MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERGENCE IN OLEIFEROUS BRASSICA SPECIES

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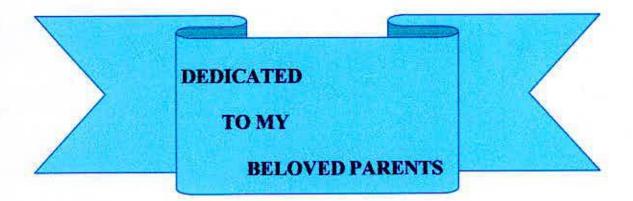
This is to certify that thesis entitled, "MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERGENCE IN OLEIFEROUS DRASSICA SPECIES" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE IN GENETICS AND PLANT DREEDING, embodies the result of a piece of bona fide research work, carried out by MOST. ISHRAT ZAHAN Registration No.26302/00580 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2006 Place: Dhaka, Bangladesh

(Dr. Md. Shahidur Rashid Bhuiyan) Supervisor





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The Author

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Møst. Ishrat Zahan

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 to study on the morphological characteristics and genetic divergence in oleiferous Brassica species. They showed wide variation and thus were categorized under three cultivated species - B. rapa, B. napus and B. juncea based on the morphological characteristics. The genotypes of three different species showed greater diversity. 41 genotypes were grouped in 6 different groups. Many of the groups comprise of the genotypes of the three different species. There is diversity among the genotypes of each species. 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 F1 and broad spectrum of variability in segregating generations. The phenotypic variance of each of characters was higher than respective genotypic variance showing the minimum role of environment on these characters. High heritability with low genetic advance was observed for the characters days to 50% flowering, days to maturity, primary branches/plant, 1000-seed weight and yield/plant. Yield/plant confirmed highly significant positive association with plant height (0.503), length of siliquae (0.277), siliquae/plant (0.658) and seed/siliquae (0.303) but insignificant negative association with days to 50% flowering (-0.058) days to maturity (-0.092).Path analysis showed that siliquae/plant had positive direct effect (0.628) on yield/plant. Path analysis revealed that days to 50% flowering had negative direct effect (-0.184) on yield/plant.

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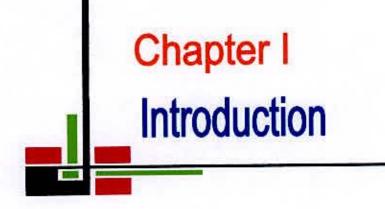


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Chapter I

INTRODUCTION

The oleiferous *Brassica* symbolized by rapeseed and mustard is one of the leading oilseed crops in our country. In Bangladesh more than 210.57 thousand metric ton of rape and mustard produced from total 279.23 thousand hectares of cultivable land in the year 2003-2004 (BBS, 2005). It is used as a condiment, salad, green manure and fodder crop, and as a leaf and stem vegetable in the various mustard growing countries of the World. There are only a few varieties of mustard in our country. So, to have sufficient in oil production we should develop high yielding mustard varieties. It is mainly self-pollinating crop, although on an average 7.5 to 30% out-crossing does occur under natural field conditions (Abraham, 1994; Rakow and Woods, 1987).

The genus *Brassica* has generally been divided into three groups namely, (i) the mustard (ii) the rapeseed and (iii) the cole. The genomic constitutions of the three elemental species of *Brassica* are as follows: 'AA' for *B. rapa*, 'BB' for *B. nigra* and 'CC' for *B. oleracea* having haploid chromosome number 10, 8 and 9, respectively. The species *B. juncea* (AABB), *B. carinata* (BBCC) and *B. napus* (AACC) are the amphidiploids, and originated by combinations 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 morpho-physiological characters (Malik *et al.*, 1995; Nanda *et al.*, 1995; Kakroo and Kumar, 1991; Singh *et al.*, 1991, Li, *et al.*, 1989).

The variability among different genotypes of a species is known as genetic diversity. It arises either due to geographical separation or due to genetic barriers to crossability. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations.

Hybridization is one of the major tools for the improvement of a crop. Before hybridization genetic diversity of the existing varieties need to be known. It is well established that the greater the genetic diversity the higher the chance of getting better hybrid or recombinant. Genetic diversity is one of the fundaments of plant breeding. It is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973; Khanna and Chaudhary, 1974, Chandra, 1977). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991).

Different types of local races, advanced lines and exotic materials of mustard and rape seed are available in our country. To utilize the variabilities, it is necessary to asses the genetic variations in respect of genetic and phenotypic co-efficient of variation, heritability, genetic advance and other relevant parameters which have been reported by many authors (Kumar *et al.*, 1996; Nanda *et al*, 1995; Biswas, 1989, Lebowitz, 1989; Yadava *et al.*, 1985). Such study can help in better and effective understanding of genetic variability and its utilization in breeding programs.

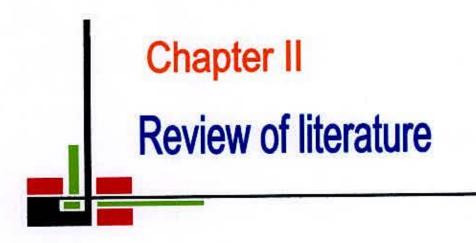
If a plant breeding program is to be advanced more rapidly and efficiently, knowledge of inter-relationships between yield contributing characters is necessary. Thus, determination of correlation between characters has a considerable importance in selection practices, since it helps in the construction of selection indices and also permits for the prediction of correlated response.

The seed yield of mustard is a complex character and is being associated with some other related plant growth characters. The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution of different plant characters to the total divergence has been carried out by several workers (Anand and Rawat, 1984, Balasch *et al.*, 1984, Ariyo, 1987, Patil *et al.*, 1987).

Precise information about the extent of genetic divergence and on characters used for discrimination among the population is crucial in any crop improvement program, because selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980; Ananda and Rawat, 1984; De *et al.*, 1988).

With conceiving the above scheme in mind, the present research work has been undertaken in order to fulfilling the following objectives:

- i. To categories the various germplasm of rapeseed and mustard under different species;
- To analyze the genetic diversity of the genotypes in respect of different morphological characters;
- iii. To screen out the suitable genotypes for future program.



Chapter II

REVIEW OF LITERATURE

Oleiferous *Brassica* is one of the common and most important oil crops of Bangladesh and as well as many countries of the world. The crop has received much attention by the researchers on various aspects of its production and utilization for different consumer uses. Many studies on the variability, correlation, heritability and genetic advance have been carried out in many countries of the world. The work so far done in Bangladesh is not adequate and conclusive. Nevertheless, some of the important and informative works and research findings have been reviewed in this chapter under the following headings:

2.1 Genetic Diversity

Cluster analysis showed a wide diversity of genotypes from the same geographical regions. An investigation was conducted by Malik *et al.* (1997) to determine the extent of diversity and relationships among the *B. juncea* germplasm from Pakistan using morphological characters and showed a comparatively low level of phenotypic variation amongst them and where genetically similar to the oilseed cultivars. However, the oilseed forms and vegetable cultivars were genetically distinct. They revealed that the evaluated germplasm appears to have a narrow genetic base which undergoes a high level of genetic erosion.

Choudhary and Joshi (2001) studied genetic diversity among 88 entries including eighty F₄ derivatives i.e., 20 each selected from *Brassica* crosses viz., *B. juncea* × *B. napus*, *B. juncea* × *B. rapa* var. *toria*, *B. juncea* × *B. rapa* var. yellow sarson and *B. tournefortii* × *B. juncea*, and eight parent genotypes was assessed through multivariate analysis and reported significant differences among the family groups as well as within the family were recorded for the trait that were studied. The multivariate (D^2) analysis revealed enormous diversity

among inter specific cross derivatives. They also calculated genetic distances among different *Brassica* species revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus*, *B. rapa* varity *toria* and *B. rapa* variety yellow sarson. They reported that the derivatives selected from cross of diverse parents revealed greater diversity. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. They also reported that the traits namely, plant height, secondary branches/plant, days to flowering and 1000-seed weight were contributed maximum towards genetic divergence.

Islam and Islam (2000) evaluated the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. 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 are days to 50% flowering, plant height, branches/plant and siliquae/plant.

Uddin (1994) reported from an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The genotypes felt into four clusters. The inter-cluster distance was larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster values were lower in all the clusters.

Reddy *et al.* (1987) conducted a study of genetic divergence of groundnut for pod yield/plant and 12 related characters by Mahalanobis' D^2 statistics. The greatest inter cluster distance was observed between clusters I (with 10 to 11 varieties depending on years) and II (4 to 6 varieties) and between clusters I and IV.

2.2 Variability

The improvement of a crop is dependent on the magnitude of genetic variability and the extent of heritability of desirable characters of the genotypes available. A critical review of genetic variability is therefore, a prerequisite for planning and evaluation of a breeding program.

Plant height is an important character which is largely influenced by genotype, soil, water availability, temperature etc. But significant genetic variability was observed by many researchers like Kumar et al. (1996), Malik et al. (1995), Kumar and Singh (1994), Singh et al. (1991), Gupta and Labana (1989), Chauhan and Singh (1985) among different genotypes of *B. napas*, *B. campestries* and *B. juncea*.

Labana *et al.* (1987) studied 39 strains of Ethiopian mustard and found low genetic variation. When Varshney *et al.* (1986) found high variability in plant height working with a number of strains of *B. napus*, *B. juncea* and *B. rapa*. Genotypic Co-efficient of Variation (GCV) for plant height in different genotypes of *B. juncea* was found to be 10.96 by Singh *et al.* (1987), 9.3 by Labana *et al.* (1980), 31.38 by Yadava (1973), 21.16 in brown sarson by Bhardwaj and Singh (1969), 12.32 in yellow sarson and 5.9 in toria by Tak and Patnaik (1977).

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 Kumar and Singh (1994), Kakroo and Kumar (1991), Yin (1989), Biswas (1989), Jain *et al.* (1988), Labana *et al.* (1987), Gupta *et al.* (1987). GCV and PCV values of 14.44 and 24.43 were reported by Singh *et al.* (1987) in different strains

of *B. juncea*. But, according to Tak and Patnaik (1977) these values were 33.2 and 57.1 in yellow sarson.

Number of siliquae/plant is one of the most important traits of oleiferous *Brassica*. In general, higher the siliquae number higher the seed yield. Variation in this mannerism was observed by several researchers. Yin (1989) worked on 8 cultivars of *B. napus* and found high genetic variation for number of siliquae/plant. Similar result was also reported by Kumar *et al.* (1996), Kudla (1993), Andrahennadi (1991), Singh *et al.* (1991), Biswas (1989). GCV and PCV for this character were 25.41 and 29.15 as observed by Singh *et al.* (1987). GCV was found to be 18.85 by Yadava (1973) and 97.3 by Bhardwaj and Singh (1969). Tak and Patnaik (1977) observed GCV and PCV in yellow sarson as 55.4 and 53.2 and in Toria as 27.1 and 23.5, respectively. From the above reviews, it is obvious that sufficient genetic variation exist in this character.

Number of the seeds per siliquae is another important component attribute. Normally higher number of seeds per siliquae is advantageous. A good number of literatures are available on the variability of this trait. Kumar *et al.* (1996) evaluated this character in 12 genotypes of Indian mustard (*B. juncea*) and found significant variability among different genotypes. Similar results were observed by Kumar and Singh (1994), Kudla (1993), Kakroo and Kumar (1991), Biswas (1989). Genotypic co-efficient of variation in 29 genotypes of *B.* juncea was observed as 14.46 by Yadava (1975), but it was 35.85 as observed by Bhardwaj and Singh (1969) in different genotypes of *B. rapa*. Again, Tak and Patnaik (1977) observed GCV 13.1 and PCV 18.5 in yellow sarson and GCV 16.3, PCV 22.6 in toria. But Singh *et al.* (1987) observed GCV and PCV in different genotypes of *B. juncea* as 6.46 and 9.5, respectively and Labana *et al.* (1980) observed 9.82 and 15.96, respectively.



Variability in consideration of days to 50% flowering, an important yield component, is very useful in selecting materials of short, medium or long duration crop. In general, early flowering genotype mature early and late flowering genotype delayed maturity. Several workers investigated the variability in respect of days to flowering. Nanda *et al.* (1995) reported from an experiment conducted with 65 strains of *Brassica napus*, *B. rapa*, *B. juncea* and *B. carinata* found days to 50% flowering varied by genotype. Singh *et al.* (1991) studied different morphological characters of 29 genotypes of *B. napus* and *B. rapa* grown under normal and stress conditions of *Brassica* production. They found the existence of significant genetic variability for days to 50% flowering. Kumar *et al.* (1996), Kumar and Singh (1994), Andrahennadi (1991), Biswas (1989), Singh *et al.* (1987), Chauhan and Singh (1985), Thurling (1983), Thakral (1982) and many other researchers worked with different genotypes of *Brassica*. In general, according to them, significant variations were observed in the character for days to 50% flowering.

Jain *et al.* (1988) in an experiment analysis of gene effects using means of six populations of a cross Varuna X YRT-3 of Indian mustard and observed that dominance gene action was important in the expression of days to flowering. Partial dominance was observed for this character by Kumar *et al.* (1991). It is evident from all these results that sufficient genetic variations exist for days to 50% flowering.

Days to maturity for any crop are most important criteria for assessment of variability. It is influenced by genotypes and various environmental factors. Significant genetic variation was found by several workers among different genotypes of rapeseed and mustard. Biswas (1989) found high GCV and PCV among 18 genotypes of *B. napus* while Sharma (1984) working with 46 genotypes of *B. juncea* and found low GCV and PCV values. Yadava (1973) found 7.6 GCV among 29 strains of *B. juncea*, while in yellow sarson Tak and Patnaik (1977) found

this value as 4.5 and 1.8, respectively. Significant variation for days to maturity was also found by Kumar and Singh (1994), Singh *et al.* (1991), Grosse and Geisler (1988), Khera and Singh (1988), Gupta *et al.* (1987), Chauhan and Singh (1985) and many other researcher in their research work.

Thousand seed weight which reflects the seed size is also an important component attribute. It differs widely from genotype to genotype and influenced by some factors of yield. A considerable number of research works have been conducted on this character. Significant variation was observed among a large number of strains of *B. rapa*, *B. napus* and *B. juncea* by Kumar and Singh (1994), Singh (1993), Yadav *et al.* (1993), Kudla (1993), Andrahennadi *et al.* (1991), Biswas (1989), Lebowitz (1989), Chowdhury *et al.* (1987). In a trail Bhardwaj and Singh (1969) observed 50.74 GCV for 1000 seed weight while same were 13.1 PCV was 16.5 in brown sarson as reported by Tak and Patnaik (1977). According to Singh *et al.* (1987), GCV and PCV in *B. juncea* were 17.86 and 21.39, respectively.

Yield is a very important character for almost every breeding program. It is a complex trait influenced largely by a number of characters and factors of crop production. A good number of research findings revealed the existence of variability among different genotypes of rapeseed and mustard. Significant variability was recorded earlier by Kumar *et al.* (1996), Kudla (1993), Kakroo and Kumar (1991), Gupta and Labana (1989), Yin (1989) and also many other researcher. 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).

From the reviews above it is clear that a wide range of variability existed for different morphological characters among different genotypes of *Brassica* oil crops and it indicates the scope of utilization of these variability for further breeding programs.

2.3 Heritability and Genetic Advance

The variation of heritability can be estimated with greater degree of accuracy when heritability in conjunction with genetic advance as percentage of mean is studied. Johnson *et al.* (1995) suggested the necessity of estimating genetic advance along with heritability in order to draw a more reliable conclusion in a selection program. Many experiments have been conducted in the investigation of heritability and genetic advance on yield and yield components of mustard. The most relevant reviews are reviewed here.

Malik *et al.* (1995) observed very high broad sense heritability (>90%) for number of primary branches, days to 50% flowering and oil content while working with different strains of *B. napus*. They also found low heritability (<50%) for number of siliquae/plant, number of seeds/siliquae, plant height and yield. But Singh *et al.* (1991) found high heritability for all these characters. Li *et al.* (1990) also recorded similar high heritability results in studies with *B. napus*.

Varshney et al. (1986) found high heritability and high genetic advance for plant height when conducted an experiment of 45 genotypes of *B. napus*, *B. rapa* and *B. juncea* species; but high heritability and genetic advance for siliquae/plant only in *B. rapa*. Singh (1986) studied 22 genotypes of *B. napus*, *B. rapa* and *B. juncea* and reported high heritability and genetic advance in seed yield, 1000 seed weight and number of seeds/siliquae. Inheritance of seed oil content was studied by Han (1990) in 7 inbreeds of *B. napus*, crossed in a diallel fashion and reported high heritability (81.16%) for this trait. However, Yadaya et al. (1985) reported low heritability for oil content in *B. juncea*. Wan and Hu (1983) observed high heritability and genetic advance for flowering time, number of primary branches/plant and plant height. Low heritability of yield was reported by many researchers like Malik *et al.* (1995), Kumar *et al.* (1988), Yadava *et al.* (1985), Chen *et al.* (1983); but Singh (1986) reported high heritability for this character.

In a study Sharma (1984) observed high heritability for plant height, days to flowering and low heritability for days to maturity when working with 46 genotypes of *B. juncea*. He also found low genetic advance for days to maturity and high genetic advance for yield/plant. In another study of Indian mustard Singh *et al.* (1987) observed high heritability (80-95%) for oil content and yield/plant. The lowest heritability (34.9%) was recorded for number of primary branches per plant.

Labana *et al.* (1980) found that plant height and number of seeds/siliquae were highly heritability, whereas, number of primary branches and seed yield per plant were less heritable when working with 104 mutants of Indian mustard. The yield variation thus principally owed to the environmental influence, for which selection would not be much effective. The selection of the material would be more practicable for plant height and number of seed/siliquae. This confirmed the finding of Chaudhari and Prasad (1968). In the same experiment the genetic advance was highest for plant height (13.75%) followed by number of seeds/siliquae (12.43%) and seed yield/plant (9.75%). This offers scope for this improvement through selection. This is because high heritability and genetic advance together provide better indication of the amount of genetic progress that can result from selection of the best individuals.

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

Thurling (1974) reported in the genotypes of *B. rapa* that the expected genetic advance in yield using a selection index technique based on simultaneous selection of several characters was significantly greater than that expected from selection for yield alone, and several indices including measurement of both yield components and vegetative characters were expected to promote a greater ratio of advance in yield than direct selection.

From the exceeding review it can be concluded that approximately all characters expected yield are high heritable in nature and the predictable genetic advance, being high for plant height, primary branches/plant, 1000 seed weight and yield, assortment is possible for high yield using number of characters in selection programs.

2.4 Character Association

Studies on relationships among different yield contributing characters are essential for effective in selection program, particularly when a number of characters are concerned.

Chaturvedi et al. (1988) found significant positive correlation between seed yield and plant height, days to flowering and days to maturity. Working with 65 strains of *B. juncea*, *B. rapa* and *B. napus*, Nanda et al. (1995) observed positive association between yield and siliquae filling period. Olsson (1990) found the similar result in *B. napus*. He also found positive correlation between siliquae density and yield.

The random mating of *B. rapa* population was evaluated by Labowitz (1989) and reported that siliquae length was positively correlated with both 1000 seed weight and seeds/siliquae. Several experiments were carried out by Chay and Thurling (1989) to study the inheritance of siliquae length among several lines of *B. napus*. Results suggested that lines with the longest siliquae generally provided significantly higher yield than those with short siliquae.

Dorn and Mitchell (1991) reported positive correlation between flowering dates while working with 12 strains of *B. rapa*. Shivahare *et al.* (1975) found days to flowering were positively correlated with primary branches/plant (+0.855). But Kumar *et al.* (1996), working with 12 genotypes of *B. juncea* found flowering time and height negatively correlated with number of primary branches/plant. Labana *et al.* (1980) also found that number of primary branches was negatively correlated with plant height and siliquae length. Number of primary branches/plant was found negatively correlated with siliquae length and 1000 seed weight, but positively with number of siliquae/plant by Singh *et al.* (1987).

Plant height was found to be negatively correlated with siliquae length (-0.208) and seeds/siliquae (-0.254) by Labana *et al.* (1980). Positive correlation of plant height with seeds/siliquae (-0.297), number of siliquae/plant (+0.81) and negative correlation with 1000 seed weight (-0.175) were reported by Chowdhury *et al.* (1987). Singh *et al.* (1987) found positive correlation of plant height with number of siliquae/plant (+0.38), number of primary branches/plant (+0.216), seeds/siliquae (+0.19) in 179 genotypes of Indian mustard. Banerzee *et al.* (1968) also found positive association of plant height with these traits in 8 strains of yellow sarson.



Yadava et al. (1978) and Chowdhury et al. (1987) found to positive associated with days to 50% flowering and days to 80% maturity in 1000 seed weight 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, number of siliquae/plant was also reported by Chowdhury et al. (1987) and Yadava et al. (1978). Significant positive association was found between days to maturity and days to flowering by Yadava et al. (1978), Varshney et al. (1986) and Chowdhury et al. (1987).

Han (1990) while working with *B. napus*, reported that oil content was positively associated with plant height, seeds/siliquae but negatively with siliquae length and number of siliquae/plant. Positive correlation with flowering time, days to maturity and 1000 seed weight was observed by Yadava *et al.* (1978) and Singh *et al.* (1987).

Yield is a complex character which is correlated with many other characters. There are a number of literatures available on the relationship of different characters with yield in mustard.

2.5 Path Co-efficient Analysis

Partitioning the correlation co-efficient into components of direct and indirect effects are necessary because correlation co-efficient alone does not give a complete picture of the causal basis of association. It is established that as the number of contributing characters increased, the indirect association becomes more complex and important. Under such circumstances, path co-efficient analysis is an effective tool in assigning the direct and indirect effects of different yield contributing traits.

Saini and Kumar (1995) conducted an experiment to evaluate the character association and path co-efficient analysis were used to determine relationships between growth and yield parameters in 28 lines of yellow and brown sarson (*B. campestries*) and their findings revealed that seeds/siliquae and seed weight had direct positive effect on yield.

