20). Similarly, cluster II ranked first for thousand seed weight (0.34). Cluster III ranked the first for length of siliqua (5.24) and thousand seed weight (0.34). Cluster IV ranked the first for Plant height (102.22) and number of seed per siliqua (40.47) (Table 6).

Table 6. Cluster mean distance of thirty *Brassica rapa* genotypes

| Characters                | Cluster |        |        |        |        |
|---------------------------|---------|--------|--------|--------|--------|
|                           | I       | II     | III    | IV     | V      |
| Plant height (cm)         | 88.30   | 92.08  | 95.50  | 102.22 | 90.57  |
| No. of primary branches   | 7.90    | 6.51   | 5.88   | 6.50   | 7.27   |
| No. of secondary branches | 10.90   | 5.23   | 3.36   | 6.87   | 5.87   |
| No. of siliqua/plant      | 239.70  | 130.22 | 102.08 | 163.90 | 145.87 |
| No. of seed/siliqua       | 14.60   | 15.27  | 15.62  | 16.23  | 15.44  |
| Siliqua length (cm)       | 5.00    | 5.11   | 5.24   | 5.12   | 5.21   |
| 1000 seed weight (g)      | 0.30    | 0.34   | 0.34   | 0.30   | 0.30   |
| Yield/plant (g)           | 6.70    | 4.12   | 3.54   | 4.83   | 5.16   |
| Yield/ha                  | 2.20    | 1.37   | 1.16   | 1.60   | 1.70   |



#### **4.3.3 Contribution of characters towards divergence of the genotypes**

The values of Vector I and Vector II are presented in Table 7. Vector I obtained from PCA expressed that no. of seed per siliqua (0.227) and yield per plant (0.490) were major characters that contribute to the genetic divergence. It was the reflection of the first axis of differentiation. In vector II no. of primary branch (0.834) and yield per hectare (21.170), showed their important role toward genetic divergence. Negative values in both vectors for plant height, number of secondary branch, number seed per plant, number of seed per siliqua, length of siliqua and thousand seed weight had lower contribution towards the divergence.

**Table 7. Latent vectors for 9 principal component characters of 30 genotypes of *Brassica rapa***

| Characters                | Vector 1 | Vector 2 |
|---------------------------|----------|----------|
| Plant height (cm)         | -0.047   | -0.142   |
| No. of primary branches   | -0.232   | 0.834    |
| No. of secondary branches | -0.327   | -0.002   |
| no. of siliqua/plant      | -0.180   | -0.026   |
| No. of seed/siliqua       | 0.227    | -0.227   |
| Siliqua length (cm)       | -0.763   | -1.271   |
| 1000 seed weight (g)      | -2.185   | -2.002   |
| Yield/plant (g)           | 0.490    | -6.589   |
| Yield/ha                  | -0.238   | 21.170   |



#### **4.3.4 Selection of genotypes as parent for hybridization programme.**

Selection of generically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960, Ghaderi *et al.* 1984, Moll *et al.* 1962, Ramanujam *et al.*, 1974).

Considering the magnitude of cluster mean and agronomic performance the genotype G16 for maximum yield per hectare from cluster I and followed by G18 for maximum silique length and thousand seed weight from cluster V I; G13 (BD-6891) for maximum yield per hectare from cluster IV were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G16 and G18; G16 and G19; G16 and G22; G16 and G28 may be suggested for future hybridization program.

## CHAPTER V

### SUMMARY AND CONCLUSION

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period of October 2010 to March 2011 to study the inter genotypic variation among advanced lines of *Brassica rapa*. The experiment was carried out to study variability, heritability, genetic advance and genetic advance in percentage of mean, genetic diversity, character associations and direct and indirect effect of different traits on yield.

The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum differences between phenotypic and genotypic coefficient of variation were 7.09% and 11.42% respectively which indicated that the plant height mostly depended on environmental effect. The highest estimated heritability among ten yield contributing characters were 38.02, 35.73, 31.58, 23.33, 20.68 % was in yield per plant, no. of seed per silique, no. of silique per plant, length of silique and seed yield per plant. The lowest heritability was 6.00% in thousand seed weight.

The maximum genetic advance in percent of mean (GAMP) was obtained for yield per hectare (30.62%) and the lowest was for lowest thousand seed weight (2.72%). The significant positive correlation at the 5% level was observed for seed yield per plant with yield per hectare at genotypic level.

Multivariate analysis was carried out through principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat



5.13 software programme. As per PCA,  $D^2$  and cluster analysis using the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V comprised 1, 13, 5, 4 and 7 genotypes, respectively.

The highest intra-cluster distance was identified in cluster IV (0.632) and the lowest intra-cluster distance was observed in cluster I (00). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used for hybridization program.

Findings of the present study indicated significant variation among the genotypes for all the character studied. Considering group distance and other agronomic performance the inter genotypic crosses between G16 and G18; G16 and G19; G16 and G22; G16 and G28 may be suggested for future hybridization program

The result of the present study revealed that a wide variability exists among the collected *Brassica rapa* genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of *Brassica rapa*. From the findings of the present study, the following conclusions could be drawn:

- i. Wide range of genetic diversity existed among the *Brassica rapa* genotypes. That variability could be used for future breeding programme of *Brassica rapa* in Bangladesh.
- ii. Selection procedure would be applied for desired characters such as increase siliqua length, number of siliqua per plant to develop high yielding varieties.
- iii. Further collection of *Brassica rapa* germplasm would be continued for getting more variability and desired traits in *Brassica rapa*.