Kudla (1994) while working with 20 genotypes of winter swede rape found that 1000 seed weight had positive direct effect and oil content had negative direct effect on yield. The direct and indirect effects of 6 main and 9 sub components of morphophysiological determinants and their contribution to oil yield were studied by Behl *et al.* (1992) in 25 diverse genotypes of *B. juncea*. The greatest effect on yield directly from seed yield and indirectly from number of siliquae/plant, 1000 seed weight, seeds/siliquae and siliquae length contributed to oil yield *via* one or more components. Gupta *et al.* (1987) also found that seed yield had the highest direct effect on oil yield. They also observed the direct effect of primary branching and 1000 seed weight of seed yield.

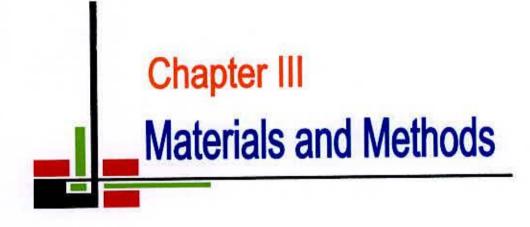
Eleven diverse *Brassica* genotypes and one of the *Eruca sativa* lines were evaluated by Chaudhary *et al.* (1990) over 5 years on the basis of morphophysilogical parameters for drought resistance. They found, days to 50% flowering and plant height contributed to plant yield indirectly *via* one or more main components. The erucic acid free rape cultivars Callypso, Semu-2080, Semu DNK-203/84 and Semu-304 were evaluated by Shabana *et al.* (1990) for 15 quantitative characters. They found the highest direct effect on number of siliquae/plant on seed yield/plant.

Kakroo and Kumar (1991), working with several strains of *B. juncea* found that 1000 seed weight and positive direct effect, but days to 50% flowering and primary branches had negative indirect effect *via* seeds/siliquae on seed yield. But Chauhan and Singh (1985) observed high positive direct effect of days to 50% flowering, plant height, primary branching, siliquae/plant, seeds/siliquae on yield. Kumar *et al.* (1988) observed the indirect

positive effect of days to 50% flowering on yield. Again Han (1990) working with *B. napus* and observed negative direct effect of number of siliquae/plant, siliquae length and positive direct effect of seeds/siliquae and plant height on yield.

Kumar et al. (1984) observed the negative indirect effect of days to flowering via plant height and siliquae length on yield in *B. juncea*. Singh et al. (1978) also found negative direct effect of these characters. But Dhillon et al. (1990) observed the highest positive direct effect of plant height on seed yield/plant.

The results of several experiments conducted by Das and Rahman (1989) in *B. rapa*, Ghosh and Chatarzee (1988) in *B. juncea*, Mishra *et al.* (1987) in *B. rapa*, Alam *et al.* (1986) in *B. juncea*, Singh *et al.* (1985) in *B. juncea*, Chen *et al.* (1983) in *B. napus*, Srivastava *et al.* (1983) in *B. juncea* and Yadav (1982) in *B. rapa*, revealed that plant height, days to maturity, 1000 seed weight, siliquae/plant and seeds/siliquae had positive direct effect and indirect effect on yield. But Varshney (1986) working with several strains of *B. rapa* and found the negative direct effect of plant height, siliquae/plant, seeds/siliquae and 1000 seed weight on yield. Chauhan *et al.* (1985) working with 20 genotypes of *B. rapa*.



Chapter II1



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 from November 2005 to March 2006 to study on the morphological characterization and genetic divergence in oleiferous *Brassica species*. The materials and methods of this experiment are presented in this chapter under the following headings -

3.1 Experimental Site

The present piece of research work was conducted in the field of Genetics and Plant Breeding Field Laboratory of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka, Bangladesh. The location of the site is 23⁰74['] N latitude and 90⁰35['] E longitude with an elevation of 8.2 meter from sea level.

3.2 Characteristics of Soil

The soil of the experimental area was loamy belonging to the Madhupur Tract (UNDP, 1988) under AEZ 28. The selected plot was medium high land.

3.3 Weather Condition of the Experimental Site

The geographical situation of the experimental site was under the subtropical climate, characterized by three distinct seasons, the monsoon or rainy season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October (Edris *et al.*, 1979). Details of the metrological data of air temperature, relative humidity, rainfalls and sunshine during the period of the experiment was collected from the weather station of Bangladesh, Sher-e Bangla Nagar, presented in Appendix I.

3.4 Planting Materials

In this research work, the seeds of oleiferous *Brassica* were used. Each of the genotypes was produced in the 2004-2005 cropping season, and the purity and germination percentage were leveled as around 100 and above 90, respectively. The source all of the genotypes used in this experiment was Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur. The name of the genotypes are presented in Table 1.

SI. No.	Genotypes	Sl. No.	Genotypes
01	6955	22	7135
02	7102	23	7136
03	7113	24	7137
04	7114	25	7138
05	7115	26	8884
06	7116	27	7126
07	7118	28	7128
08	7125	29	7788
09	7129	30	7789
10	7837	31	7790
11	7958	32	7815
12	9061	33	7830
13	SAU-YC	34	7831
14	7104	35	7832
15	7107	36	7833
16	7117	37	7834
17	7127	38	7835
18	7131	39	7836
19	7132	40	9101
20	7133	41	9102
21	7134		

Table 1. Name of oleiferous Brassica genotypes used in the present study

3.5 Layout of the Experiment

The experiment was laid out in the Randomized Complete Block Design (RCBD) with three replications. The layout of the experiment was prepared for distributing the genotypes into the every plot of each block. There were 41 plots, each measuring $2.5 \text{ m} \times 1.0 \text{ m}$ in each of 3 replications. The 41 genotypes of the experiment were assigned at random into 41 plots of each replication. The distance maintained between two plots was 50 cm between blocks was 75 cm.

3.6 Preparation of the Main Field

The plot selected for the experiment was opened in the first week of November 2005 with a power tiller, and was exposed to the sun for a week, after one week the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain a good tilth. Weeds and stubbles were removed, and finally obtained a desirable tilth of soil for sowing of *Brassica* seeds. The experimental plot was partitioned into the unit plots in accordance with the experimental design mentioned in 3.5. Recommended doses of well-rotten cowdung manure and chemical fertilizers as indicated in 3.7 were mixed with the soil of each unit plot.

3.7 Application of Manure and Fertilizers

The fertilizers N, P, K, S and B in the form of urea, TSP, MP, Gypsum and borax, respectively were applied. The entire amount of TSP, MP, Gypsum, Zinc sulphate and borax was applied during the final preparation of land. Urea was applied in two equal installments at before sowing and flowering. The dose and method of application of fertilizer are shown in Table 2.

Fertilizers	Dose (kg/ha)	Application (%)	
		Basal	Before flowering
Urea	250	50	50
TSP	170	100	
MP	85	100	
Gypsum	150	100	
Borax	60	100	in Flor

Table 2. Dose and method of application of fertilizers in Brassica field

Source: Krishi Projukti Hatboi, BARI, Joydebpur, Gazipur

3.8 Sowing of Seeds in the Field

The seeds were sown in lines each having a line to line distance of 40 cm under direct sowing in the well prepared plot on 17 November 2005.

3.9 After Care

When the seedlings started to emerge in the beds it was always kept under careful observation. After emergence of seedlings, various intercultural operations were accomplished for better growth and development of the *Brassica* seedlings.

3.9.1 Irrigation

Light over-head irrigation was provided with a watering cane to the plots once immediately after germination and continued for three times for proper growth and development of the plants.

3.9.2 Thinning and Gap Filling

The seedling were first thinned from all of the plots at 10 Days after sowing (DAS) 2nd thinning was carried out after 7 days for maintaining proper spacing the experimental plots.

3.9.3 Weeding and Mulching

Weeding and mulching were done to keep the plots free from weeds, easy aeration of soil and to conserve soil moisture, which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully after complete emergence of *Brassica* seedlings and whenever necessary. Breaking the crust of the soil, when needed were done through mulching.

3.9.4 Top Dressing

After basal dose, the remaining doses of urea were top-dressed in 2 equal installments. The fertilizers were applied on both sides of plant rows and mixed well with the soil.

3.10 Plant Protection

Malathion 57 EC insecticide was applied after one month of seeds sowing at 12 days interval for 3 times with 1 ml in 2.5 liters water as a preventative measure against different fungal diseases.

3.11 Harvesting, threshing and cleaning

The crop was harvested depending upon the maturity of each genotype. Harvesting was done manually. Enough care was taken for harvesting, threshing and also cleaning of *Brassica* seed.

3.12 Species identification

The 41 genotypes used in the present study were not under single mustard rape seed species. They showed wide variation and thus were categorized under three cultivated species – *B. rapa*, *B. napus* and *B. juncea* based on the morphological characteristics.

3.13 Data recording

3.13.1 Days to 50% flowering

Difference between the dates of sowing to the date of flowering of a plot was counted as days to 50% flowering. Days to 50% flowering was recorded when 50% flowers of a plot were at the flowering stage.

3.13.2 Days to maturity

Maturities of the crops of 41 genotypes were recorded considering the maturity symptom such as color changing of the plant from greenish to straw colored appearance.

3.13.3 Plant height

The height of plant was recorded in centimeter (cm) at harvest in the experimental plots. Data were recorded as the average of 10 plants selected at random from the inner rows of each plot after harvest. The height was measured from the ground level to the tip of the growing point of the main branch.

3.13.4 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.

3.13.5 Number of secondary branches/plant

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

3.13.6 Number of siliquae/plant

The total numbers of siliquae of the randomly selected 10 plants of a plot were recorded and then average numbers of siliquae were estimated.

3.13.7 Length of siliquae

Distance between the ends of the peduncle to the starting point of the beak was recorded as siliquae length and was presented in centimeter (cm).

3.13.8 Number of seed/siliquae

Ten siliquae from each plant were selected randomly and number of seeds was counted and the average number of seed per siliquae was determined.

3.13.9 1000 seed weight

One thousand seeds were counted randomly from the total seeds of cleaned harvested seeds and then weighted in grams.

3.13.10 Yield/plant

Seed weight per plant was measured from the randomly selected plants and then average was designated as seed yield per plant.

3.14 Statistical analysis

The data obtained for different characters were statistically analyzed to find out the significance of the difference among the *Brassica* genotypes. The mean values of all the characters were evaluated and analysis of variance was performing by the 'F' test. The significance of the difference among the treatments means was estimated by the least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984). Correlation coefficient was estimated according to Singh and Chaudhury (1985).

3.15 Analysis of genetic divergence

3.15.1 Score index for selection

The breeding population of even a single species differs significantly in many characteristics. Therefore, in the present experiment which included 41 genotypes, score index for selection was used. The score index was prepared considering two groups of characteristics viz. Plant characters (Group I) and seed and siliquae characters (Group II). These grouping also helped in finding out the best performance for a group of characters and all characters together.

Group I (Plant characters)

i. Days to 50% flowering	: 25-30=1; 30-35=2; 35-40=3, 40-45=4; rest 5
ii. Days to 80% maturity	: 60-70=1; 70-80=2; 80-90=3; 90-100=4; rest 5

iii. Plant height (cm): above 140=1, 140-120=2, 120-100=3, 100-80=4; rest 5iv. Number of primary branches/plant: above 8 =1; 8-7=2; 7-6=3; 6-5=4; rest 5v. Number of secondary branches/plant: above 8 =1; 8-7=2; 7-6=3; 6-5=4; rest 5

Group II (Seed and siliquae characters):

i. Number of siliquae/plant	: above 170=1; 170-140=2; 140-110=3; 110-80=4; rest 5
ii. Length of siliquae (cm)	: above 5=1; 5-4.5=2, 4.5-4.0=3; 4.0-3.5=4; rest 5
iii. Number of seed/siliquae	: above 30=1, 30-25=2, 25-20=3; 20-15=4; rest 5
iv. 1000 seed weight (g)	: 5.0-4.5=1; 4.5-4.0=2; 4.0-3.5=3; 3.5-3.0=4; rest 5
v. Yield/plant (g)	: 9-8=1, 8-7=2; 7-6=3, 6-5=4; rest 5

[Note: 1, 2, 3, 4 and 5 represent most desired to less and less desired one among the genotypes]

Genetic divergences among the genotypes studied were assessed by using Mahalanobis' D² statistics and its auxiliary analysis. Both techniques estimate divergences among a set of genotypes on multivariate scale.

3.15.2 Mahalanobis' D² statistics

First the variation among the materials were tested by Wilkin's criteria 'A'.

 $\frac{|W|}{|S|} = \frac{|W|}{|Determination of error matrix|}$

Now, 'v' $_{(stat)} = -m \log_{e^{-}} = - \{n-(p+q+1)/2\} \log_{e^{-}}$

Where,

$$m = n-(p+q+1)/2$$

$$p = number of variables or characters$$

$$q = number of varieties - 1 (or df for population)$$

$$n = df for error + varieties$$

$$e = 2.7183$$

Data were then analysed for D^2 statistics according to Rao (1952). Error variance and covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Using the pivotal elements the original means of the characters (X₁, X₂-----X₈) were transformed into a set of uncorrelated variables (Y₁, Y₂-----Y₈). Now, the genetic divergence between two varieties/lines (suppose Vi and Vj was calculated

$$D^2 ij = \sum_{k=1}^{8} (Vik - Vjk)^2$$

Where,

as -

D²ij = Genetic divergence between 'i' th and 'j' th genotypes

Vik = Transformed mean of the 'i' th genotype for 'k' th character

Vik = Transformed mean of the 'j' th genotype for 'k' th character

The D² values between all varieties were arranged in order of relative distances from each other and were used for clusters formation, as suggested by Rao, 1952.

Average intra-cluster $D^2 =$

$$\frac{\sum D^2 i}{n}$$

Where,

\sum D²i = Sum of distances between all possible combinations (n) of the genotypes included in a cluster.

n = All possible combinations

3.16 Estimation of variability

Genotypic and phenotypic coefficient of variation and heritability were estimated by using the following formulae:

3.16.1 Estimation of components of variance from individual environment

Genotypic and phenotypic variances were estimated with the help of the following formula suggested by Johnson *et al.* (1955). The genotypic variance (σ^2_g) was estimated by

subtracting error mean square (σ_e^2) from the genotypic mean square and dividing it by the number of replication (r). This is given by the following formula -

Genotypic variance $(\sigma_g^2) = \frac{MS_V - MS_E}{r}$ Where, $MS_V = \text{genotype mean square}$

 MS_E = error mean square

r = number of replication

The phenotypic variance (σ_p^2) , was derived by adding genotypic variances with the error variance, as given by the following formula –

Phenotypic variance $(\sigma_{ph}^2) = \sigma_g^2 + \sigma_c^2$

Where,

 σ_{ph}^{2} = phenotypic variance σ_{g}^{2} = genotypic variance σ_{e}^{2} = error variance

3.16.2 Estimation of genotypic co-efficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were

calculated following formula as suggested by Burton (1952):

% Genotypic coefficient of variance = $\frac{\sigma_8}{x} \times 100$

Where,

 σ_g = genotypic standard deviation

 $\overline{\mathbf{x}}$ = population mean

% Phenotypic coefficient of variance =

$$\frac{\sigma_{ph}}{x} \times 100$$

Where,

 σ_{ph} = phenotypic standard deviation

 $\overline{\mathbf{x}}$ = population mean

3.16,3 Estimation of heritability

Heritability in broad sense was estimated following the formula as suggested by Johnson et al. (1955):

Heritability (%) = $\frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$ Where,

> σ_{g}^{2} = genotypic variance σ_{ph}^{2} = phenotypic variance

3.16.4 Estimation of genetic Advance

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960) :

$$GA = \frac{\sigma_g^2}{\sigma_p^2} \times K \sigma_p$$

Where,

GA = Genetic advance

- σ_{g}^{2} = genotypic variance
- σ^{2}_{ph} = phenotypic variance

 σ_{ph} = phenotypic standard deviation

K = Selection differential which is equal to 2.64 at 5%

selection intensity

3.16.5 Estimation of Genetic Advance in percentage of mean

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

Genetic Advance in percentage of mean =

 $\frac{\text{Genetic advance}}{\overline{x}} \times 100$

3.17 Estimation of correlation

Simple correlation was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985):

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

Where,

 $\Sigma =$ Summation

x and y are the two variables

N = Number of observations

3.18 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect of independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say x_1 , x_2 , x_3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as given below:

 $ryx_1 = Pyx_1 + Pyx_2rx_1x_2 + Pyx_3rx_1x_3$

 $ryx_2 = Pyx_1rx_1x_2 + Pyx_2 + Pyx_3rx_2x_3$

 $ryx_3 = Pyx_1rx_1x_3 + Pyx_2rx_2x_3 + Pyx_3$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (unknown). P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows :

 $Pyx_1 =$ The direct effect of x_1 on y

 $Pyx_1rx_1x_2 =$ The indirect effect of x_1 via x_2 on y

 $Pyx_1rx_1x_3 =$ The indirect effect of x_1 via x_3 on y

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

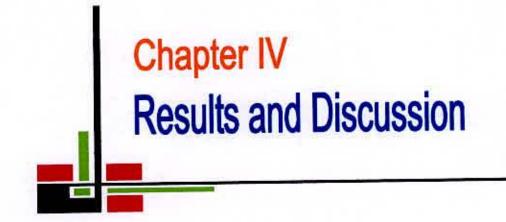
 $P^2RY = 1 - \sum Piy.riy$

Where,

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

Piy = Direct effect of the character on yield

riy = Correlation of the character with yield



Chapter IV

RESULTS AND DISCUSSION

The present experiment was conducted to determine the breeding values in respect of genotypic effects and comparative performances of *Brassica* genotypes which were used in this experiment. Firstly, all of the genotypes were categorized on the basis of the characteristics of the species *Brassica rapa*, *B. juncea and B. napus*.

The inflorescence is the key distinguish different species of *Brassica*. However, this is to some extent uncertain as far as the *Brassica* species in the triangle of U are concerned. Systematization according to the color is also not reliable since there are more than five different colors. The shape of the inflorescence can generally provide indication to distinguish species. *B. oleracea* has the buds at a higher level than the flowers just opened. This character is dominant in the hybrids *B. napus* and *B. juncea* whereas in *B. rapa* the buds are at lower level than the flowers just opened. However, there are exceptions to this rule, and in *B. napus* with the same bud position as in *B. rapa* may be found (Plate 2).

The morphological and other characteristics of *Brassica* differ from the common genotypes between *B. rapa*, *B. juncea*, *B. napus*. *Brassica* is a dicotyledonous herbaceous annual. It grows to a height of 2-3 ft as soon as the plants become 30 to 90 days old. They bear numerous beautiful yellow flowers. The flowers bloom gradually from below upwards and bear pods in the same order. In *B. rapa*, the leaves of the inflorescence grasp the stalk completely but in case of *napus* the grasp the stalk partially. In *B. juncea* the lamina of the upper leaf does not reach the stalk (Plate 1).

The most reliable characters used for distinguishing the *Brassica* spices in the generative phase is the shape of the upper leaves, exception in this character are almost never found. In

the basic species *B. rapa* the lower part of the blade, whereas in *B oleracea* the blade just reaches the stalk (Plate 1). The hybrid *B. juncea* has obtained much of these characters but the petiole is short (Bengtsson *et al.*, 1972).





Leaves of B. napus



Leaves of B. rapa

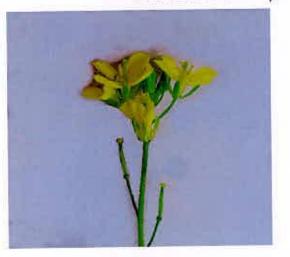


Leaves of B. juncea

Plate 1. Photographs represent the distinguishing characters among *B.* napus, *B. rapa* and *B. juncea* leaves



Inflorescence of B. napus



Inflorescence of B. rapa



Inflorescence of G. juneea

Plate 2. Photographs represent the distinguishing characters among *B.* napus, *B.* rapa and *B.* juncea inflorescence



Siliquae of B. napus

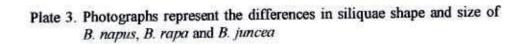


Siliquae of Brassica spp



Siliquae of B. rapa

Siliquae of B. juncea



The flowering habit of *B. napus and B. juncea* is such that the open flowers appear below the flower buds but the situation is reverse in case of *B. rapa*, i.e. the fresh open flowers appear above the flower buds (plate 3). With the help of clear-cut morphological characteristics 41 genotypes were categorized as *B. napus*, *B. rapa* and *B. juncea*. Categorization of *Brassica* species on the basis of morphological characteristics. Among the 41 genotypes, 15 genotypes were categorized as *B. napus*, 13 genotypes were *B. rapa* and rest 13 genotypes were *B. napus*.

B. napus	B. rapa	B. juncea
BD-7126	BD-6955	BD-7104
BD-7128	BD-7102	BD-7107
BD-7788	BD-7113	BD-7117
BD-7789	BD-7114	BD-7127
BD-7790	BD-7115	BD-7131
BD-7815	BD-7116	BD-7132
BD-7830	BD-7118	BD-7133
BD-7831	BD-7125	BD-7134
BD-7832	BD-7129	BD-7135
BD-7833	BD-7837	BD-7136
BD-7834	BD-7958	BD-7137
BD-7835	BD-9061	BD-7138
BD-7836	SAU-YC	BD-8884
BD-9101	-	
BD-9102	and the second sec	-

Table 3. Genotypes of 41 Brassica categorized in B. napus, B. rapa and B. juncea

4.1 GENETIC DIVERGENCE

4.1.1 Genetic Divergence for Brassica

Study of genetic diversity among 41 genotypes of *Brassica* was assessed through Mahalanobis' D² to measure the degree of diversification among the genotypes. Using this technique, grouping of genotypes was done in six clusters where genotypes grouped together were less divergent than the ones placed in different clusters. The clusters separated by greatest statistical distance exhibited maximum divergence. Composition of different clusters with their corresponding genotypes and their source are shown in Table 4. Among the cluster formed the number III and V was found to be the largest comprising with 10 genotypes followed by cluster IV and VI with 8 and 7 genotypes producing second and third largest group respectively. While the cluster I and II was found with 3 genotypes in each.