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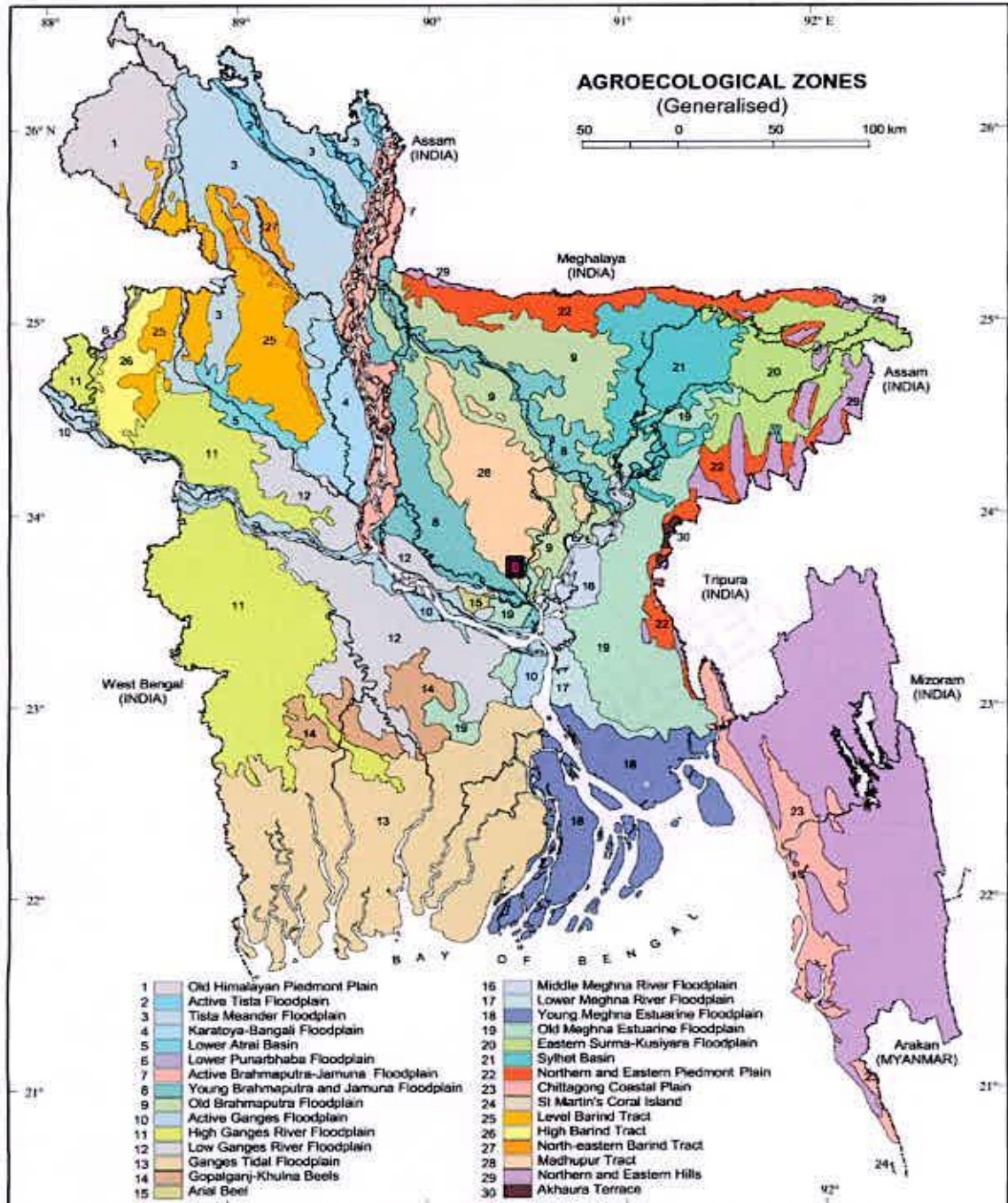
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## APPENDICES

### Appendix I. Map showing the experimental site under the study



REFERENCE ONLY

**Appendix II. Physical characteristics and chemical composition of soil of the experimental plot**

| Soil characteristics  | Analytical results    |
|-----------------------|-----------------------|
| Agrological Zone      | Madhupur Tract        |
| p <sup>H</sup>        | 6.00 – 6.63           |
| Organic matter        | 0.84                  |
| Total N (%)           | 0.46                  |
| Available phosphorous | 21 ppm                |
| Exchangeable K        | 0.41 meq / 100 g soil |

Source: Soil Resource and Development Institute (SRDI), Dhaka

**Appendix III: Mean performance of different parameters of thirty *Brassica rapa* genotypes**

| Identifier                | Minimum | Maximum | Mean   |
|---------------------------|---------|---------|--------|
| Plant height              | 81.20   | 124.00  | 93.52  |
| No. of primary branches   | 5.30    | 8.00    | 6.627  |
| No. of secondary branches | 1.80    | 10.90   | 5.477  |
| No. of siliqua/plant      | 81.70   | 239.7   | 137.3  |
| No. of seed/siliqua       | 12.10   | 19.30   | 15.47  |
| Siliqua length (g)        | 4.40    | 6.00    | 5.153  |
| 1000 seed weight          | 0.30    | 0.40    | 0.3233 |
| Yield/plant               | 2.80    | 7.10    | 4.44   |
| Yield/ha                  | 0.90    | 2.30    | 1.469  |

সত্যাবস্থা তথ্য বিশ্ববিদ্যালয় গাইবান্ধা  
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