Cluster group	Number of genotypes	Name of the Genotypes
I	3	BD-7789, BD-7127, BD-8884
Ш	3	BD-7136, BD-7102, BD-7834
ш	10	BD-7114, BD-7958, BD-7830, BD-7129, SAU-YC, BD-7131, BD-7132, BD-7118, BD-7125, BD-7107
IV	8	BD-7104, BD-6955, BD-7113, BD-7133, BD-7135, BD-7115, BD-9061, BD-7836
v	10	BD-7837, BD-7137, BD-7833, BD-9101, BD-9102, BD-7116, BD-7117, BD-7138, BD-7128, BD-7832
VI	7	BD-7134, BD-7815, BD-7831, BD-7126, BD-7788, BD-7835, BD-7790

Table 4. Clustering pattern of 41 Brassica genotypes by Tocher's method

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50%	49.22	35.22	38.22	36.83	40.9	45.98
flowering						
Days to maturity	89.11	77.11	80.37	80.63	82.07	86.98
Plant height	138.99	83.39	88,75	84.52	89.21	88.78
Number of primary branches/plant	7.66	18.76	71.14	6.25	5.3	6.0
Number of scondary	7.66	7.96	4.5	4.07	3.24	3.35
branches/plant						
Number of siliquae/plant	184.23	108.58	132.4	102.32	78.33	47.72
Length of siliquae	3.99	4.1	4.2	3.93	4.21	3.97
Number of seed/siliquae	16.74	18.71	19.9	18.93	16.86	12.15
1000 seed weight / plant	3.17	3.14	2.9	3.14	2.94	2.69
Yield/plant	7.88	4.15	5.19	4.12	3.22	1.51

Table 5. Cluster means for 10 characters of 41 Brassica genotypes

From the cluster mean value (5) it was observed that the mean value of cluster I ranked first for days to 50% flowering, days to maturity, plant height, siliquae per plant, 1000 seed weight per plant and yield per plant. Cluster II ranked first for primary branches per plant and secondary branches per plant. Cluster III ranked for length of siliquae and seed per siliquae.

The result revealed that the average value of inter cluster were always higher than the average of intra cluster distance (Table 6) suggesting wider genetic diversity among the genotypes of the groups. Cluster II had the highest intra-cluster distance of 0.813 followed by the cluster V (0.801). On the contrary cluster IV had the lowest intra cluster distance of 0.378 followed by cluster number VI (0.447).

Clusters	I	II	III	IV	v	VI
I	0.668 (0.817)	3.385 (1.840)	8.225 (2.868)	6.548 (2.559)	2.389 (1.546)	3.749 (1.936)
II		0.813 (0.902)	4.183 (2.45)	9.112 (3.019)	3.507 (1.873)	6.033 (2.456)
ш			0.524 (0.724)	8.477 (2.912)	3.989 (1.997)	8.089 (2.844)
IV				0.378 (0.615)	7.558 (2.749)	3.889 (1.972)
v			_		0,801 (0.895)	7.155 (2.675)
VI						0.447 (0.669)

Table 6. Average intra (bold) and inter-cluster D² and D values of 6 clusters for 41 Brassica genotypes formed by Torcher's method

The cluster distances denoted by the average of inter and intra-cluster is the approximate measure of the cluster divergence. Inter cluster distance was maximum (9.112) between clusters II and IV followed by clusters III and IV (8.477). 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 segregating generations. So, wide crossing should be possible between different group and intra specific crossing should be possible between same groups.

Golakiya and Makne (1991) while assessing genetic diversity of 23 genotypes and grouped them into six clusters. Inter and intra cluster values (D) were reported to be ranged from 9.50 to 22.20 and 5.18 to 8.45 (Katule *et al.*, 1991), Reddy and Reddy (1993) reported on 48 genotypes of which were grouped into 11 clusters. On the other hand Baydar and Bayraktar (1994) reported 35 genotypes which were divided into 6 clusters of different genetic divergences. Badignnavar *et al.* (2002), Joel and Mylsamy (1998), Islam *et al.* (1995) were found the same results. Islam *et al.* (1995) observed that inter cluster distances were larger than that of intra cluster distances. Reddy *et al.* (1987) found maximum inter cluster distance between cluster I and II in his work. All these findings are in support with the present result.

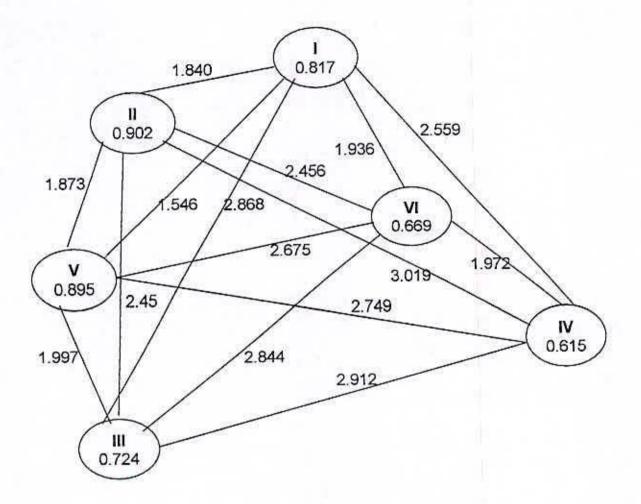


Figure1. Diagram showing intra and inter cluster distances (D) of 41 Brassica genotypes

4.1.2 Genetic Divergence for B. napus

Study of genetic diversity among 15 genotypes of *B. napus* assessed through Mahalanobis' D^2 statistics to measure the degree of diversification among the genotypes. Using this technique, grouping of genotypes was done in six clusters where genotypes grouped together were less divergent than the ones placed in different clusters. The clusters separated by greatest statistical distance exhibited maximum divergence. Composition of different clusters with their corresponding genotypes and their source are shown in Table7. Cluster VI was the largest cluster comprising of 6 genotypes followed by cluster IV with 3 genotypes.

Cluster group	Number of genotypes	Name of the genotypes			
Ι	1	BD-7789			
П	2	BD-7834, BD-7830			
Ш	1	BD-7836			
IV	3	BD-7833, BD-9101, BD-9102			
v	2	BD-7128, BD-7832			
VI	6	BD-7815, BD-7831, BD-7126, BD-7788, BD-7835, BD-7790			

Table 7. Clustering pattern of 15 Brassica napus genotypes by Tocher's method

From the cluster mean value (8) it was observed that the mean value of cluster I ranked first for days to maturity, plant height, primary branches per plant, siliquae per plant, seed per siliquae, 1000 seed weight per plant and yield per plant. Cluster II ranked first for secondary branches per plant. Cluster III ranked for length of siliquae.



Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50%	51	41	38	39.78	43.17	47.58
flowering						
Days to maturity	94	83.75	81.33	81.89	81.67	87.11
Plant height	112.5	82.1	83.36	79.94	85.52	87.86
Number of primary	10.5	10	5.97	4.98	4.74	5.73
branches/plant						
Number of secondary	5.13	6.15	3.5	2.71	2.6	3.21
branches/plant						
Number of	145.25	71.74	66.73	60.86	61.38	37.78
siliquae/plant	835/202	15/10	20220	0.022	1.00	
Length of siliquae	5.46	5.6	6.03	4.95	4.92	4.13
Number of seed/siliquae	21.88	17.89	16.11	17.4	17.08	11.94
1000 seed weight / plant	3.31	3.2	3.27	3.12	3.19	2.66
Yield/plant	8.38	1.97	1.77	1.45	1.54	1.16

Table8. Cluster means for 10 characters of 15 B. napus genotypes

The average inter cluster distance were always higher than the average intra cluster distance (Table 9) in most of the cases suggesting wider genetic diversity among the genotypes of the groups. Cluster II had the highest intra-cluster distance (0.789) followed by cluster VI (0.666). Cluster I and III had no intra cluster distance (0.00) because only one genotype was felt in both the cluster. So, wide crossing should be possible between different groups.

Clusters	I	II	Ш	IV	V	VI
I	0.00	5.258	6.212	7.111	4.485	2.358
	(0.00)	(2.293)	(2.492)	(2.667)	(2.118)	(1.536)
П		0.789	6.478	3.133	8.114	3.587
		(0,888)	(2.545)	(1.770)	(2.849)	(1.894)
Ш			0.00	9.557	5.879	6.000
0.355349			(0.00)	(3.091)	(2.425)	(2.449)
IV				0.645	3.515	9.335
				(0.803)	(1.875)	(3.055)
V					0.333	6.582
					(0.577)	(2.566)
VI						0.666
						(0.816)

Table 9.Average intra (bold) and inter-cluster D² and D values of 6 clusters for 15B. napus genotypes formed by Torcher's method.

Cluster distances denoted by the average inter and intra-cluster distances are the approximate measure of the cluster divergence. Inter cluster distance was maximum between cluster II and IV (9.557), followed by clusters IV and VI (9.335). 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 segregating generations.

Golakiya and Makne (1991) while assessing genetic diversity of 23 genotypes and grouped them into six clusters. Inter and intra cluster values (D) were reported to be ranged from 9.50 to 22.20 and 5.18 to 8.45 (Katule *et al.*, 1991), Reddy and Reddy (1993) reported on 48 genotypes of which were grouped into 11 clusters. On the other hand Baydar and Bayraktar (1994) reported 35 genotypes which were divided into 6 clusters of different genetic divergences.

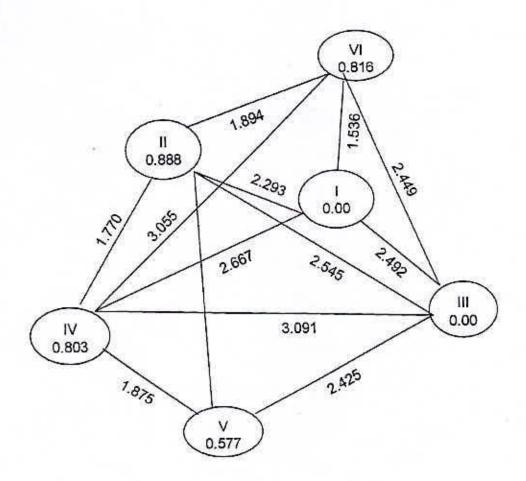


Figure2. Diagram showing intra and inter cluster distances (D) of 15 B. napus genotypes

4.1.3 Genetic Divergence for B. rapa

Study of genetic diversity among 13 genotypes of *B. rapa* assessed through Mahalanobis' D^2 statistics to measure the degree of diversification among the genotypes. Using this technique, grouping of genotypes was done in six clusters where genotypes grouped together were less divergent than the ones placed in different clusters. The clusters separated by greatest statistical distance exhibited maximum divergence. Composition of different clusters with their corresponding genotypes and their source are shown in Table 10. Cluster III and IV was the largest cluster comprising with 4 *B. rapa* genotypes followed by cluster II with 2 genotypes. So, crossing should be possible between different cluster groups.

Number of genotypes	Name of the genotypes				
1	BD-7102				
2	BD-7958, BD-7114				
4	BD-7129, SAU-YC, BD-7118, BD-7125				
4	BD-6955, BD-7113, BD-7115, BD-9061				
1	BD-7837				
1	BD-7116				
	Number of genotypes 1 2 4 4 1 1 1 1 1 1 1 1 1 1 1				

Table 10. Clustering pattern of 13 B. rapa genotypes by Tocher's method

Table11. Cluster	means for	10 characters of	15 B	. rapa	genotypes
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Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50% flowering	27	30.33	41.36	36.8	43.33	42.33
Days to maturity	67.67	76	81.1	80.7	79.67	82.67
Plant height	57.78	71.52	93.01	75.20	103.3	88.77
Number of primary branches/plant	4.36	5.55	7.28	5.29	5.3	5.4
Number of scondary branches/plant	8.12	7.48	0	1.85	0	0
Number of siliquae/plant	144.33	146.65	97.4	76.61	65.3	73.3
Length of siliquae	3,58	4.21	4.37	4.08	35.2	4.51
Number of seed/siliquae	22.8	17.88	24.65	25.85	22	22.5
1000 seed weight / plant	3.09	2.74	3.14	2.68	3.48	2.72
Yield/plant	4.02	4.41	6.14	4.19	5.92	4.9

From the cluster mean value (11) it was observed that the mean value of cluster I ranked first secondary branches per plant. Cluster II ranked first for siliquae per plant. Cluster III ranked for primary branches per plant and yield per plant. length of siliquae and seed per siliquae. Cluster IV ranked for seed per siliquae. Cluster V ranked for days to 50% flowering, plant height, 1000 seed weight per plant. Cluster V ranked for days to maturity.

The average inter distance cluster were always higher than the average intra cluster distance (Table 12) that suggesting wider genetic diversity among the genotypes of the groups. Cluster II had the highest intra-cluster distance (0.901) followed by cluster III (0.666). Cluster I, V and VI had the lowest intra cluster distance (0.00) followed by cluster IV (0.421).

Clusters	I	П	ш	IV	V	VI	
I	0.00 (0.00)	5.336 (2.310)	7.558 (2.749)	8.557 (2.925)	4.892 (2.212)	6.223 (2.495)	
п		0.901 (0.949)	5.328 (2.308)	7.665 (2.769)	5.712 (2.390)	3.598 (1.897)	
ш			0.666 (0.816)	6.325 (2.515)	7.253 (2.693)	3.278 (1.811)	
IV				0.421 (0.649)	5.444 (2.333)	5.478 (2.341)	
v					0.00 (0.00)	6.195 (2.489)	
VI						0.00 (0.00)	

 Table 12.
 Average intra (bold) and inter-cluster D² and D values of 6 clusters for 13

 Brassica rapa genotypes formed by Torcher's method

Cluster distances denoted by the average inter and intra-cluster distances are the approximate measure of the cluster divergence. Inter cluster distance was maximum (8.557) between clusters I and IV, followed by clusters II and IV (7.665). 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 segregating generations.

Golakiya and Makne (1991) while assessing genetic diversity of 23 genotypes and grouped them into six clusters. Inter and intra cluster values (D) were reported to be ranged from 9.50 to 22.20 and 5.18 to 8.45 (Katule *et al.*, 1991), Reddy and Reddy (1993) reported on 48 genotypes of which were grouped into 11 clusters.

On the other hand Baydar and Bayraktar (1994) reported 35 genotypes which were divided into 6 clusters of different genetic divergences. Badignnavar *et al.* (2002), Joel and Mylsamy (1998), Islam *et al.* (1995) were found the same results. Islam *et al.* (1995) observed that inter cluster distances were larger than that of intra cluster distances. Reddy *et al.* (1987) found.

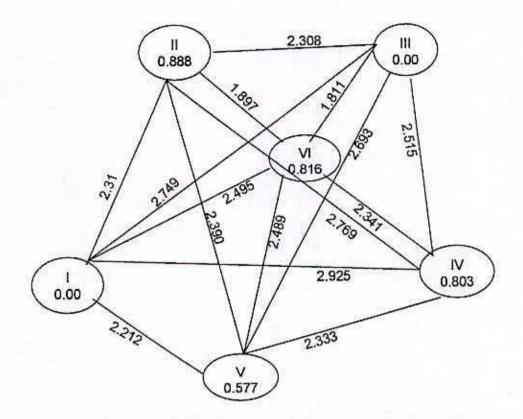


Figure: Diagram showing intra and inter cluster distance(D) of 13 Brassica rapa genotypes

maximum inter cluster distance between cluster I and II. All these findings are in support with the present results.

4.1.4 Genetic Divergence for B. juncea

Study of genetic diversity among 13 genotypes of *B. juncea* evaluated through Mahalanobis' D^2 statistics to measure the degree of diversification among the genotypes. Using this technique, grouping of genotypes was done in six clusters where genotypes grouped together were less divergent than the ones placed in different clusters. The clusters separated by greatest statistical distance exhibited maximum divergence. Composition of different clusters with their corresponding genotypes and their source are shown in Table 13. Cluster III was the largest cluster comprising of 4 genotypes followed by cluster V with 3 genotypes.

Number of genotypes	Name of the genotypes
2	BD-7127, BD-8884
1	BD-7136
4	BD-7131, BD-7132, BD-7107, BD-7104
2	BD-7133, BD-7135
3	BD-7137, BD-7117, BD-7138
1	BD-7134
	2 1 4 2 2

Table 13. Clustering pattern of 13 B. juncea genotypes by Tocher's method

Characters	Cluster	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50%	48.33	37	36.5	39.83	39.22	36.33
flowering						
Days to maturity	86.67	79	80.5	81.33	83.11	86
Plant height	152.23	105.13	101.42	101.48	96.39	94.27
Number of primary	6.23	9.4	7.93	6.52	5.97	7.6
branches/plant	0.00	6.40	7.50	6.20	3.34	4.2
Number of scondary	8.93	6.43	7.59	6.38	5.54	4.4
branches/plant	203.72	77.23	162.65	133.27	113.14	107.4
Number of	205.12	11.25	102.05	133.61	113.14	107.4
siliquae/plant Length of siliquae	3.25	3.58	3.41	3.01	3.13	3.02
NT A COM	14.17	14.77	13.68	13.11	12.58	13.4
Number of	14.17	14.77	15.00	13.11	12.56	15.4
seed/siliquae 1000 seed weight /	3.1	3.15	2.69	2.63	2.48	2.89
plant	ីរ៉ាំំ	0.10	2.05			
Yield/plant	7.62	5,95	5.35	5.84	4.66	3.62

Table14. Cluster means for 10 characters of 13 B. juncea genotypes

From the cluster mean value (14) it was observed that the mean value of cluster I ranked first for days to 50% flowering, days to maturity, plant height, secondary branches per plant, siliquae per plant, seed per siliquae, 1000 seed weight per plant and yield per plant. Cluster II ranked first for primary branches per plant, length of siliquae, 1000 seed weight per plant.



The average inter cluster were mostly higher than the average intra cluster distance (Table 15) that suggesting wider genetic diversity among the genotypes of the groups. Cluster I had the highest intra-cluster distance (0.779) followed by cluster V (0.763); cluster III (0.748) and IV (0.488) in order. While cluster II and VI had the lowest (0.00) or no intra cluster distance.

Inter cluster distance was maximum (8.912) between clusters I and IV, followed by clusters II and V (8.332). 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 segregating generations.

 Table 15.
 Average intra (bold) and inter-cluster D² and D values of 6 clusters for 13 B.

 juncea genotypes formed by Torcher's method

 Clusters
 I

 II
 III

Clusters	I	п	ш	IV	V	VI
I	0.779 (0.883)	4.225 (2.055)	5.212 (2.283)	8.912 (2.985)	5.221 (2.285)	2.958 (1.719)
n		0.00 (0.00)	7.526 (2.743)	3.558 (1.886)	8.332 (2.887)	5.558 (2.358)
ш			0.748 (0.865)	2.338 (1.529)	5.338 (2.310)	7.338 (2.709)
IV				0.488 (0.699)	2.552 (1.597)	3.889 (1.972)
v					0.763 (0.874)	5.111 (2.261)
VI						0.00 (0.00)

Reddy and Reddy (1993) reported on 48 genotypes of which were grouped into 11 clusters. On the other hand Baydar and Bayraktar (1994) reported 35 genotypes which were divided into 6 clusters of different genetic divergences. Badignnavar *et al.* (2002), Joel and Mylsamy (1998), Islam *et al.* (1995) were found the same results.

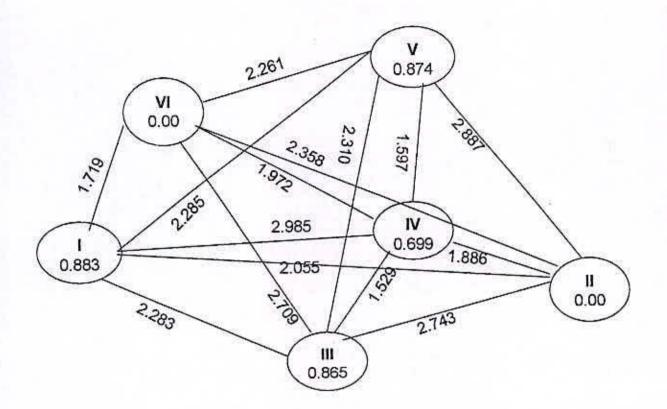


Figure4. Diagram showing intra and inter cluster distances (D) of 13B. juncea genotyp

4.2 ANALYTICAL RESULTS

4.2.1 Analytical results for Brassica

The present experiment was conducted to determine the breeding values in respect of genotypic effects and comparative performances of *Brassica* genotypes which were used in this experiment. Analytical results of 41 genotypes have been estimated under different sections of phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic diversity, correlation co-efficient among different important yield contributing characters and also direct and indirect effect of yield related traits on yield.

The analysis of variance (ANOVA) of the data on different yield components and yield of *Brassica* are given in Table 12. The results have been presented and discussed, and possible interpretations have been given under the following headings:

The mean square values from one way analysis for different characters are presented in Table 12. The mean values for all the recorded characters are presented in Table 13 and genotypic and phenotypic variances also presented in Table 14.

4.2.1.1 Days to 50% Flowering

Analysis of variance of the data for days to 50% flowering showed highly significant difference among the genotypes of *Brassica* used in the present experiment. The mean squares value regarding to days to 50% flowering (Table 12) indicated the presence of variability among the genotypes. Maximum days to 50% flowering (51.33) was recorded in genotype BD-7788 and BD-7789 (Table 13) followed by 8884 and 7126 (49.33) and the minimum days to 50% flowering (27.00) was recorded in the genotypes BD-7102 followed by BD-9061, BD-7958 and BD-7113, respectively (29.00, 29.33, respectively).

The phenotypic variance (41.13) was slightly higher than the genotypic variance (33.24) indicating less environmental influence on this characters (Table 14) which was supported by narrow difference between phenotypic (15.82%) and genotypic (14.22%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their earlier experiment. Low phenotypic co-efficient of variation was also noticed by Prakash *et al.* (2000) which also supported the present experimental result. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.1.2 Days to Maturity

A significant variation was recorded among the genotypes in consideration of days to maturity (Table 16). Maximum identical days to maturity (94.67, 94.00 and 93.67 days) were recorded in *Brassica* genotypes BD-7788, BD-7789, BD-7790. Minimum days to maturity (67.67 days) were obtained from the genotype BD-7102 followed by BD-7958 as 75.33 days (Table 17).

The phenotypic variance for days to maturity (27.59) was found higher than the genotypic variance (22.83). The phenotypic co-efficient of variation (6.377%) was also higher than the genotypic co-efficient of variation (5.801%) indicating the presence of considerable influence of environmental factors for expressing this character (Table 18). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation in their study.



Plate 4. Photograph of showing morphology of different lines of three Brassica spp



Plate 5. Photograph of showing morphology of different lines of B. rapa with B. napus



Plate 6. Photograph of showing morphology of different lines of B. rapa with B. juncea



Plate 7. Photograph of short duration B. rapa line



Plate 8. Photograph of medium duration B. rapa line



Plate 9. Photograph of medium duration B. napus line



Plate 10. Photograph of long duration B. napus line





Plate 11. Photograph of two lines of *B. juncea* showing differences in maturity

Table 16. Analysis of variance of the data of 10 important characters in respect of 41 Brassica genotypes

Source of variation	Degrees	Mean square											
	of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)		
Replication	2	16.415	4.683	75.270	3.360	0.440	583.603	0.257	5.199	0.129	0.567		
Genotypes	40	107.615**	73.247**	1469.95**	13.980**	34.632**	7868.88**	2.312**	105.569**	1.273**	15.299**		
Error	80	7.890	4.766	27.921	0.794	0.668	256.633	0.043	3.411	0.045	1.417		
Coefficient variation	of	6.93	2.65	5.78	13.71	8.61	15.83	5.06	10.66	7,31	9.63		

** Significant at 1% level of probability

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
BD-6955	40.67 f-k	80.33 e-j	95.87f-i	3,70 pq	0.00 o	52.43 k-n	3.83 i	29.02 b	4.52 a	5.01 c-f
BD-7102	27.00 n	67.671	57.93 rs	4.33 n-q	8.20 cd	144.33 d-f	3.58 ij	22.80 cd	3.09 b-j	4.03 d-j
BD-7113	29.33 n	78.33 h-k	59.72 г	5.13 k-q	4.03 j-n	98.63 h-j	4.88 d-f	16.68 h-m	0.34 p	4.00 d-j
BD-7114	31.67 mn	76.67 i-k	65.37 gr	5.10 k-q	9.30 bc	142.63 d-f	4.25 gh	16.43 h-n	2.78 g-l	2.95 f-l
BD-7115	43.00 d-i	84.67 b-e	78.33 l-p	7.30 f-j	0.00 0	59.22 k-n	3.62 ij	35.51 a	3.15 b-h	4.19 d-i
BD-7116	42.33 d-j	82.67 c-g	88.77 i-k	5.40 k-p	0.00 o	73.30 j-1	4.51 f-h	22.50 с-е	2.72 i-m	4.90 c-f
BD-7118	38.67 g-1	84.67 b-e	108.70 cd	9.17 b-e	0.00 o	122.00 f-h	3.44 i-l	20.77 d-g	3.46 bc	5.75 с-е
BD-7125	43.67 c-g	80.33 e-j	92.03 h-k	6.43 g-l	0.00 o	64.03 kl	4.73 ef	34.27 a	3.04 d-j	5.41c-e
BD-7129	40.33 f-1	83.33 c-g	97.00 e-i	8.10 d-g	0,00 0	109.40 g-i	4.27 gh	21.93 c-f	3.11 b-j	6.15 b-d
BD-7837	43.33 c-h	79.67 f-j	103.30 d-g	5.30 k-p	0.00 0	65.30 kl	3.52 i-k	22.00 c-f	3.48 b	5.92 b-e
BD-7958	29.00 n	75.33 k	77,67 m-p	6.00 i-n	5.67 g-i	150.67 c-f	4.18 h	19.33 d-i	2.70 j-m	5.88 b-e
BD-9061	29.00 n	77.00 i-k	50.20 s	4.57 m-q	6.43 fg	135.25 e-g	3.82 i	14.89 k-r	2.73 h-m	2.31 h-l
SAU-YC	44.00 c-g	76.33 jk	73.70 o-q	5.10 k-q	0.00 0	83.33 i-k	5.14 cd	24.49 c	2.95 e-1	7.23 a-c
BD-7104	35.00 lm	80.67 e-i	105.73 с-е	10.30 b	5.87 gh	139.77 ef	3.24 j-m	13.03 n-t	2.76 g-m	4.04 d-j
BD-7107	36.67 k-m	79.33 g-k	76.30 n-p	5.67 j-o	14.67 a	189.23 b	3.64 ij	13.26 m-t	2.21 n	4.76 d-g
BD-7107 BD-7117	39.00 g-l	84.00 b-f	87.73 i-l	4.80 l-q	6.50 e-g	128.43 e-h	3.13 k-n	11.93 q-u	2.27 n	5.61 c-e
BD-7127	47.33 a-d	85,33 b-d	148.47 a	7,93 d-h	10.10 b	232.23 a	2.78 no	15.97 i-p	1.82 o	7.16 a-c
BD-7127 BD-7131	36.67 k-m	84.00 b-f	113.67 c	7.30 f-j	5.00 g-k	170.67 b-d	3.29 j-m	13.87 l-s	2.92 f-1	6.26 b-d
BD-7132	37.67 i-1	78.00 h-k	109.97 cd	8.47 c-f	4.83 h-1	150.93 c-f	3.45 i-1	14.57 k-r	2.85 f-1	6.36 b-d
BD-7132 BD-7133	38.67 g-1	80.00 f-j	100.83 d-h	6.33 h-m	4.83 h-l	132.50 e-g	3.47 i-l	11.95 q-u	3,06 c-j	6.26 b-d
BD-7133 BD-7134	36.33 k-m	86.00 bc	94.27 g-j	7.60 e-I	4.20 i-m	107.40 g-i	3.02 mn	13.40 m-t	2.89 f-l	3.62 e-k
BD-7134 BD-7135	41.00 e-k	82.67 c-g	102.13 d-g	6.70 g-k	7.93 c-e	134.03 e-g	2.55 0	14.27 l-r	2.21 n	5.42 c-e
DD-1155	11.00 0-K	02.01 0 8								

Table 17. Mean performance of 10 important characters in respect of 41 Brassica genotypes

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
BD-7136	37.00 j-1	79.00 g-k	105.13 c-f	9.40 b-d	6.43 fg	151.23 c-f	3.58 ij	14.77 k-r	3.15 b-h	5.95 b-e
BD-7137	39.67 f-1	82.67 c-g	107.43 cd	5.57 j-o	7.40 d-f	101.27 h-j	3.09 l-n	12.61 o-u	2.80 g-l	4.37 d-h
BD-7138	39.00 g-1	82.67 c-g	94.00 g-j	7.53 e-i	5.13 g-j	109.73 g-i	3.17 k-m	13.23 m-t	2.37 mn	4.01 d-j
BD-8884	49.33 ab	88.00 b	156.00 a	4.53 n-q	7.63 d-f	175.20 bc	3.73 i	12.37 p-u	4.38 a	8.09 ab
BD-7126	49.33 ab	82.00 c-h	84.20 j-n	6.50 g-l	2.97 mn	54.70 k-n	3.75 i	12.29 q-u	2.54 l-n	1.281
BD-7128	42.33 d-j	80.00 f-j	82.83 k-o	5.30 k-p	2.63 n	66.87 kl	4.67 ef	19.07 e-i	3.40 b-d	1.96 i-l
BD-7788	51.33 a	94.67 a	89.67 i-k	8.00 d-h	5.83 gh	17.83 o	3.47 i-l	11.33 r-u	2.18 n	0.921
BD-7789	51.33 a	94.00 a	114.17 c	10.50 b	5.20 g-j	154.50 с-е	5.55 b	22.33 с-е	3.37 b-e	8,95 a
BD-7790	48.67 a-c	93.67 a	129.17 b	6.00 i-n	3.00 mn	60.17 k-m	3.30 j-m	9.17 u	2.58 k-n	1.211
BD-7815	46.33 a-f	83.00 c-g	91.44 h-k	3.70 pg	0.00 0	45.901-0	4.28 gh	17.99 g-k	3.14 b-i	1.68 kl
BD-7830	44.67 b-f	86.00 bc	72.70 pq	9.83 bc	5.50 g-j	141.60 d-f	5.60 b	19.55 d-h	3,13 b-i	1.49 kl
BD-7831	47.33 a-d	84.00 b-f	71.00 pq	5.37 k-p	4.00 j-n	29.00 no	5.35 bc	10.25 tu	2.80 g-l	0.921
BD-7832	44.00 c-g	83.33 c-g	88.20 i-1	4.20 o-q	2.57 n	55.83 k-n	5.17 cd	15.11 j-q	2,98 e-k	1.121
BD-7832	41.33 e-k	84.00 b-f	64.97 gr	6.43 g-l	2.77 mn	67.13 kl	5.25 b-d	15.97 i-p	3.03 d-j	1.51 kl
BD-7833	41.67 e-k	84.67 b-e	87.10 i-m	13.67 a	9.10 bc	30.17 m-o	5.16 cd	18.57 f-j	3.18 b-g	2.48 g-l
BD-7834 BD-7835	42.33 d-j	85.33 b-d	61.67 r	4.83 l-q	3.43 1-n	19.07 o	4.60 e-g	10.60 s-u	2.70 j-m	0.941
BD-7836	38,00 h-l	81.33 d-h	83.37 k-o	5.97 i-o	3.50 k-n	66.73 kl	6.03 a	16.11 h-o	3.27 b-f	1.77 j-l
BD-7830 BD-9101	40.00 f-l	82.00 c-h	87.83 i-J	4.97 k-q	5.37 g-j	54.17 k-n	4.63 e-g	19.13 e-i	3.15 b-i	1.67 kl
BD-9101 BD-9102	38.00 h-l	79.67 f-j	87.03 i-m	3.53 g	0.00 0	61.27 kl	4.98 c-e	17.10 h-l	3.18 b-g	1.171
Range	27-51.33	67.7-94.7	50.20-156	3.53-13.67	0.00-14.67	17.8-232.2	2.55-6.03	9.17-35.5	0.34-4.52	0.92-8.95
Mean	40.54	82.37	91,36	6.50	4.39	101.17	4.09	17.33	2.89	4.02

In a column means having similar letter(s) or without letter are identical and those having dissimilar letter(s) differ significantly as per 0.05 level of probability.

Table 18. Estimation of genetic parameters for yield and yield contributing characters of 41 genotypes of Brassica

Characters	Genotypic Variance (σ_{g}^{2})	Phenotypic Variance (σ_p^2)	% Genotypic Coefficient of Variation	% Phenotypic Coefficient of Variation	Heritability (%)	Genetic Advance (GA)	GA in percentage of mean
Days to 50% Flowering	33.242	41.132	14.223	15.819	80.818	13.683	33.751
Days to Maturity	22.827	27.593	5.801	6.377	82.728	11,473	13.928
Plant Height	480,676	508.597	23.997	24.685	94.510	56.269	61.590
Primary Branch (No.)	4.395	5,189	32.246	35,046	84.699	5.094	78.365
Secondary Branch (No)	11.321	11,989	76.651	78.884	94.428	8.633	196.650
Length of Siliquae	0.756	0.799	21.247	21.858	94.621	2.233	54.601
No. of Seed/Siliquae	34.053	37.464	33.676	35.320	90,895	14.688	84.756
No. of Siliquae/Plant	2537.416	2794.049	49.790	52.248	90.815	126.730	125.265
1000 Seed Weight	0.409	0,454	22.145	23.322	90.095	1.603	55,471
Yield/Plant	4.627	6.044	53.507	61.169	76.557	4.970	123.629

4.2.1.3 Plant Height

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for plant height indicating genotypic differences among the genotypes used under the present study (Table 16). From the mean value it was found that the tallest (156.0 cm) genotype was BD-8884 (Table 17) which was identical with BD-7127 (148.5 cm) while the shortest (50.20 cm) genotype was BD-9061 followed by BD-7102 (57.93 cm).

The phenotypic variance (508.60) was considerably higher than the genotypic variance (480.68) and the phenotypic and genotypic co-efficient of variations were 24.69 % and 23.99 %, respectively (Table 18). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001) in their study.

4.2.1.4 Number of Primary Branches/Plant

Analysis of variance of the data for number of primary branches/plant showed highly statistically significant difference among the genotypes of *Brassica* used in the present piece of work. The mean squares value regarding the trait indicated the presence of variability among the genotypes (Table 16). Maximum number of primary branches/plant (13.67) was recorded in genotype BD-7834 (Table 17) followed by BD-7104 (10.30). On the other hand the minimum number of primary branches/plant (3.53) was recorded in the genotypes BD-7815 (3.70).

The phenotypic variance (5.189) was slightly higher than the genotypic variance (4.395) indicating less environmental influence on this characters (Table 18) which was supported by

narrow difference between phenotypic (35.05%) and genotypic (32.25%) co-efficient of variation. Kuriakose and Joseph (1986), Alam *et al.* (1985) and Uddin *et al.* (1995) reported the similar results earlier.

4.2.1.5 Number of Secondary Branches/Plant

In the present experiment analysis of variance of the data for number of secondary branches/plant showed highly significant difference among the genotypes included in the present experiment. The mean squares value regarding to number of secondary branches/plant (Table 16) indicated the presence of variability among the genotypes. Highest number of secondary branches/plant (14.67) was recorded in genotype BD-7107 (Table 17) followed by the genotypes BD-7127 (10.10). On another way the genotypes BD-6955, BD-7115, BD-7116, BD-7118, BD-7125, BD-7129, BD-7837, BD-9102, and accession SAU-YC produced no secondary branches per plant.

The phenotypic variance (11.99) was similar with the genotypic variance (11.32) indicating less environmental influence on this characters (Table 18) which was supported by slight difference between phenotypic (78.88%) and genotypic (76.65%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the said character in their experiment earlier. Low phenotypic co-efficient of variation in this respect was noticed by Prakash *et al.* (2000) which also supported the results of the present experiment. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.1.6 Number of Siliquae/Plant

The mean square value due to genotype from the analysis of variance was found statistically significant differences at 1% level of probability for number of siliquae/plant among the genotypes used as experimental material under the present experiment (Table 16). From the

mean value it was found that the highest number of siliquae/plant (232.2) was recorded for the genotype BD-7127 which was closely followed by the genotypes BD-7107 (189.2) while the minimum number (17.83) was recorded for the genotype BD-7788 which was identical with the genotype BD-7835 (19.07).

The phenotypic variance (2794.05) was considerably higher than the genotypic variance (2537.42) and the phenotypic and genotypic co-efficient of variations were 52.25% and 49.79%, respectively (Table 18). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for number of siliquae / plant were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

4.2.1.7 Length of Siliquae (cm)

A significant variation was recorded among the genotypes in consideration of length of siliquae (Table 16). Maximum length of siliquae (6.03 cm) were recorded in *Brassica* genotypes BD-7836 followed by BD-7830 and BD-7789 (5.60 and 5.55 cm, respectively). Minimum length of siliquae (2.55 cm) was recorded for the genotype BD-7135 (Table 17).

The phenotypic variance (0.799) was similar to the genotypic variance (0.756). The phenotypic co-efficient of variation (21.86%) was also similar to the genotypic co-efficient of variation (21.25%) indicating the presence of considerable influence of environmental factors on this trait (Table 18). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.2.1.8 Number of Seed/Siliquae

The value of the analysis of variance of the data for the number of seed/siliquae showed highly significant difference among the genotypes of *Brassica* used in the present experiment. The mean squares value regarding to the character (Table 16) indicated the presence of variability among the genotypes. Maximum number of seed/siliquae (35.51) was recorded in genotype BD-7115 (Table 17) which was identical by the genotypes BD-7125 (34.27) and the minimum (9.17) was recorded in the genotypes BD-7790 followed by BD-7831 (10.25).

The phenotypic variance (37.46) was slightly higher than the genotypic variance (34.05) indicating less environmental influence on this characters (Table 18) which was supported by narrow difference between phenotypic (35.32%) and genotypic (33.68%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their earlier investigation. Low phenotypic co-efficient of variation regarding this in earlier noticed by Prakash *et al.* (2000) which also supported the results of the present experiment. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.1.9 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for 1000 seed weight indicating genotypic differences among the genotypes used under the present experiment (Table 16). From the mean value it was found that the highest 1000 seed weight (4.52 g) was recorded in the genotype BD-6955 which was identical with BD-8884 (4.38 g) while the lowest 1000 seed weight (0.344 g) was in the BD-7113 followed by the genotype BD-7127 (1.82 g).

The phenotypic variance (0.454) was considerably higher than the genotypic variance (0.409) and the phenotypic and genotypic co-efficient of variations were 23.32% and 22.15%, respectively (Table 18) for 1000 seed weight of *Brassica* genotypes. The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for 1000 seed weight were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

4.2.1.10 Yield/Plant (g)

Analysis of variance of the data for yield/plant showed statistically highly significant difference among the genotypes of *Brassica* used in the present piece of work. The mean square values for to the trait indicated the presence of variability among the genotypes (Table 16). The highest yield/plant (8.95 g) was recorded in genotype BD-7789 (Table 17) followed by the genotypes BD-8884 (8.09 g). On the other hand the lowest yield/plant (0.921 g) was recorded in the genotypes BD-7831.

The phenotypic variance (6.044) was higher than the genotypic variance (4.627) indicating less environmental influence on yield/plant for *Brassica* (Table 18) which was supported by narrow difference between phenotypic (61.17%) and genotypic (53.51%) co-efficient of variation. Almost similar results were observed by Uddin *et al.* (1995), Islam and Rasul (1998), Nazzar *et al.* (2000) and Azad and Hamid (2000).

4.2.2 Analytical results for B. napus

This experiment was conducted to determine the breeding values in respect of genotypic effects and comparative performances of *B. napus* entries that included in this trial. Analytical results of 15 genotypes have been estimated under different sections of phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic

diversity, correlation co-efficient among different important yield contributing characters and also direct and indirect effect of yield related traits on yield.

The analysis of variance (ANOVA) of the data on different yield components and yield of *B. napus* are given in Table 19. The results have been presented and discussed, and possible interpretations have been given under the following headings:

The mean square values from one way analysis for different characters are presented in Table 18. The mean values for all the recorded characters are presented in Table 20 and genotypic and phenotypic variances also presented in Table 21.

4.2.2.1 Days to 50% Flowering

Analysis of variance of the data for days to 50% flowering showed highly significant in difference among the *B. napus* genotypes used in the present experiment. The mean squares value regarding to days to 50% flowering (Table 19) indicated the presence of variability among the genotypes. Maximum days to 50% flowering (51.33) was recorded in genotype BD-7788 and BD-7789 (Table 20) followed by BD-7126 (49.33) and the minimum days to 50% flowering (38.00) was recorded in the genotypes BD-7836 and BD-9102.

The phenotypic variance (25.56) was slightly higher than the genotypic variance (16.99) indicating less environmental influence on this characters (Table 21) which was supported by slender difference between phenotypic (11.38%) and genotypic (9.28%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their earlier experiment. Low phenotypic co-efficient of variation was also noticed by Prakash *et al.* (2000) which also supported the results of the present experiment.

4.2.2.2 Days to Maturity

A significant variation was recorded among the genotypes in consideration of days to maturity (Table 19. Maximum identical days to maturity (94.67, 94.00 and 93.67 days) were recorded in *B. napus* genotypes BD-7788, BD-7789, BD-7790, respectively followed by BD-7830 (86.00 days). Minimum days to maturity (79.67 days) were obtained from the genotype BD-9102 (Table 20).

The phenotypic variance (27.01) was higher than the genotypic variance (23.35). The phenotypic co-efficient of variation (6.101%) was also higher than the genotypic co-efficient of variation (5.67%) indicating the presence of considerable influence of environmental factors on this character (Table 21). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.2.2.3 Plant Height

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for plant height indicating genotypic differences among the *B. napus* entries used under the present trial (Table 19). Starting the mean value it was found that the tallest (129.17 cm) genotype was BD-7790 (Table 20) which was identical with BD-7789 (114.17 cm) while the shortest (61.67 cm) genotype was BD-7835.

The phenotypic variance (319.78) was considerably higher than the genotypic variance (286.35) and the phenotypic and genotypic co-efficient of variations were 20.71 % and 19.60 %, respectively (Table 21). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed Azad and Hamid (2000) and Venkatramana *et al.* (2001).

Table 19. Analysis of variance of the data of 10	mportant characters in respect	of 15 genotypes of B. napus
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Source of	Degrees					Mean so	juare				
variation	of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
Replication	2	0.822	1.089	30.489	5.411	2.070	325.547	0.461	17.867	0.159	1.379
Genotypes	14	59.556**	73.708**	892.488**	23.771**	15.830**	4558.983**	1.930**	48.633**	0.358**	11.850**
Error	28	8.560	3.660	33.426	1.548	0.650	104.822	0.056	2.342	0.060	0.468
Coefficient variation	of	6.58	2.25	6.69	18.89	21.65	16.60	4.93	9.79	8.26	35.28

** Significant at 1% level of probability



Table 20. Mean performance of 10 important characters in respect of 15 genotypes of B. napus

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
DD 7126	49.33 ab	82.00 cdef	84.20 c	6.50 de	2.97 d	54.70 bc	3.75 f	12.29 e	2.54 de	1.28 bc
BD-7126	49.33 ad 42.33 cdef	80.00 ef	82.83 c	5.30 efg	2.63 d	66.87 b	4.67 de	19.07 b	3.40 a	1.96 bc
BD-7128		94.67 a	89.67 b	8.00 cd	5.83 b	17.83 e	3.47 fg	11.33 ef	2.18 e	0.92 c
BD-7788	51.33 a		114.17 a	10.50 b	5.20 bc	154.50 a	5.55 b	22.33 a	3.37 a	8.95 a
BD-7789	51.33 a	94.00 a	Concernance and the second	6.00 def	3.00 d	60.17 bc	3.30 g	9.17 f	2.58 de	1.21 bc
BD-7790	48.67 ab	93.67 a	129.17 a	Concession of the second second	0.00 e	45.90 cd	4.28 e	17.99 bc	3.14 abc	1.68 bc
BD-7815	46.33 abcd	83.00 bcdef	91.44 d	3.70 fg	the second se	141.60 a	5.60 b	19.55 b	3.13 abc	1.49 bc
BD-7830	44.67 bcde	86.00 b	72.70 de	9.83 bc	5.50 b	29.00 de	5.35 bc	10.25 ef	2.80 bcd	0.92 c
BD-7831	47.33 abc	84.00 bcd	71.00 c	5.37 efg	4.00 cd		Construction and a	15.11 d	2.98 abcd	1.12 c
BD-7832	44.00 bcde	83.33 bcde	88.20 de	4.20 efg	2.57 d	55.83 bc	5.17 bc		3.03 abc	1.51 bc
BD-7833	41.33 def	84.00 bcd	64.97 c	6.43 de	2.77 d	67.13 b	5.25 bc	15.97 cd	3.18 ab	2.48 b
BD-7834	41.67 def	84.67 bcd	87.10 e	13.67 a	9.10 a	30,17 de	5.16 bc	18.57 bc		1 - C. C. C. C. C. C. C.
BD-7835	42.33 cdef	85.33 bc	61.67 e	4.83 efg	3.43 d	19.07 e	4.60 de	10.60 ef	2.70 cd	0.94 c
	38.00 f	81.33 def	83.37 c	5.97 def	3.50 d	66.73 b	6.03 a	16.11 cd	3.27 ab	1.77 bc
BD-7836			87.83 c	4.97 efg	5.37 bc	54.17 bc	4,63 de	19.13 b	3.15 abc	1.67 bc
BD-9101	40.00 ef	82.00 cdef		3.53 g	0.00 e	61.27 bc	4.98 cd	17.10 bcd	3.18 ab	1.17 bc
BD-9102	38.00 f	79.67 f	87.03 c	-	0.00-9.10	17.83-154.50	3.30-6.03	9.17-22.33	2.18-3.39	0.917-8.95
Range	38.00-51.33	79.67-94.67	61.67-129	3.53-13.67	The Corporation of the second	61.66	4.79	15.64	2.98	1.94
Mean	44.44	85.18	86.36	6.59	3.72	01.00	14.02			

In a column means having similar letter(s) or without letter is identical and those having dissimilar letter(s) differ significantly as per 0.05 level of probability.

Table 21. Estimation of genetic parameters for yield and yield contributing characters of 15 genotypes of B. Napus

Characters	Genotypic Variance (σ_g^2)	Phenotypic Variance (σ_p^2)	% Genotypic Coefficient of Variation	% Phenotypic Coefficient of Variation	Heritability (%)	Genetic Advance (GA)	GA in percentage of mean
Days to 50% Flowering	16.999	25.559	9.277	11.376	66.508	8.877	19.974
Days to Maturity	23.349	27.009	5.673	6,101	86.449	11.861	13.925
Plant Height	286.354	319.780	19.596	20,707	89.547	42.274	48.953
Primary Branch (No.)	7.408	8.956	41.324	45.438	82.715	6.536	99.222
Secondary Branch (No)	5.060	5.710	60.392	64.178	88.616	5.591	150.144
No. of Siliquae/Plant	1484.720	1589.542	62.489	64.657	93.406	98.313	159.439
Length of Siliquae	0.625	0.681	16.524	17.234	91.773	1.999	41.755
No. of Seed/Siliquae	15.430	17.772	25.118	26.960	86.822	9.664	61.795
1000 Seed Weight	0.099	0.159	10.588	13.412	62.343	0,657	22.074
Yield/Plant	3.794	4.262	100.516	106.553	89.019	4.853	250.411

4.2.2.4 Number of Primary Branches/Plant

Analysis of variance of the data for number of primary branches/plant showed highly statistically significant difference among the genotypes of *B. napus* used in the present piece of experiment. The mean squares value regarding to the individuality indicated the incidence of variability among the genotypes (Table 19). Maximum number of primary branches/plant (13.67) was recorded in genotype BD-7834 (Table 20). On the other hand the minimum number of primary branches/plant (3.53) was recorded in the genotypes BD-9102 followed by BD-7815 (3.70).

The phenotypic variance (8.96) was slightly higher than the genotypic variance (7.41) indicating less environmental influence on this characters (Table 21 which was supported by narrow difference between phenotypic (45.44%) and genotypic (41.32%) co-efficient of variation. Alam *et al.* (1985) and Uddin *et al.* (1995) reported the same results earlier.

4.2.2.5 Number of Secondary Branches/Plant

In the present experiment analysis of variance of the data for number of secondary branches/plant showed highly significant difference among the *B. napus* genotypes used in the present experiment. The mean squares value regarding to number of secondary branches/plant (Table 19 indicated the presence of variability among the genotypes. Highest number of secondary branches/plant (9.10) was recorded in genotype BD-7834 (Table 20). On another way the genotypes BD-9102 and BD-7815 had no secondary branches/plant.

The phenotypic variance (5.71) was similar with the genotypic variance (5.06) indicating less environmental influence on this characters (Table 21) which was supported by slight difference between phenotypic (64.18%) and genotypic (60.39%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their experiment earlier. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.2.6 Number of Siliquae/Plant

The mean square value due to genotype from the analysis of variance was found statistically significant differences at 1% level of probability for number of siliquae/plant among the genotypes used under the present experiment (Table 19). From the mean value it was found that the highest number of siliquae/plant (154.50) was recorded for the genotype BD-7789 which was statistically identical with the genotypes BD-7830 (141.60) while the minimum number (17.83) was recorded for the genotype BD-7788 which was identical with the genotype BD-7788 which was identical with the genotype BD-7835 (19.07).

The phenotypic variance (1589.54) was considerably higher than the genotypic variance (1484.72) and the phenotypic and genotypic co-efficient of variations were 64.66% and 62.49%, respectively (Table 21). The result indicated the existence of inherent variability among the population with possibility of high potential for selection.

4.2.2.7 Length of Siliquae (cm)

A significant variation was recorded among the genotypes in consideration of length of siliquae (Table 19). Maximum length of siliquae (6.03 cm) were recorded in *B. napus* genotypes BD-7836 followed by BD-7830 and BD-7789 (5.60 and 5.55 cm, respectively). Minimum length of siliquae (3.30 cm) was recorded for the genotype BD-7790 (Table 20).

The phenotypic variance (0.681) was similar than the genotypic variance (0.625). The phenotypic co-efficient of variation (17.23%) was also similar than the genotypic co-efficient of variation (16.52%) indicating the presence of considerable influence of environmental factors on this character (Table 21). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.2.2.8 Number of Seed/Siliquae

The value of the analysis of variance of the data for number of seed/siliquae showed highly significant difference among the genotypes of *B. napus* used in the present experiment. The mean squares value regarding to the character indicated the presence of variability among the genotypes. Maximum number of seed/siliquae (22.33) was recorded in genotype BD-7789 (Table 20) and the minimum (9.17) was recorded in the genotypes BD-7790 followed by BD-7831 (10.25).

The phenotypic variance (17.77) was slightly higher than the genotypic variance (15.43) indicating less environmental influence on this characters (Table 21) which was supported by narrow difference between phenotypic (26.96%) and genotypic (25.11%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their earlier experiment.

4.2.2.9 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for 1000 seed weight indicating genotypic differences among the entries used under the present experiment (Table 19). From the mean value it was found that the highest 1000 seed weight (3.40 g) was recorded in the genotype BD-7128 which was identical with BD-7789 (3.37 g) while the lowest 1000 seed weight (2.18 g) was in the BD-7788.

The phenotypic variance (0.159) was considerably higher than the genotypic variance (0.099) and the phenotypic and genotypic co-efficient of variations were 13.41% and 10.59%, respectively (Table 21) for 1000 seed weight. The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations

for 1000 seed weight were also observed by Azad and Hamid (2000) and Venkatramana et al. (2001).

4.2.2.10 Yield/Plant (g)

Analysis of variance of the data for yield/plant showed highly statistically significant difference among the genotypes used in the present piece of trial. The mean squares value regarding to the traits indicated the presence of variability among the genotypes (Table 19). The highest yield/plant (8.95 g) was recorded in genotype BD-7789 (Table 21). On the other hand the lowest yield/plant (0.92 g) was recorded in the genotypes BD-7788 and BD-7831, respectively which was identical with the genotypes BD-7835 (0.943).

The phenotypic variance (4.26) was higher than the genotypic variance (3.79) indicating less environmental influence on yield/plant for *B. napus* (Table 21) which was supported by narrow difference between phenotypic (106.55%) and genotypic (100.52%) co-efficient of variation. Almost similar results were observed by Nazzar *et al.* (2000) and Azad and Hamid (2000).

4.2.3 Analytical results for B. rapa

Analytical results of 13 genotypes of *B. rapa* have been estimated and presented under different sections for phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic diversity, correlation co-efficient among different important yield contributing characters and also direct and indirect effect of different traits related to yield.

The analysis of variance (ANOVA) of the data on different yield components and yield of *B. rapa* are given in Table 22. The results have been presented and discussed, and possible interpretations have been given under the following headings: The mean square values from one way analysis for different characters are presented in Table 22. The mean values for all the recorded characters are presented in Table 23 and genotypic and phenotypic variances also presented in Table 24.

4.2.3.1 Days to 50% Flowering

Analysis of variance of the data for days to 50% flowering showed highly significant difference among the genotypes of *B rapa* used in the present experiment. The mean squares value regarding to days to 50% flowering (Table 22) indicated the presence of variability among the genotypes. Maximum days to 50% flowering (44.00) was recorded in genotype SAU-YC (Table 23) which was statistically identical with BD-7125 (43.67), BD-7837 (43.33) and BD-7116 (43.00) and the minimum days to 50% flowering (27.00) was recorded for the genotype BD-7115 followed by BD-9061, BD-7958 and BD-7113 (29.00, 29.33, respectively).

The phenotypic variance (48.35) was slightly higher than the genotypic variance (43.385) indicating less environmental influence on this characters (Table 24) which was supported by narrow difference between phenotypic (18.753%) and genotypic (17.766%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their earlier experiment. Low phenotypic co-efficient of variation was also noticed by Prakash *et al.* (2000) which also supported the results of the present experiment. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.3.2 Days to Maturity

A significant variation was recorded among the genotypes in consideration of days to maturity (Table 22). Maximum identical days to maturity (84.67) were recorded in *B. rapa* genotypes BD-7115, BD-7118, respectively followed by BD-7129 (83.33 days). Minimum

days to maturity (67.67 days) was obtained from the genotype BD-7102 followed by (75.33) in BD-7958 (Table 23).

The phenotypic variance (24.406) was higher than the genotypic variance (20.214). The phenotypic co-efficient of variation (6.253%) was also higher than the genotypic co-efficient of variation (5.691%) indicating the presence of considerable influence of environmental factors on this character (Table 24). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.2.3.3 Plant Height

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for plant height indicating genotypic differences among the *B. rapa* genotypes used under the present experiment (Table 22). From the mean value it was found that the tallest (108.70 cm) genotype was BD-7118 (Table 23) which was identical with BD-7837 (103.30 cm) while the shortest (50.20 cm) genotype was BD-9061.

The phenotypic variance (362.593) was considerably higher than the genotypic variance (340.138) and the phenotypic and genotypic co-efficient of variations were 23.607 % and 22.865 %, respectively (Table 24). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

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Source of	Degrees					Mean se	quare			10010	D Buch
variation	of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
Replication	2	6.077	3.692	44.20	0.696	0.002	73.398	0.025	4.887	0.003	2,230
Genotypes	12	135.120**	64.833**	1042.87**	7.307**	39.120**	3895.288**	0.931**	122.852**	2.524**	5.656**
Error	24	4.966	4.192	22.455	0.178	0.242	202.439	0.049	5.388	0.016	1.450
Coefficient variation	of	6.01	2.59	5.87	7.26	19.00	14.22	5.33	10.04	4.25	24.57

Table 22. Analysis of variance of the data of 10 important characters in respect of 13 genotypes of Brassica rapa

** Significant at 1% level of probability

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
BD-6955	40.67 ab	80.33 bc	95.87 bc	3.70 i	0.00 e	52.43 f	3.83 de	29.02 b	4.52 a	5.01 abc
BD-7102	27.00 d	67.67 f	57.93 ef	4.33 hi	8.20 b	144.33 ab	3.58 e	22.80 cd	3.09 c	4.03 bcd
BD-7113	29.33 cd	78.33 cde	59.72 e	5.13 fg	4.03 d	98.63 cd	4.88 ab	16.68 efg	0.34 f	4.00 bcd
BD-7114	31.67 c	76.67 cde	65,37 e	5.10 fgh	9.30 a	142.63 ab	4.25 c	16.43 fg	2.78 de	2.95 cd
BD-7115	43.00 a	84.67 a	78.33 d	7.30 c	0.00 e	59.22 ef	3.62 e	35.51 a	3.15 c	4.19 bcd
BD-7116	42.33 ab	82.67 ab	88.77 c	5.40 ef	0.00 e	73.30 ef	4.51 bc	22.50 cd	2.72 de	4.90 bc
BD-7118	38.671 b	84.67 a	108.70 a	9.17 a	0.00 e	122.00 bc	3.44 e	20.77 cde	3.46 b	5.75 ab
BD-7125	43.67 a	80.33 bc	92.03 c	6.43 d	0.00 e	64.03 ef	4.73 b	34.27 a	3.04 c	5.41 ab
BD-7129	40.33 ab	83.33 ab	97.00 bc	8.10 b	0.00 e	109.40 c	4.27 c	21.93 cd	3.11 c	6.15 ab
BD-7837	43.33 a	79.67 bcd	103.30 ab	5.30 efg	0.00 e	65.30 ef	3,52 e	22.00 cd	3.48 b	5.92 ab
BD-7958	29.00 cd	75.33 e	77.67 d	6.00 de	5.67 c	150.67 a	4.18 cd	19.33 def	2.70 e	5.88 ab
BD-9061	29.00 cd	77.00 cde	50.20 f	4.57 gh	6.43 c	135.25 ab	3.82 de	14.89 g	2.73 de	2.31 d
SAU-YC	44.00 a	76.33 de	73.70 d	5.10 fgh	0.00 e	83.33 de	5.14 a	24.49 c	2.95 cd	7.23 a
Range	27.00-43.67	67.67-84.67	50.2-108.7	3.70-9.17	0.00-9.30	52.43-150.67	3.44-5.14	14.89-35.51	0.34-4.52	2.31-7.23
Mean	37.08	79.00	80.66	5.82	2.59	100.04	4.14	23,12	2.93	4.90

Table 23. Mean performance of 10 important characters in respect of 13 genotypes of Brassica rapa

In a column means having similar letter(s) or without letter are identical and those having dissimilar letter(s) differ significantly as per 0.05 level of probability



Table 24. Estimation of genetic parameters for yield and yield contributing characters of 13 genotypes of Brassica rapa

Characters	Genotypic Variance	Phenotypic Variance (σ^2_p)	% Genotypic Coefficient of Variation	% Phenotypic Coefficient of Variation	Heritability (%)	Genetic Advance (GA)	GA in percentage of mean
	(σ ² g)		17.766	18,753	89.729	16.471	44.423
Days to 50% Flowering	43.385	48.351	17.700		00.004	10.802	13.673
Days to Maturity	20.214	24,406	5.691	6,253	82.824	10.802	104-049245-02465
	240 129	362.593	22.865	23.607	93.807	47,158	58.464
Plant Height	340.138			27,466	93.031	3.925	67.459
Primary Branch (No.)	2.376	2.554	26.487	27.400		0.115	363.947
Secondary Branch (No)	12.959	13.201	139,157	140.433	98.167	9.415	305.947
Secondary Branch (140)		1422 280	35.071	37.844	85.877	85.834	85.799
No. of Siliquae/Plant	1230.950	1433.389			95 714	1.326	32.061
Length of Siliquae	0.294	0.343	13.104	14,168	85.714	1.520	
	20.155	44,543	27.058	28.862	87.904	15.488	66.978
No. of Seed/Siliquae	39.155	41.212		21 502	98.122	2.391	81.603
1000 Seed Weight	0.836	0.852	31.195	31,502	70.122		44.716
Yield/Plant	1.402	2.852	24.153	34.455	49.158	2.192	44.716

4.2.3.4 Number of Primary Branches/Plant

Analysis of variance of the data for number of primary branches/plant showed highly statistically significant difference among the genotypes of *B. rapa* used in the present piece of research work. The mean squares value regarding to the traits indicated the presence of variability among the genotypes (Table 22). Maximum number of primary branches/plant (9.17) was recorded in genotype BD- 7118 (Table 19) followed by BD-7129 (8.10). On the other hand the minimum number of primary branches/plant (3.70) was recorded in the genotypes BD-6955 followed by BD-7102 (4.33).

The phenotypic variance (2.554) was slightly higher than the genotypic variance (2.376) indicating less environmental influence on this characters (Table 24) which was supported by narrow difference between phenotypic (27.466%) and genotypic (26.487%) co-efficient of variation. Kuriakose and Joseph (1986), Alam *et al.* (1985) and Uddin *et al.* (1995) reported the same results earlier.

4.2.3.5 Number of Secondary Branches/Plant

In the present experiment analysis of variance of the data for number of secondary branches/plant showed highly significant difference among the *rapa* genotypes used in the present experiment. The mean squares value regarding to number of secondary branches/plant (Table 22) indicated the presence of variability among the genotypes. Highest number of secondary branches/plant (9.30) was recorded in genotype BD-7114 (Table 23) followed by the genotypes BD-7102 (8.20). On another way the genotypes BD-6955, BD-7115, BD-7116, BD-7118, BD-7125, BD-7129, BD-7837, SAU-YC had no secondary branches/plant.

The phenotypic variance (13.201) was similar with the genotypic variance (12.959) indicating less environmental influence on this characters (Table 24) which was supported by

slight difference between phenotypic (140.433%) and genotypic (139.157%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their experiment earlier. Low phenotypic co-efficient of variation in this respect was noticed by Prakash *et al.* (2000) which also supported the results of the present experiment. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.3.6 Number of Siliquae/Plant

The mean square value due to genotype from the analysis of variance was found statistically significant differences at 1% level of probability for number of siliquae/plant among the *rapa* genotypes used as experimental material under the present experiment (Table 22). From the mean value it was found that the highest number of siliquae/plant (150.67) was recorded for the genotype BD-7958 while the minimum number (52.43) was recorded for the genotype BD-6955.

The phenotypic variance (1433.389) was considerably higher than the genotypic variance (1230.950) and the phenotypic and genotypic co-efficient of variations were 37.844% and 35.071%, respectively (Table 24). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations in number of siliquae/plant were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

4.2.3.7 Length of Siliquae (cm)

A significant variation was recorded among the *B. rapa* genotypes in consideration of length of siliquae (Table 22). Maximum length of siliquae (5.14 cm) were recorded in *B. rapa*

genotypes SAU-YC followed by BD-7113 (4.88 cm). Minimum length of siliquae (3.44 cm) was recorded for the genotype BD-7118 (Table 23).

The phenotypic variance (0.343) was similar than the genotypic variance (0.294). The phenotypic co-efficient of variation (14.168%) was also similar than the genotypic co-efficient of variation (13.104%) indicating the presence of considerable influence of environmental factors on this trait (Table 24). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.2.3.8 Number of Seed/Siliquae

The value of the analysis of variance of the data for number of seed/siliquae showed highly significant difference among the genotypes of *B. rapa* used in the present experiment. The mean squares value regarding the character (Table 22) indicated the presence of variability among the genotypes. Maximum number of seed/siliquae (35.51) was recorded in genotype BD-7115 (Table 23) which was identical by the genotypes BD-7125 (34.27) and the minimum (14.89) was recorded in the genotypes BD-9061.

The phenotypic variance (44.543) was slightly higher than the genotypic variance (39.155) indicating less environmental influence on this characters (Table 24) which was supported by narrow difference between phenotypic (28.862%) and genotypic (27.058%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters in their earlier investigation. Low phenotypic co-efficient of variation regarding this in earlier noticed by Prakash *et al.* (2000) which also supported the results of the present experiment. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.3.9 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for 1000 seed weight indicating genotypic differences among the genotypes used under the present experiment (Table 22). From the mean value it was found that the highest 1000 seed weight (4.52 g) was recorded in the genotype BD-6955 while the lowest 1000 seed weight (0.34 g) was in the BD-7113.

The phenotypic variance (0.852) was slightly higher than the genotypic variance (0.836) and the phenotypic and genotypic co-efficient of variations were 31.502% and 31.195%, respectively (Table 24) for 1000 seed weight of *B. rapa* genotypes. The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic coefficient of variations for 1000 seed weight were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

4.2.3.10 Yield/Plant (g)

Analysis of variance of the data for yield/plant showed highly statistically significant difference among the genotypes of *B. rapa* used in the present piece of research work. The mean squares value regarding to the traits indicated the presence of variability among the genotypes (Table 22). The highest yield/plant (7.23 g) was recorded in genotype SAU-YC77 (Table 23). On the other hand the lowest yield/plant (2.31 g) was recorded in the genotypes BD-9061 which was identical with the genotypes BD-7114 (2.95 g).

The phenotypic variance (2.852) was higher than the genotypic variance (1.402) indicating less environmental influence on yield/plant for *B. rapa* (Table 24) which was supported by

narrow difference between phenotypic (34.455%) and genotypic (24.153%) co-efficient of variation. Almost similar results were observed by Uddin *et al.* (1995), Islam and Rasul (1998), Nazzar *et al.* (2000) and Azad and Hamid (2000).

4.2.4 Analytical results for B. juncea

Results of 13 genotypes of *B. juncea* have been predictable under different subdivision of phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic diversity, correlation co-efficient among different important yield contributing characters and also direct and indirect effect of yield associated character on yield.

The analysis of variance (ANOVA) of the data on different yield components and yield of *B. juncea* are presented in Table 25. The results have been discussed, and possible interpretations have been given under the following headings:

The mean square values from one way analysis for different characters are presented in Table 25. The mean values for all the recorded characters are presented in Table 26 and genotypic and phenotypic variances also presented in Table 27.

4.2.4.1 Days to 50% Flowering

Analysis of variance of the data for days to 50% flowering showed highly significant difference among the genotypes of *B. juncea* used in the present experiment. The mean squares value regarding to days to 50% flowering (Table 25) indicated the presence of variability among the genotypes. Maximum days to 50% flowering (49.33) was recorded in genotype BD-8884 which was statistically identical (47.33) with the *juncea* genotypes BD-7127 (Table 26) and the minimum days to 50% flowering (35.00) was recorded in the genotypes BD-7104.

The phenotypic inconsistency (24.58) was higher than the genotypic variance (14.89) indicating less environmental influence on this characters (Table 27) which was supported by narrow difference between phenotypic (12.56%) and genotypic (9.77%) co-efficient of variation. Hossain and Alam (1989) and Deshmukh *et al.* (1986) reported similar results for the characters. Low phenotypic co-efficient of variation was also noticed by Prakash *et al.* (2000) which also supported the results of the present experiment.

4.2.4.2 Days to Maturity

Statistically significant variation was recorded among the genotypes of *juncea* in consideration of days to maturity (Table 25). Maximum days to maturity (88.00 days) were recorded in *B. juncea* genotypes BD-884. Minimum days to maturity (78.00 days) were obtained from the genotype BD-7132 followed by BD-7107 (Table 26).

The phenotypic variance (12.79) was higher than the genotypic variance (7.01). The phenotypic co-efficient of variation (4.33%) was also higher than the genotypic co-efficient of variation (3.21%) indicating the presence of considerable influence of environmental factors on this character (Table 27). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

Source of	Degrees	and the second second				Mean squ	iare			1.251	
variation	of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
Replication	2	29.410	19.718	13.434	0.339	0.294	636.679	0.001	0.037	0.103	0.525
Genotypes	12	54.368**	26.812**	1469.20**	8.900**	24.093**	4062.660**	0.348**	4.227*	1.201**	5.321*
Error	24	9.688	5.774	30.547	0.405	1.066	493.044	0.010	1.782	0.051	2.429
Coefficient o		7.88	2.91	5,13	8.98	14.83	15.01	3.12	9,90	8.25	28.18

Table 25. Analysis of variance of the data of 10 important characters in respect of 13 genotypes of B. Juncea

Significant at 5% level of probability
Significant at 1% level of probability

Table 26. Mean performance of 10 important characters in respect of 13 genotypes of B. juncea

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of Siliquae/ plant	Length of siliquae (cm)	Number of seed/ siliquae	1000 seed weight (g)	Yield/ plant (g)
BD-7104	35.00 b	80.67 cde	105.73 bc	10,30 a	5.87 def	139.77 cdef	3.24 ef	13.03 bc	2.76 b	4.04 c
BD-7107	36.67 b	79.33 de	76.30 f	5.67 fg	14.67 a	189.23 b	3.64 ab	13.26 bc	2.21 cd	4.76 bc
BD-7117	39.00 b	84.00 abc	87,73 e	4.80 g	6.50 cde	128.43 def	3.13 efg	11.93 c	2.27 c	5.61 abc
BD-7127	47.33 a	85.33 ab	148.47 a	7.93 c	10.10 b	232.23 a	2.78 h	15.97 a	1.82 d	7.16 ab
BD-7131	36.67 b	84.00 abc	113.67 b	7.30 cde	5.00 ef	170.67 bcd	3.29 de	13.87 abc	2.92 b	6.26 abc
BD-7132	37.67 b	78.00 e	109.97 bc	8.47 bc	4.83 ef	150.93 bcde	3.45 cd	14.57 ab	2.85 b	6.36 abc
BD-7133	38.67 b	80.00 cde	100.83 cd	6.33 ef	4.83 ef	132.50 def	3.47 bc	11.95 с	3.06 b	6.26 abc
BD-7134	36.33 b	86.00 ab	94.27 de	7.60 cd	4.20 f	107.40 f	3.02 g	13.40 bc	2.89 b	3.62 c
BD-7135	41.00 b	82.67 bcd	102.13 cd	6.70 def	7.93 c	134.03 cdef	2.55 i	14.27 abc	2.21 cd	5.42 abc
BD-7136	37.00 b	79.00 de	105.13 bc	9.40 ab	6.43 cde	151.23 bcde	3.58 abc	14.77 ab	3.15 b	5.95 abc
BD-7137	39.67 b	82.67 bcd	107.43 bc	5.57 fg	7.40 cd	101.27 f	3.09 fg	12.61 bc	2.80 b	4.37 bc
BD-7138	39.00 b	82.67 bcd	94.00 de	7.53 cd	5.13 ef	109.73 ef	3.17 efg	13.23 bc	2.37 c	4.01 c
BD-8884	49.33 a	88.00 a	156.00 a	4.53 g	7.63 cd	175.20 bc	3.73 a	12.37 bc	4.38 a	8.09 a
Range	35,00-49.33	78.00-88.00	76.30-156.00	4.53-10.3	4.20-14.67	101.27-232.23	2.55-3.73	11.93-15.97	1.82-4.38	4.01-8.09
Mean	39.49	82,49	107.82	7.09	6.96	147.90	3.24	13.48	2.75	5.53

In a column means having similar letter(s) or without letter are identical and those having dissimilar letter(s) differ significantly as per 0.05 level of probability

Table 27. Estimation of genetic parameters for yield and yield contributing characters of 13 genotypes of B. Juncea

Characters	Genotypic Variance (σ_g^2)	Phenotypic Variance (σ_p^2)	% Genotypic Coefficient of Variation	% Phenotypic Coefficient of Variation	Heritability (%)	Genetic Advance (GA)	GA in percentage of mean
Days to 50% Flowering	14.893	24.581	9.773	12.556	60.588	7.930	20.084
Days to Maturity	7.013	12.787	3.210	4.334	54.844	5.176	6.275
Plant Height	479.551	510.098	20.311	20.947	94.012	56.054	51,988
Primary Branch (No.)	2.832	3.237	23.748	25.385	87,487	4.155	58,630
Secondary Branch (No)	7.676	8.742	39.790	42.461	87.806	6.855	98,428
No. of Siliquae/Plant	1189.872	1682.916	23.324	27.738	70.703	76,572	51.774
Length of Siliquae	0.113	0.123	10.370	10.833	91.848	0.851	26.268
No. of Seed/Siliquae	0,815	2.597	6,700	11.960	31.382	1.336	9.909
1000 Seed Weight	0,383	0.434	22.550	24.007	88.258	1.535	55.937
Yield/Plant	0.964	3,393	17.754	33.303	28.411	1.382	24.979

4.2.4.3 Plant Height

The mean square due to genotype from the analysis of variance was found statistically significant for plant height indicating genotypic differences among the genotypes used under the present experiment (Table 25). From the mean value it was found that the tallest (156.0 cm) genotype was BD-8884 (Table 10) which was identical with BD-7127 (148.5 cm) while the shortest (76.30 cm) genotype was BD-7107.

The phenotypic variance (510.10) was considerably higher than the genotypic variance (479.55) and the phenotypic and genotypic co-efficient of variations were 20.95 % and 20.31 %, respectively (Table 27). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Mishra and Yadav (1992) and Venkatramana *et al.* (2001).

4.2.4.4 Number of Primary Branches/Plant

Analysis of variance of the data for number of primary branches/plant showed statistically significant variation among the genotypes of *B. juncea* used in the present trail. The mean squares value regarding to the traits indicated the presence of variability among the genotypes (Table 25). Maximum number of primary branches/plant (10.30) was recorded in genotype BD-7104 (Table 26). On the other hand the minimum number of primary branches/plant (4.53) was recorded in the genotypes BD-8884.

The phenotypic variance (3.237) was slightly higher than the genotypic variance (2.832) indicating less environmental influence on this characters (Table 27) which was supported by narrow difference between phenotypic (25.39%) and genotypic (23.75%) co-efficient of variation.

4.2.4.5 Number of Secondary Branches/Plant

In the present trail analysis of variance of the data for number of secondary branches/plant showed highly significant variation among the genotypes of *B. juncea* used. The mean squares value regarding to number of secondary branches/plant (Table 25) indicated the presence of variability among the genotypes. Highest number of secondary branches/plant (14.67) was recorded in genotype BD-7107 (Table 26). On another way the genotypes BD-7134 produced the lowest (4.20) secondary branches/plant. In *B. juncea* all the genotypes produced secondary branches.

The phenotypic variance (8.742) was similar with the genotypic variance (7.676) indicating less environmental influence on this characters (Table 27) which was supported by slight difference between phenotypic (42.46%) and genotypic (39.79%) co-efficient of variation. Low phenotypic co-efficient of variation in this respect was noticed by Prakash *et al.* (2000) which also supported the results of the present experiment.

4.2.4.6 Number of Siliquae/Plant

The mean square value due to genotype from the analysis of variance was found statistically significant differences for number of siliquae/plant among the genotypes used as experimental material under the present trail (Table 25). From the mean value it was found that the highest number of siliquae/plant (232.23) was recorded for the genotype BD-7127 which was closely followed by the genotypes BD-7107 (189.23) while the minimum number (101.27) was recorded for the genotype BD-7137.

The phenotypic variance (1682.92) was considerably higher than the genotypic variance (1189.87) and the phenotypic and genotypic co-efficient of variations were 27.74% and 23.32%, respectively (Table 27). Genotypic and phenotypic co-efficient of variations in

number of siliquae/plant were also observed by Azad and Hamid (2000) and Venkatramana et al. (2001).

4.2.4.7 Length of Siliquae (cm)

A significant variation was recorded among the genotypes in consideration of length of siliquae (Table 25). Maximum length of siliquae (3.73 cm) were recorded in. *juncea* genotypes BD-8884 followed by BD-7107 (3.64). Minimum length of siliquae (2.55 cm) was recorded for the genotype BD-7135 (Table 26).

The phenotypic variance (0.123) was similar to the genotypic variance (0.113). The phenotypic co-efficient of variation (10.83%) was also similar than the genotypic co-efficient of variation (10.37%) indicating the presence of considerable influence of environmental factors on this character (Table 27). Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.2.4.8 Number of Seed/Siliquae

The value of the analysis of variance of the data for number of seed/siliquae showed highly significant difference among the genotypes of *B. juncea* used in the present piece of experiment. The mean squares value regarding to the character (Table 25) indicated the presence of variability among the genotypes. Maximum number of seed/siliquae (15.97) was recorded in genotype BD-7127 (Table 26) and the minimum (11.93) was recorded in the genotypes BD-7117.

The phenotypic variance (2.597) was higher than the genotypic variance (0.815) indicating less environmental influence on this characters (Table 27) which was supported by narrow difference between phenotypic (11.96%) and genotypic (6.70%) co-efficient of variation. Yogendra *et al.* (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.2.4.9 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant for 1000 seed weight indicating genotypic differences among the genotypes used under the present experiment (Table 25). From the mean value it was found that the highest 1000 seed weight (4.38 g) was recorded in the genotype BD-8884 while the lowest 1000 seed weight (1.82 g) was in the BD-7127.

The phenotypic variance (0.434) was considerably higher than the genotypic variance (0.383) and the phenotypic and genotypic co-efficient of variations were 24.01% and 22.55%, respectively (Table 27) for 1000 seed weight of *B. juncea* genotypes. The result indicated the existence of inherent variability among the population with possibility of high potential for selection.

4.2.4.10 Yield/Plant (g)

Analysis of variance of the data for yield/plant showed highly statistically significant difference among the genotypes of *B. juncea* used in the present piece of experiment. The mean squares value regarding to the traits indicated the presence of variability among the genotypes (Table 25). The highest yield/plant (8.09 g) was recorded in genotype BD-8884 (Table 26). On the other hand the lowest yield/plant (4.01 g) was recorded in the genotypes BD-7138 which was identical with the genotypes BD-7107.

The phenotypic variance (3.393) was higher than the genotypic variance (0.964) indicating less environmental influence on yield/plant for *B. juncea* (Table 27) which was supported by difference between phenotypic (33.30%) and genotypic (17.75%) co-efficient of variation. Almost similar results were observed by Uddin *et al.* (1995), Islam and Rasul (1998).



4.3 HERITABILITY AND GENETIC ADVANCE

4.3.1 Heritability and Genetic Advance for Brassica

Results of analysis of variance revealed that the genotypes of *Brassica* differed significantly for all the characters under study and indicating the prevalence of genetic variation and providing scope to find out the superior genotypes through selection. Results of the heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 18.

4.3.1.1 Days to 50% Flowering

Days of 50% flowering showed high heritability (80.82%) with genetic advance (13.68%) and genetic advance in percentage of mean (33.75) revealing possibility of predominance of additive gene action in the inheritance of this character as compared to other yield contributing characters and also indicating limited possibility of involvement of additive gene effect with less response to selection.

4.3.1.2 Days to Maturity

The magnitude of heritability in broad sense (h^2b) of this character was high (82.73%) and low genetic advance (11.47%) and low genetic advance in percentage of mean (13.93). These results indicate both additive and non-additive genes involvements in the expression of the character and this with limited scope of improvement by direct selection. These results were reported by Alam *et al.* (1985) and Hossain (1988).

4.3.1.3 Plant Height

Very high heritability (94.51%) together with high genetic advance (56.27%) and genetic advance in percentage of mean (61.59) revealing possibility of predominance of additive

gene action in the inheritance of this character as has been reported by Singh and Singh (1999).

4.3.1.4 Number of Primary Branches/Plant

Number of primary branches/plant showed high heritability (84.70%) coupled with low genetic advance (5.094%) and high genetic advance in percentage of mean (61.59). These findings revealed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

4.3.1.5 Number of Secondary Branches/Plant

High heritability (94.428%) coupled with low genetic advance (8.633%) and high genetic advance in percentage of mean (196.650) was calculated in respect of number of secondary branches/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection which was also earlier reported by Kumar *et al.* (1998).

4.3.1.6 Number of Siliquae/Plant

Number of siliquae/plant showed very high heritability (90.82%) coupled with very high genetic advance (126.73%) and very high genetic advance in percentage of mean (125.27). As this trait possessed high variation, it was high potential for effective selection for further genetic improvement of this trait.

4.3.1.7 Length of Siliquae (cm)

Length of siliquae/plant showed very high heritability (94.62%) connected with very low genetic advance (2.233%) and high genetic advance in percentage of mean (54.60) which findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.1.8 Number of Seed/Siliquae

The magnitude of heritability in broad sense (h²b) of this trait was high (90.90%) and low genetic advance (14.697%) and high genetic advance in percentage of mean (84.76). These results indicate both additive and non-additive genes involvements in the expression of the character and this with limit scope of improvement by direct selection.

4.3.1.9 1000 Seed Weight (g)

Very high heritability (90.10%) associated with very low genetic advance (1.603%) and high genetic advance in percentage of mean (55.47) was calculated in respect of 1000 seed weight of *Brassica* genotypes. These findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.1.10 Yield/Plant (g)

High heritability (76.56%) coupled with low genetic advance (4.970%) and high genetic advance in percentage of mean (123.63) was recorded in respect of yield/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.2 Heritability and Genetic Advance for B. napus

Results of analysis of variance revealed that the genotypes of *B. napus* differed significantly for all the characters under study and indicating the prevalence of genetic variation and providing scope to find out the superior genotypes through selection. Findings of the heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 21.

4.3.2.1 Days to 50% Flowering

Days of 50% flowering showed high heritability (66.51%) with genetic advance (8.88%) and genetic advance in percentage of mean (19.97) revealing possibility of predominance of additive gene action in the inheritance of this character as compared to other yield contributing characters and also indicating limited possibility of involvement of additive gene effect with less response to selection.

4.3.2.2 Days to Maturity

The magnitude of heritability in broad sense (h^2b) of this character was high (86.45%) and low genetic advance (11.86%) and low genetic advance in percentage of mean (13.93). These results indicate both additive and non-additive genes involvements in the expression of the character and this with limit scope of improvement by direct selection. These results were reported by Alam *et al.* (1985) and Hossain (1988).

4.3.2.3 Plant Height

Very high heritability (89.55%) together with high genetic advance (42.27%) and genetic advance in percentage of mean (48.95) revealing possibility of predominance of additive gene action in the inheritance of this character as has been reported by Singh and Singh (1999).

4.3.2.4 Number of Primary Branches/Plant

Number of primary branches/plant showed high heritability (82.72%) coupled with low genetic advance (6.54%) and high genetic advance in percentage of mean (99.22). These findings revealed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

4.3.2.5 Number of Secondary Branches/Plant

High heritability (88.62%) coupled with low genetic advance (5.59%) and high genetic advance in percentage of mean (150.14) was calculated in respect of number of secondary branches/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection which was also earlier reported by Kumar *et al.* (1998).

4.3.2.6 Number of Siliquae/Plant

Number of siliquae/plant showed very high heritability (93.41%) coupled with very high genetic advance (98.31%) and very high genetic advance in percentage of mean (159.44). As this trait possessed high variation, it was high potential for effective selection for further genetic improvement of this trait.

4.3.2.7 Length of Siliquae (cm)

Length of siliquae/plant showed very high heritability (91.77%) connected with very low genetic advance (1.999%) and high genetic advance in percentage of mean (41.76) which findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.2.8 Number of Seed/Siliquae

The magnitude of heritability in broad sense (h^2b) of this trait was high (86.82%) and low genetic advance (9.664%) and high genetic advance in percentage of mean (61.80). These results indicate both additive and non-additive genes involvements in the expression of the character and this with limited scope of improvement by direct selection.

4.3.2.9 1000 Seed Weight (g)

Very high heritability (62.34%) associated with very low genetic advance (0.657%) and high genetic advance in percentage of mean (22.07) was calculated in respect of 1000 seed weight

of *B. napus* genotypes. These findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.2.10 Yield/Plant (g)

High heritability (89.02%) coupled with low genetic advance (4.853%) and high genetic advance in percentage of mean (250.41) was recorded in respect of yield/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.3 Heritability and Genetic Advance for B. rapa

Results of analysis of variance revealed that the genotypes of *Brassica* differed significantly for all the characters under study and indicating the prevalence of genetic variation and providing scope to find out the superior genotypes through selection. Results of the heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 24.

4.3.3.1 Days to 50% Flowering

Days of 50% flowering showed high heritability (89.729%) with genetic advance (16.471%) and genetic advance in percentage of mean (44.423) revealing possibility of predominance of additive gene action in the inheritance of this character as compared to other yield contributing characters and also indicating limited possibility of involvement of additive gene effect with less response to selection.

4.3.3.2 Days to Maturity

The magnitude of heritability in broad sense (h^2b) of this character was high (82.824%) and low genetic advance (10.802%) and low genetic advance in percentage of mean (13.673). These results indicate both additive and non-additive genes involvements in the expression of the character and this with limited scope of improvement by direct selection. Similar results were also reported by Alam et al. (1985) and Hossain (1988).

4.3.3.3 Plant Height

Very high heritability (93.807%) together with high genetic advance (47.158%) and genetic advance in percentage of mean (58.464) revealing possibility of predominance of additive gene action in the inheritance of this character as has been reported by Singh and Singh (1999).

4.3.3.4 Number of Primary Branches/Plant

Number of primary branches/plant showed high heritability (93.031%) coupled with low genetic advance (3.925%) and high genetic advance in percentage of mean (67.459). These findings revealed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

4.3.3.5 Number of Secondary Branches/Plant

High heritability (98.167%) coupled with low genetic advance (9.415%) and high genetic advance in percentage of mean (363.95) was calculated in respect of number of secondary branches/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection which was also earlier reported by Kumar *et al.* (1998).

4.3.3.6 Number of Siliquae/Plant

Number of siliquae/plant showed very high heritability (85.88%) coupled with very high genetic advance (85.83%) and very high genetic advance in percentage of mean (85.80). As this trait possessed high variation, it was highly potential for effective selection for further genetic improvement of this trait.

4.3.3.7 Length of Siliquae (cm)

Length of siliquae/plant showed very high heritability (85.71%) connected with very low genetic advance (1.326%) and high genetic advance in percentage of mean (32.061) which expressed the action of additive gene effect on the expression of this character as well as having scope of improvement through selection.

4.3.3.8 Number of Seed/Siliquae

The magnitude of heritability in broad sense (h^2b) of this trait was high (87.90%) and low genetic advance (15.49%) and high genetic advance in percentage of mean (66.98). These results indicate both additive and non-additive genes involvements while the expressing of the character with limited scope of improvement by direct selection.

4.3.3.9 1000 Seed Weight (g)

Very high heritability (98.12%) associated with very low genetic advance (2.391%) and high genetic advance in percentage of mean (81.60) was calculated in respect of 1000 seed weight of *B. rapa* genotypes. These findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.3.10 Yield/Plant (g)

High heritability (49.16%) coupled with low genetic advance (2.19%) and high genetic advance in percentage of mean (44.72) was recorded in respect of yield/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.4 Heritability and Genetic Advance for B. juncea

Results of analysis of variance showed that the genotypes of *B. juncea* differed statistically significant for all the characters under trial and indicating the prevalence of genetic variation and providing scope to find out the advanced genotypes through selection. Results of the

heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 27.

4.3.4.1 Days to 50% Flowering

Days of 50% flowering showed high heritability (60.59%) with genetic advance (7.930%) and genetic advance in percentage of mean (20.084) enlightening possibility of predominance of additive gene with action the inheritance of this character as compared to other yield contributing factors and also indicating limited possibility of involvement of additive gene effect with less response to selection.

4.3.4.2 Days to Maturity

The magnitude of heritability in broad sense (h²b) of this character found to be high (54.84%) with low genetic advance (5.176%) and low genetic advance in percentage of mean (6.275). These results indicate both additive and non-additive genes involvements in the expression of the character and with limited scope of improvement by direct selection.

4.3.4.3 Plant Height

Very high heritability (94.01%) together with high genetic advance (56.05%) and with high genetic advance in percentage of mean (51.99) revealing possibility of predominance of additive gene action in the inheritance of this trait as has been reported by Singh and Singh (1999).

4.3.4.4 Number of Primary Branches/Plant

Number of primary branches/plant showed high heritability (87.49%) coupled with low genetic advance (4.155%) and high genetic advance in percentage of mean (58.63). These findings revealed the action of additive gene effect on the expression of this character as well

as a scope of improvement through selection which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

4.3.4.5 Number of Secondary Branches/Plant

High heritability (87.81%) coupled with low genetic advance (6.86%) and high genetic advance in percentage of mean (98.43) was calculated in respect of number of secondary branches/plant.

4.3.4.6 Number of Siliquae/Plant

Number of siliquae/plant showed very high heritability (70.70%) coupled with very high genetic advance (76.57%) and very high genetic advance in percentage of mean (51.77). As this trait possessed high variation, it was high potential for effective selection for further genetic improvement of this trait.

4.3.4.7 Length of Siliquae (cm)

Length of siliquae/plant showed very high heritability (91.85%) connected with very low genetic advance (0.851%) and high genetic advance in percentage of mean (26.27) which findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.4.8 Number of Seed/Siliquae

The magnitude of heritability in broad sense (h^2b) of this trait was high (31.38%) and low genetic advance (1.336%) and high genetic advance in percentage of mean (9.909). These results indicate both additive and non-additive genes involvements in the expression of the character which limits the scope of improvement by direct selection.

4.3.4.9 1000 Seed Weight (g)

Very high heritability (88.26%) associated with very low genetic advance (1.535%) and high genetic advance in percentage of mean (55.94) was calculated in respect of 1000 seed weight of *B. juncea* genotypes. These findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.3.4.10 Yield/Plant (g)

High heritability (28.41%) coupled with low genetic advance (1.382%) and high genetic advance in percentage of mean (24.98) was recorded in respect of yield/plant. These findings discovered the action of additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.4 CORRELATION MATRIX

4.4.1 Correlation Matrix for Brassica

Correlation matrix analysis was done to measure the mutual relationship between eight different yield and yield contributing characters and to determine the component characters on which selection could be based for improvement in yield of 41 *Brassica* genotypes (Table 28).

4.4.1.1 Days to 50% Flowering

Days to 50% flowering in *Oleiferous Brassica* genotypes independent of species showed significant positive association with days to maturity (0.760), plant height (0.424) and 1000 seed weight (0.206) while insignificant association with primary branches (0.129) and siliquae length (0.130) was observed. The results revealed that early flowering plants produced tallest plant, having maximum days to maturity would increase considerably with more 1000 seed weight. On the other hand secondary branches/plant and siliquae/plant showed the negative significant relation with on days to 50% flowering. This suggested that

Table 28. Correlation matrix among the yield and yield contributing characters of 41 genotypes of Brassica

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	1.00	0.760**	0.424**	0.129	-0.208*	0.130	-0.023	-0.292**	0.206*	-0.058
Days to maturity		1.00	0.440**	0.314**	-0.046	0.007	-0.225*	-0.179*	0.033	-0.092
Plant height (cm)			1.00	0.266**	0.081	-0.407**	-0.118	0.379**	0.241**	0.503*
Primary branches/ plant (No.)				1.00	0.243**	0.009	0.037	0.214*	-0.014	0.206*
Secondary branches/plant (No.)					1.00	-0.259**	0.439**	0.575**	-0.290**	0.118
Length of siliquae (cm)						1.00	0.259**	-0.372**	0.172	-0.277*
Seed/ siliquae (No.)							1.00	-0.104	0.342**	0,303*
Siliquae/ plant (No.)		1. 						1.00	-0.101	0.658*
1000 seed weight (g)					1		-1.		1.00	0.155
Yield/ plant (g)										1.00

Significant at 1% level of probability
Significant at 5% level of probability



early days to 50% flowering genotypes were more potential to allocate their photosynthates towards siliquae formation.

4.4.1.2 Days to Maturity

Days to maturity confirmed highly significant positive association with plant height (0.440) and primary branches/plant (0.314) but insignificant association with length of siliquae (0.007) and 1000 seed weight (0.033). The results revealed that with the increase in days to maturity increase plant height and more number of primary branches/plant increased considerably. On the other hand, days to maturity showed significant negative correlation with seed/siliquae (-0.225) and siliquae/plant (-0.179) and insignificant negative relation with secondary branches/plant (-0.046) and yield/plant (-0.092). Reasons behind these the reverse phenomenons were probably damaged or prevent development of mature pods before harvest ultimately resulting in reduced yield/plant. Negative association of days to maturity with plant height has also been reported by Kumar and Yadava (1982) which don't support with the findings of the presents experiment.

4.4.1.3 Plant Height

Plant height had significant negative association (-0.407) with length of siliquae among the genotypes suggesting that tall genotypes were not physiologically potential for siliquae length. In addition, plant height showed simple significant negative association with seed/siliquae (-0.118). The results revealed that even though tall plants do not produced highest number of seed/siliquae, their ultimate results in the lowest yield/plant. Plant height showed the positive relation with yield/plant (0.503). Hossain (1988) reported negative association of plant height with length of siliquae which also support the present experiment in relation with correlation matrix.

4.4.1.4 Number of Primary Branches/Plant

Number of primary branches/plant established highly significant positive association with plant height (0.440), secondary branches/plant (0.243) and yield/plant (0.206) and positive insignificant association with length of siliquae (0.009) and seed/siliquae (0.037). The results revealed that with the increase in number of primary branches/plant increase plant height and increase considerably more secondary primary branches/plant. On the other hand, number of primary branches/plant showed negative correlation with 1000 seed weight (-0.014). Negative association of number of primary branches/plant and 1000 seed weight has also been reported by Kumar and Yadava (1982) which also support with the findings of the presents study.

4.4.1.5 Number of Secondary Branches/Plant

Number of secondary branches/plant showed significant positive association with seed/siliquae (0.439) and siliquae/plant (0.575). The results revealed that highest numbers of secondary branches are the ultimate result of maximum number of primary branches/plant. On the other hand, length of siliquae (-0.259), 1000 seed weight (-0.290) and also days to 50% flowering showed the negative significant correlation on number of secondary branches/plant. This suggested that highest number of secondary branches/plant genotypes were more potential to apportion their photosynthesis to siliquae formation and maximum siliquae/plant.

4.4.1.6 Number of Siliquae/Plant

Number of siliquae/plant had significant negative association (-0.407) with plant height among the genotypes suggesting that tall genotypes were not physiologically potential for producing highest number of siliquae/plant. In addition, number of siliquae/plant showed simple significant negative association with 1000 seed weight (-0.101). The results revealed that highest number of seed/siliquae never ensured though tall plants. Number of siliquae/plant showed the positive relation with yield/plant (0.658). Hossain (1988) reported negative association of plant height with length of siliquae which also support the present experiment in relation with correlation.

4.4.1.7 Length of Siliquae (cm)

Length of siliquae showed highly significant positive association with number of seed/siliquae (0.259) but insignificant association was found with primary branches/plant (0.009), 1000 seed weight (0.172) and days to flowering (0.130). On the other hand, length of siliquae showed significant negative correlation with siliquae/plant (-0.372). Negative association of length of siliquae with 1000 seed weight has also been reported by Kumar and Yadava (1982) which also support with the findings of the presents experiment.

4.4.1.8 Number of Seed/Siliquae

Number of seed/siliquae showed significant positive association with secondary branches/plant (0.439), length of siliquae (0.259) and 1000 seed weight (0.342). The results revealed that number of seed/siliquae would increase considerably more 1000 seed weight. On the other hand the negative significant correlation was found in days to maturity (-0.225).

4.4.1.9 1000 Seed Weight (g)

1000 seed weight showed significant negative association with secondary branches (-0.290). 1000 seed weight height showed the positive relation with plant height (0.241), seed/siliquae (0.342).

4.4.1.10 Yield/Plant (g)

Yield/plant confirmed highly significant positive association with plant height (0.503) and primary branches/plant (0.206) but insignificant association with secondary branches/plant (0.118), 1000 seed weight (0.155). On the other hand, yield/plant showed significant negative

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correlation with length of siliquae (-0.277) and insignificant negative relation with days to flowering (-0.058), days to maturity (-0.092).

4.4.2 Correlation Matrix for B. napus

Correlation matrix analysis was done to measure the mutual relationship between eight different yield and yield contributing characters and to determine the component characters on which selection could be based for improvement in yield of 15 *B. napus* genotypes (Table 29)

4.4.2.1 Days to 50% Flowering

Days to 50% flowering showed significant positive association with days to maturity (0.742) and plant height (0.362). The results revealed that early flowering plants ensure early maturity. On the other hand length of siliquae and 1000 seed weight showed the negative significant correlation on days to 50% flowering. This suggested that early days to 50% flowering genotypes were more potential to allocate their photosynthesis to enlargement of siliquae.

4.4.2.2 Days to Maturity

Days to maturity confirmed highly significant positive association with plant height (0.534), primary branches/plant (0.391), secondary branches/plant (0.357) and yield/plant (0.373) but insignificant association with siliquae/plant (0.188). The results revealed that with the increase in days to maturity the above traits under study increase considerably in Brassica with exception to siliquae/plant. On the other hand, it showed significant negative correlation with 1000 seed weight (-0.329) and insignificant negative relation with length of siliquae (-0.317) and seed/siliquae (-0.201).

Table 29. Correlation matrix among the yield and yield contributing characters of 15 genotypes of B. napus

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	1.00	0.742**	0.362*	0.192	0.134	-0.406**	-0.245	0.111	-0.358**	0.275
Days to maturity	-	1.00	0.534**	0.391**	0.357**	-0.317	-0.201	0,188	-0,329*	0.373**
Plant height (cm)			1.00	0.183	0.035	-0.330*	0.071	0,286	-0.006	0.439**
Primary branches/ plant (No.)		1		1.00	0.848**	0.245	0.351*	0.338*	0.089	0.466**
Secondary branches/ plant (No.)					1.00	0,181	0.184	0.071	-0.015	0,254
Length of siliquae (cm)						1.00	0.578**	0.461**	0.658**	0.352*
Seed/ siliquae (No.)							1.00	0.635**	0.761**	0.595**
Siliquae/ plant (No.)								1.00	0.488**	0.689**
1000 seed weight (g)									1.00	0.458**
Yield/ plant (g)										1.00

** Significant at 1% level of probability * Significant at 5% level of probability

4.4.2.3 Plant Height

Plant height had significant negative association (-0.330) with length of siliquae among the genotypes suggesting that tall genotypes were not physiologically potential for siliquae length. In addition, plant height showed simple significant negative association with 1000 seed weight (-0.006). The results revealed that even though tall plants do not produced highest number of seed/siliquae, they are ultimately results in the lowest yield/plant. Plant height showed the positive relation both with days to flowering and maturity (0.362 and 0.534) yield/plant (0.439).

4.4.2.4 Number of Primary Branches/Plant

Number of primary branches/plant established highly significant positive association with secondary branches/plant (0.848), seed/siliquae (0.351), siliquae/plant (0.338) and yield/plant (0.466) and also showed positive insignificant association with length of siliquae (0.245) and 1000 seed weight (0.089). The results revealed that with the increase in number of primary branches/plant the considerably increase in secondary branches/plant helped to produce more siliquae / plant sowing ultimate increase in yield.

4.4.2.5 Number of Secondary Branches/Plant

Number of secondary branches/plant showed significant positive association with primary branches/plant (0.848) and days to maturity (0.357). It appears the results that the highest numbers of secondary branches are the ultimate result of maximum number of primary branches/plant. On the contrary, 1000 seed weight (-0.015) showed the negative insignificant correlation for number of secondary branches/plant.

4.4.2.6 Number of Siliquae/Plant

Number of siliquae/plant showed the positive relation with 1000 seed weight (0.488), length of siliquae (0.461), seed/siliquae (0.635) and yield/plant (0.689). Hossain (1988) reported

negative association of plant height with length of siliquae which also do not support the present experiment in relation with correlation.

4.4.2.7 Length of Siliquae (cm)

Length of siliquae showed highly significant positive association with number of seed/siliquae (0.578), siliquae/plant (0.461), 1000 seed weight (0.658). The results revealed that with the increase of 1000 seed weight with the result of increasing trend of siliquae length. On the other hand, length of siliquae showed significant negative correlation with days to flowering (-0.406) and plant height (-0.330).

4.4.2.8 Number of Seed/Siliquae

Number of seed/siliquae showed significant positive association with primary branches/plant (0.351), length of siliquae (.578), siliquae/plant (0.635) and 1000 seed weight (0.761) and yield/plant (0.595). The results revealed that number of seed/siliquae would attribute considerably for ultimate more yield/plant. On the other hand the negative correlation was found in days to flowering (-0.245) and for days to maturity (-0.371).

4.4.2.9 1000 Seed Weight (g)

1000 seed weight showed significant positive association with length of siliquae (0.658), seed/siliquae (0.761), siliquae / plant (0.488) and yield/plant (0.458). 1000 seed weight showed the negative relation with days to flowering (-0.358) and days to maturity (-0.329) seed.

4.4.2.10 Yield/Plant (g)

Yield/plant confirmed highly significant positive association with days to maturity (0.373) plant height (0.439) and primary branches/plant (0.466), length of siliquae (0.352), seed/siliquae (0.595), and siliquae/plant (0.689) and 1000 seed weight (0.458). Insignificant

association was observed with days to flowering (0.275) and for secondary branches/plant (0.254).

4.4.3 Correlation Matrix for B. rapa

Correlation matrix analysis was done to measure the mutual relationship between eight different yield and yield contributing characters and to determine the component characters on which selection could be based for improvement in yield of 13 *B. rapa* genotypes (Table 30)

4.4.3.1 Days to 50% Flowering

Days to 50% flowering showed significant positive association with days to maturity (0.663), plant height (0.678), seed/siliquae (0.595), 1000 seed weight (0.438) and yield/plant (0.415). The results revealed that the tallest plant initiated with early flowering required maximum days to maturity would increase considerably with more 1000 seed weight gained for highest seed yield. On the other hand secondary branches/plant and siliquae/plant showed the negative significant correlation (-0.861 and -0.746) on days to 50% flowering. This suggested that early days to 50% flowering genotypes were more potential to allocate their photosynthates for maximum plant height, maximum viable seeds per siliquae with maximum seed weight gained towards highest yield per plant.

4.4.3.2 Days to Maturity

Days to maturity confirmed highly significant positive association with plant height (0.594) and primary branches/plant (0.580) but insignificant association with seed/siliquae (0.276), 1000 seed weight (0.142) and yield / plant (0.123). The results revealed that with the increase in days to maturity the plant height increased considerably with more primary branches/plant. On the other hand, days to maturity showed significant negative correlation with secondary branches/plant (-0.692) and siliquae/plant (-0.515) and insignificant negative relation with

length of siliquae (-0.045). Reasons behind these where reverse phenomenon's were probably damaged or rotting on development of mature pods before harvest ultimately resulting in reduced yield/plant. Negative association of days to maturity with plant height has also been reported by Kumar and Yadava (1982) which do not support the findings of the presents experiment.

4.4.3.3 Plant Height

Plant height had significant negative association (-0.748) with secondary branches/plant and for number of siliquae/plant (-0.430) suggesting that tall genotypes were not physiologically potential for both. In addition, plant height showed simple non significant negative association with length of siliquae (-0.169). The results revealed that even though tall plants do not produced longest siliquae it showed the positive relation with primary branches/plant (0.530) seed/siliquae (0.420), 1000 seed weight (0.541) and yield/plant (0.570). Hossain (1988) reported negative association of plant height with length of siliquae which also support the present experiment in relation with correlation matrix.

4.4.3.4 Number of Primary Branches/Plant

Number of primary branches/plant established highly significant positive association with days to maturity (0.530), plant height (0.530) and positive insignificant association with seed/siliquae (0.179) and siliquae/plant (0.063), 1000 seed weight (0.046) and yield/plant (0.274). The results revealed that with the increase in number of primary branches/plant the trait plant height and days to maturity increased considerably. On the other hand, number of primary branches/plant showed negative correlation with secondary branches/plant (-0.402). Negative association of number of primary branches/plant and 1000 seed weight has also been reported by Kumar and Yadava (1982) which also support with the findings of the presents study.

Table 30. Correlation matrix among the yield and yield contributing characters of 13 genotypes of Brassica rapa

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	1.00	0.663**	0.678**	0.304	-0.861**	0.118	0.595**	-0.746**	0.438**	0.415**
Days to maturity		1.00	0.594**	0.580**	-0.692**	-0.045	0.276	-0,515**	0.142	0.123
Plant height (cm)			1.00	0.530**	-0.748**	-0.169	0.420**	-0.430**	0.541**	0.570**
Primary branches/ plant (No.)				1,00	-0.402**	-0.123	0,179	0.063	0.046	0.274
Secondary branches/ plant (No.)					1.00	-0.077	-0.559**	0.788**	-0.324*	-0.515*
Length of siliquae (cm)						1.00	0.011	-0.069	-0,496**	0.243
Seed/ siliquae (No.)							1.00	-0.609**	0.438**	0.361*
Siliquae/ plant (No.)								1.00	-0.234	-0.175
1000 seed weight (g)									1.00	0.271
Yield/ plant (g)										1.00

** Significant at 1% level of probability * Significant at 5% level of probability



4.4.3.5 Number of Secondary Branches/Plant

Number of secondary branches/plant showed significant positive association with siliquae/plant (0.788). The results revealed that highest numbers of secondary branches are the ultimate result of maximum number of siliquae/plant. On the other hand, seed / siliquae (-0.559), 1000 seed weight (-0.324) and yield/plant (-0.515) showed the negative significant correlation on number of secondary branches/plant. This suggested that the genotypes with highest number of secondary branches/plant were more potential to apportion for their photosynthates to siliquae formation and maximum siliquae/plant.

4.4.3.6 Number of Siliquae/Plant

Number of siliquae/plant had significant negative association (-0.746) with days to 50% flowering, (0.515) for days to maturity, (-0.430) for plant height and (-0.609) for seed / siliquae production. In addition, number of siliquae/plant showed simple significant negative association with 1000 seed weight (-0.234) and for yield/plant (-0.175). The results revealed that highest number of seed/siliquae never ensured though tall plants. Number of siliquae/plant showed the positive insignificant relation with number of primary branches/plant (0.063). Hossain (1988) reported negative association of plant height with length of siliquae which also support the present experiment in relation with correlation.

4.4.3.7 Length of Siliquae (cm)

Length of siliquae showed positive association with days to 50% flowering (0.118) but insignificant association was found with seed/siliquae (0.011) and yield/plant (0.243). On the other hand, length of siliquae showed significant negative correlation with 1000 seed weight (-0.496). Negative association of length of siliquae with 1000 seed weight has also been reported by Kumar and Yadava (1982) which also support with the findings of the presents experiment.

4.4.3.8 Number of Seed/Siliquae

Number of seed/siliquae showed significant positive association with plant height (0.420), 1000 seed weight (0.438) and yield/plant (0.361). The results revealed that number of seed/siliquae would increase considerably more 1000 seed weight. On the other hand the negative significant correlation was found in siliquae/plant (-0.609) and for secondary branches/plant (-0.559).

4.4.3.9 1000 Seed Weight (g)

1000 seed weight showed significant negative association with secondary branches (-0.324) and length of siliquae (-0.496). 1000 seed weight showed the positive insignificant relation with days to maturity (0.142), number of primary branches/plant (0.046) and yield/plant (0.271).

4.4.3.10 Yield/Plant (g)

Yield/plant confirmed highly significant positive association with days to flowering (0.415), plant height (0.570) and number of seed/siliquae (0.361) but insignificant association with days to maturity (0.123), number of primary branches/plant (0.274), siliquae length (0.243) and for 1000 seed weight (0.271). On the other hand, yield/plant showed significant negative correlation with secondary branches/plant (-0.515) and insignificant negative relation with siliquae/pant (-0.175).

4.4.4 Correlation Matrix for B. juncea

Correlation matrix analysis of the *B. juncea* was done to measure the communal relationship between eight different yield and yield contributing characters and to conclude the component characters on which selection could be based for enhancement in yield of the genotypes (Table 31).

4.4.4.1 Days to 50% Flowering

Days to 50% flowering showed significant positive association with days to maturity (0.725), plant height (0.689), siliquae/plant (0.383) and for yield/plant (0.395). The results discovered that early flowering plants produced tallest plant height; maximum days to maturity would increase considerably with more siliquae/plant. On the other hand primary branches/plant showed the negative significant correlation (-0.307) on days to 50% flowering.

4.4.4.2 Days to Maturity

Days to maturity confirmed highly significant positive association with plant height (0.431) but insignificant association with siliquae/plant (0.085), 1000 seed weight (0.174) and yield/plant (0.087). The results revealed that with the increase in days to maturity increase siliquae production also increase 1000 seed weight. On the other hand, days to maturity showed significant negative correlation (-0.312) with primary branches/plant and insignificant negative relation with secondary branches/plant (-0.011), length of siliquae (-0.246) and seed/siliquae (-0.077). Negative association of days to maturity with plant height has also been reported by Kumar and Yadava (1982) which don't support with the findings of the presents experiment.

4.4.4.3 Plant Height

Plant height had significant positive association (0.523) with siliquae/plant, 1000 seed weight (0.422) and yield/plant (0.610) the genotypes suggesting that tall genotypes were not physiologically potential for siliquae production. Plant height showed the positive insignificant relation with primary and secondary branches/plant, (0.003 and 0.004), seed/siliquae and siliquae length (0.290 and 0.034). Hossain (1988) reported negative association of plant height with siliquae/plant which also supports the present experiment in relation with correlation matrix.

Table 31. Correlation matrix among the yield and yield contributing characters of 13 genotypes of B. juncea

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	1.00	0.725**	0.689**	-0.307*	0.255	-0.093	0.135	0.383*	0.174	0.395*
Days to maturity		1.00	0.431**	-0.312*	-0.011	-0.246	-0.077	0.085	0.174	0,087
Plant height (cm)			1,00	0.003	0.004	0.034	0.290	0.523**	0.422**	0.610**
Primary branches/ plant (No.)				1,00	-0.253	-0.076	0.460**	0.111	-0,130	-0.110
Secondary branches/ plant (No.)					1.00	0,088	0.202	0,569**	-0.307*	0.161
Length of siliquae (cm)						1.00	-0.182	0.146	0.617**	0.255
Seed/ siliquae (No.)							1.00	0.490**	-0.123	0.396*
Siliquae/ plant (No.)								1.00	-0.061	0.679**
1000 seed weight (g)									1.00	0,320*
Yield/plant (g)										1.00

** Significant at 1% level of probability
* Significant at 5% level of probability

4.4.4.4 Number of Primary Branches/Plant

Number of primary branches/plant established highly significant positive association with seed/siliquae (0.460) and positive insignificant association with plant height (0.003) and siliquae/plant (0.111). The results expressed that with the increase in number of primary branches/plant increase plant height and increase considerably more secondary siliquae/plant. On the other hand, number of primary branches/plant showed negative significant correlation with days to flowering and days to maturity (-0.307 and -0.312). Negative association of number of primary branches/plant and days to flowering has also been reported by Kumar and Yadava (1982) which also support with the findings of the presents study.

4.4.4.5 Number of Secondary Branches/Plant

Number of secondary branches/plant showed significant positive association with siliquae/plant (0.569). The results revealed that highest numbers of secondary branches are the ultimate result of maximum number of siliquae/plant. On the other hand, days to maturity (-0.011), primary branches/plant (-0.253) showed negative insignificant differences while 1000 seed weight (-0.307) showed the negative significant correlation on number of secondary branches/plant. This suggested that genotypes with highest number of secondary branches/plant were more potential to apportion their photosynthates to siliquae formation and maximum siliquae/plant.

4.4.4.6 Number of Siliquae/Plant

Number of siliquae/plant had negative insignificant association (-0.061) with 1000 seed weight among the genotypes studied. Number of siliquae/plant showed significantly positive relation with days to flowering (0.383), plant height (0.523), secondary branches/plant (0.569), seed/siliquae (0.490) and yield/plant (0.679). Hossain (1988) reported negative

association of plant height with length of siliquae which also support the present experiment in relation with correlation.

4.4.4.7 Length of Siliquae (cm)

Length of siliquae showed highly significant positive association with 1000 seed weight (0.617) but insignificant association was found with plant height (0.034), secondary branches/plant (0.088), siliquae/plant (0.146) and yield/plant (0.255). On the other hand, length of siliquae showed negative correlation with days to flowering and maturity (-0.093 and -0.246) and primary branches/plant (-0.076).

4.4.4.8 Number of Seed/Siliquae

Number of seed/siliquae showed significant positive association with primary branches/plant (0.460), siliquae/plant (0.490) and yield/plant (0.396). The results revealed that number of seed/siliquae would increase considerably more seed yield. On the other hand the negative association was recorded in days to maturity (-0.077).

4.4.4.9 1000 Seed Weight (g)

1000 seed weight showed significant negative association with secondary branches (-0.307) while positive significant association was observed for plant height (0.422), length of siliquae (0.617) and yield/plant (0.320).

4.4.4.10 Yield/Plant (g)

Yield/plant confirmed highly significant positive association with days to flowering (0.395), plant height (0.610), seed/siliquae (0.396) siliquae/plant (0.679) and 1000 seed weight (0.320) but insignificant association with days to maturity (0.087) secondary branches/plant (0.161) length of siliquae (0.255). On the other hand, yield/plant showed negative correlation with primary branches/plant (-0.110).

4.5. PATH CO-EFFICIENT ANALYSIS

4.5.1 Path Co-efficient Analysis for Brassica

Path co-efficient analysis screens the components of correlation co-efficient into direct and indirect effects and indicates the relationship in more meaningful way. Path co-efficient were analyzed using the genotypic correlation only. The results of the path co-efficient using genotypic correlation are presented in Table 32.

4.5.1.1 Yield/plant vs. Days to 50% Flowering

Path analysis revealed that days to 50% flowering had negative direct effect (-0.184) on yield/plant (Table 28). It showed negligible negative indirect effect through branches/plant and pods/plant. Days to 50% flowering showed positive indirect effect through number of primary and secondary branches/plant, seed/siliquae. Yadava *et al.* (1994), Deshmark *et al.* (1986) reported direct effect of days of 50% flowering on yield/plant.

4.5.1.2 Yield/plant vs. Days to Maturity

Days to maturity showed positive direct effect (0.205) on yield/plant (Table 28). The positive correlation between days to maturity and yield was probably due to cumulative indirect influence of negatively associated traits. However, days to maturity had indirect negative effect also through days to flowering, plant height, primary and secondary branches. Yadava *et al.* (1984) founds days to maturity exerting significant positive direct and indirect effects on pod yield/plant. Similar direct positive effect of days to maturity on plant yield was reported by Kumar and Yadava (1978) and Hossain (1988).

4.5.1.3 Yield/plant vs. Plant Height

Plant height had positive direct effect (0.405) on yield and negative indirect effects through days to flowering, primary branches/plant (Table 28). The correlation coefficient between yield/plant and plant height was also negative due to the negative contribution of others

characters towards yield. On the contrary, plant height had positive contribution via days to 50% flowering, days to maturity. Oleagineux (1983) also showed that plant height had a direct negative effect on plant yield.

4.5.1.4 Yield/plant vs. Number of Primary Branches/Plant

Path analysis showed that number of primary branches/plant had positive direct effect (0.311) on yield/plant (Table 28). It showed negligible negative indirect effect through secondary branches/plant, seed/siliquae. Number of primary branches/plant showed positive indirect effect through days to flowering and days to maturity, length of siliquae and siliquae/plant.

4.5.1.5 Yield/plant vs. Number of Secondary Branches/Plant

Number of secondary branches/plant had positive direct effect (0.119) on yield and negative indirect effects through days to maturity, length of siliquae. On the contrary, number of secondary branches/plant had positive contribution via days to flowering, number of primary branches/plant, seed/siliquae, siliquae/plant and 1000 seed weight.

4.5.1.6 Yield/plant vs. Length of Siliquae (cm)

Length of siliquae had negative direct effect (-0.378) on yield and negative indirect effects through days to flowering and maturity, secondary branches/plant. On the other hand, length of siliquae had positive contribution via plant height, primary branches/plant, and seed/siliquae.

4.5.1.7 Yield/plant vs. Number of Seed/Siliquae

Path analysis showed that number of seed/siliquae had positive direct effect (0.504) on yield/plant (Table 28). It showed negligible negative indirect effect through primary branches/plant, length of siliquae and siliquae/plant, while positive indirect effect through days to flowering and days to maturity, plant height and secondary branches/plant observed.



Table 32.	Partitioning of genetic correlation into direct (bold) and indirect effects of yield contributing characters on yield of 41	
	genotypes of <i>Brassica</i> by path analysis	

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	-0.184	0.037	0.063	-0.058	-0.012	0.015	-0.042	0.085	0.038	-0.058
Days to maturity	-0.064	0.205	-0.039	-0.013	-0.008	-0.022	-0.084	0.006	-0,073	-0.092
Plant height (cm)	-0.092	0.047	0,405	-0.029	0.055	0.042	0,026	0.039	0.010	0,503
Primary branches/ plant (No.)	0.016	0.082	0.029	0.311	-0.038	0.075	-0,038	0.018	-0.249	0.206
Secondary branches/ plant (No.)	0,045	-0.078	-0.022	0.030	0.119	-0.068	0.032	0.019	0,041	0.118
Length of siliquae (cm)	-0.008	-0.068	0.025	0.078	-0.045	-0.378	0.023	0.051	0.045	-0.277
Seed/ siliquae (No.)	0.098	0.047	0.025	-0.088	0.099	-0.087	0.504	-0,055	-0,240	0.303
Siliquae/ plant (No.)	0.012	-0.078	-0.033	0.011	0,032	0.095	0.024	0.628	-0.033	0.658
1000 seed weight (g)	0.077	0.033	0,112	0.096	0.032	-0,088	0.069	0.092	-0,268	0.155

Residual effect =0.4533

4.5.1.8 Yield/plant vs. Number of Siliquae/Plant

Number of siliquae/plant had positive direct effect (0.628) on yield and negative indirect effects through days to maturity, plant height and 1000 seed weight. On the other hand, number of siliquae/plant had positive contribution via days to flowering, primary and secondary branches/plant, length of siliquae and seed/siliquae.

4.5.1.9 Yield/plant vs. 1000 Seed Weight (g)

Path analysis showed that 1000 seed weight had negative direct effect (-0.268) on yield/plant (Table 28). It showed negligible negative indirect effect through length of siliquae and positive indirect effect through days to flowering and days to maturity, plant height, primary and secondary branches/plant siliquae/plant and seeds/siliquae.

4.5.2 Path Co-efficient Analysis for B. napus

Path co-efficient analysis screens the components of correlation co-efficient into direct and indirect effects and indicates the relationship in more meaningful way. Path co-efficient were analyzed using the genotypic correlation only. The results of the path co-efficient using genotypic correlation are presented in Table 33.

4.5.2.1 Yield/plant vs. Days to 50% Flowering

Path analysis revealed that days to 50% flowering had positive direct effect (0.398) on yield/plant (Table 29). It showed negligible negative indirect effect through primary and secondary branches/plant, seed/siliquae and 1000 seed weight. Days to 50% flowering showed positive indirect effect through days to maturity, plant height, length of siliquae and siliquae/plant. Yadava *et al.* (1994), Deshmark *et al.* (1986) reported direct effect of days of 50% flowering on yield/plant.

4.5.2.2 Yield/plant vs. Days to Maturity

Days to maturity showed negative direct effect (-0.175) on yield/plant (Table 29). The positive correlation between days to maturity and yield was probably due to cumulative indirect influence of negatively associated traits. However, days to maturity had indirect negative effect also through plant height, secondary branches/plant, seed/siliquae and 1000 seed weight.

4.5.2.3 Yield/plant vs. Plant Height

Plant height had positive direct effect (0.388) on yield and negative indirect effects through days to flowering, primary branches/plant, length of siliquae and siliquae/plant (Table 29). On the contrary, plant height had positive contribution via days to maturity, secondary branches and 1000 seed weight.

4.5.2.4 Yield/plant vs. Number of Primary Branches/Plant

Path analysis showed that number of primary branches/plant had negative direct effect (-0.125) on yield/plant (Table 29). It showed negligible negative indirect effect through secondary branches/plant, seed/siliquae and 1000 seed weight. Number of primary branches/plant showed positive indirect effect through days to flowering and days to maturity, plant height, length of siliquae and siliquae/plant.

4.5.2.5 Yield/plant vs. Number of Secondary Branches/Plant

Number of secondary branches/plant had positive direct effect (0.228) on yield and negative indirect effects through days to flowering and maturity, plant height, and length of siliquae. On the contrary, number of secondary branches/plant had positive contribution via number of primary branches/plant, seed/siliquae, siliquae/plant and 1000 seed weight.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	0.398	0.303	0.088	-0.198	-0.087	0,007	-0.240	0.142	-0.138	0.275
Days to maturity	0,123	-0.175	-0.101	0.214	-0.008	0.322	-0.084	0.151	-0.069	0.373**
Plant height (cm)	-0.119	0.278	0.388	-0.094	0.166	-0.187	0.002	-0.005	0.010	0,439**
Primary branches/ plant (No.)	0.005	0.038	0.122	-0.125	-0.108	0.375	-0,015	0.205	-0,031	0.466**
Secondary branches/ plant (No.)	-0.032	-0.018	-0.111	0.145	0.228	-0,006	0.021	0.007	0.020	0.254
Length of siliquae (cm)	-0.011	-0.007	0.205	0.177	-0.046	-0.342	0.178	-0.001	0.199	0.352*
Seed/ siliquae (No.)	0.235	0.097	-0.038	-0.060	0.277	-0.087	0,266	-0,055	-0.040	0.595**
Siliquae/ plant (No.)	-0.054	-0.018	-0,107	0.155	-0.031	0.095	0.198	0.455	-0.004	0.689**
1000 seed weight (g)	0.127	0,006	0.085	-0.092	0.039	-0.081	0.069	0.091	0.214	0.458**

Table 33. Partitioning of genetic correlation into direct (bold) and indirect effects of yield contributing characters on yield of 15 genotypes of *B. napus* by path analysis

Residual effect =0.4852

** Significant at 1% level of probability

* Significant at 5% level of probability

4.5.2.6 Yield/plant vs. Length of Siliquae (cm)

Length of siliquae had negative direct effect (-0.342) on yield and negative indirect effects through days to flowering and maturity, secondary branches/plant. On the other hand, length of siliquae had positive contribution via plant height, primary branches/plant, seed/siliquae and 1000 seed weight.

4.5.2.7 Yield/plant vs. Number of Seed/Siliquae

Path analysis showed that number of seed/siliquae had positive direct effect (0.266) on yield/plant (Table 29). It showed negligible negative indirect effect through plant height, primary branches/plant, length of siliquae, siliquae/plant and 1000 seed weight and positive indirect effect through days to flowering and days to maturity, and secondary branches/plant.

4.5.2.8 Yield/plant vs. Number of Siliquae/Plant

Number of siliquae/plant had positive direct effect (0.455) on yield and negative indirect effects through days to flowering and maturity, plant height, secondary branches/plant and 1000 seed weight. On the other hand, number of siliquae/plant had positive contribution via primary branches/plant, length of siliquae and seed/siliquae.

4.5.2.9 Yield/plant vs. 1000 Seed Weight (g)

Path analysis showed that 1000 seed weight had positive direct effect (0.214) on yield/plant (Table 29). It showed negligible negative indirect effect through primary branches/plant, length of siliquae and positive indirect effect through days to flowering and days to maturity, plant height, secondary branches/plant seed/siliquae and siliquae/plant.

4.5.3 Path Co-efficient Analysis for B. rapa

Path co-efficient analysis screens the components of correlation co-efficient into direct and indirect effects and indicates the relationship in more meaningful way. Path co-efficient were analyzed using the genotypic correlation only. The results of the path co-efficient using genotypic correlation are presented in Table 34.

4.5.3.1 Yield/plant vs. Days to 50% Flowering

Path analysis revealed that days to 50% flowering had positive direct effect (0.351) on yield/plant (Table 30). It showed negligible negative indirect effect through plant height, primary branches/plant and seed/siliquae. Days to 50% flowering showed positive indirect effect through days to maturity, number of secondary branches/plant, length of siliquae, siliquae/plant. Yadava *et al.* (1994), Deshmark *et al.* (1986) reported direct effect of days of 50% flowering on yield/plant.

4.5.3.2 Yield/plant vs. Days to Maturity

Days to maturity showed positive direct effect (0.339) on yield/plant (Table 30). The positive correlation between days to maturity and yield was probably due to cumulative indirect influence of negatively associated traits. However, days to maturity had indirect negative effect also through plant height, secondary branches/plant and 1000 seed weight. Yadava *et al.* (1984) founds days to maturity exerting significant positive direct and indirect effects on pod yield/plant. Similar direct positive effect of days to maturity on plant yield was reported by Kumar and Yadava (1978) and Hossain (1988).

4.5.3.3 Yield/plant vs. Plant Height

Plant height had negative direct effect (0.398) on yield and negative indirect effects through days to flowering, secondary branches/plant, and seed/siliquae (Table 30). The correlation coefficient between yield/plant and plant height was also negative due to the negative contribution of majority of characters towards yield. On the contrary, plant height had positive contribution via days to maturity, primary branches/plant. Oleagineux (1983) also showed that plant height had a direct negative effect on plant yield.

4.5.3.4 Yield/plant vs. Number of Primary Branches/Plant

Path analysis showed that number of primary branches/plant had positive direct effect (0.458) on yield/plant (Table 30). It showed negligible negative indirect effect through days to maturity, seed/siliquae, siliquae/plant, 1000 seed weight. Number of primary branches/plant showed positive indirect effect through days to flowering, plant height, secondary branches/plant and length of siliquae.

4.5.3.5 Yield/plant vs. Number of Secondary Branches/Plant

Number of secondary branches/plant had positive direct effect (0.331) on yield and negative indirect effects through days to maturity, plant height, length of siliquae and 1000 seed weight. On the contrary, number of secondary branches/plant had positive contribution via number of primary branches/plant, siliquae/plant.

4.5.3.6 Yield/plant vs. Length of Siliquae (cm)

Length of siliquae had negative direct effect (-0.256) on yield and negative indirect effects through primary branches/plant and 1000 seed weight. On the other hand, length of siliquae had positive contribution via days to flowering and days to maturity, plant height, secondary branches/plant, seed/siliquae and siliquae/plant.

4.5.3.7 Yield/plant vs. Number of Seed/Siliquae

Path analysis showed that number of seed/siliquae had positive direct effect (0.129) on yield/plant (Table 30). It showed negligible negative indirect effect through days to flowering, plant height, primary branches/plant, length of siliquae, 1000 seed weight and positive indirect effect through days to maturity and secondary branches/plant, siliquae/plant.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	0.351	0.297	-0.214	-0,110	0.058	0.251	-0.194	0.211	-0.235	0.415**
Days to maturity	0.111	0.339	-0.445	0.255	-0,108	0.027	0.089	0.012	-0.157	0.123
Plant height (cm)	-0.258	0.308	-0,398	0.147	-0.117	0.397	-0.142	0.245	0.388	0.570**
Primary branches/ plant (No.)	0.118	-0.145	0,184	0.458	0.089	0.375	-0.238	-0,318	-0.249	0.274
Secondary branches/ plant (No.)	0.005	-0.103	-0.030	0.185	0.331	-0.358	-0.295	0.019	-0.269	-0.515**
Length of siliquae (cm)	0.107	0.028	0.089	-0.134	0.075	-0.256	0.214	0.129	-0.009	0.243
Seed/ siliquae (No.)	-0.018	0.187	-0.168	-0.158	0.199	-0.030	0.129	0.355	-0,135	0.361*
Siliquae/ plant (No.)	-0.007	0,147	-0.070	-0.311	0.022	-0.277	0.082	0.407	-0.168	-0.175
1000 seed weight (g)	0.128	-0.052	0.222	0.055	-0.006	-0.031	0.169	0.145	-0.359	0.271

Table 34. Partitioning of genetic correlation into direct (bold) and indirect effects of yield contributing characters on yield of 13 genotypes of *Brassica rapa* by path analysis

Residual effect =0.5833

** Significant at 1% level of probability * Significant at 5% level of probability



4.5.3.8 Yield/plant vs. Number of Siliquae/Plant

Number of siliquae/plant had positive direct effect (0.407) on yield and negative indirect effects through days to flowering, plant height, primary branches/plant, length of siliquae and 1000 seed weight. On the other hand, number of siliquae/plant had positive contribution via days to maturity, secondary branches/plant, and seed/siliquae.

4.5.3.9 Yield/plant vs. 1000 Seed Weight (g)

Path analysis showed that 1000 seed weight had negative direct effect (-0.359) on yield/plant (Table 30). It showed negligible negative indirect effect through days to maturity, length of siliquae and positive indirect effect through days to flowering and, plant height, primary branches/plant seed/siliquae and siliquae/plant.

4.5.4 Path Co-efficient Analysis for B. juncea

Path co-efficient analysis screens the components of correlation co-efficient into direct and indirect effects and indicates the relationship in more momentous way. Path co-efficient were analyzed using the genotypic correlation only. The results of the path co-efficient using genotypic correlation are presented in Table 35.

4.5.4.1 Yield/plant vs. Days to 50% Flowering

Path analysis revealed that days to 50% flowering had negative direct effect (-0.245) on yield/plant (Table 31). It showed negligible negative indirect effect through secondary branches/plant and 1000 seed weight. Days to 50% flowering showed positive indirect effect through plant height, primary branches/plant, length of siliquae and seed/siliquae. Yadava *et al.* (1994), Deshmark *et al.* (1986) reported direct effect of days of 50% flowering on vield/plant.

4.5.4.2 Yield/plant vs. Days to Maturity

Days to maturity showed negative direct effect (-0.165) on yield/plant (Table 31). However, days to maturity had indirect negative effect also through plant height, secondary branches/plant, siliquae/plant and 1000 seed weight. On the other hand positive indirect effect also recorded through days to flowering, primary branches/plant, length of siliquae, seed/siliquae.

4.5.4.3 Yield/plant vs. Plant Height

Plant height had negative direct effect (-0.289) on yield and negative indirect effects through days to flowering and length of siliquae (Table 31). On the contrary, plant height had positive contribution via days to maturity, primary and secondary branches/plant, seed/siliquae, siliquae/plant and 1000 seed weight. Oleagineux (1983) also showed that plant height had a direct negative effect on plant yield.

4.5.4.4 Yield/plant vs. Number of Primary Branches/Plant

Path analysis showed that number of primary branches/plant had positive direct effect (0.171) on yield/plant (Table 31). It showed negligible negative indirect effect through days to maturity, secondary branches/plant, seed/siliquae, siliquae/plant and 1000 seed weight. Number of primary branches/plant showed positive indirect effect through days to maturity, length of siliquae and seed/siliquae and 1000 seed weight.

4.5.4.5 Yield/plant vs. Number of Secondary Branches/Plant

Number of secondary branches/plant had negative direct effect (-0.221) on yield and negative indirect effects through days to flowering, plant height, primary branches/plant, and siliquae/plant. On the contrary, number of secondary branches/plant had positive contribution via days to maturity, length of siliquae, seed/siliquae and 1000 seed weight.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant (No.)	Secondary branches/ plant (No.)	Length of siliquae (cm)	Seed/ siliquae (No.)	Siliquae/ plant (No.)	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	-0.245	-0.121	0.217	0.009	-0.202	0.321	0,196	0.235	-0.015	0.395*
Days to maturity	0.129	-0.165	-0.111	0.210	-0.042	0.081	0.209	-0.132	-0.092	0.087
Plant height (cm)	-0.151	0.012	-0,289	0.143	0.147	-0.015	0.321	0.288	0.154	0.610**
Primary branches/ plant (No.)	0.247	-0.027	0.133	0.171	-0.192	0.033	-0.244	-0.082	-0.149	-0.110
Secondary branches/ plant (No.)	-0.086	0.129	-0.147	-0.168	-0.221	0.235	0.309	-0.055	0.165	0.161
Length of siliquae (cm)	0.111	-0.032	0,122	0.113	-0.107	-0.155	0.068	0.174	-0.039	0.255
Seed/ siliquae (No.)	-0.042	0.149	0.269	-0,126	0.237	-0.105	0.309	-0.055	-0.240	0,396*
Siliquae/ plant (No.)	0.055	0.031	-0.079	0.289	0.139	0.095	-0.228	0.425	-0.048	0.679**
1000 seed weight (g)	0.147	-0,104	0.142	-0,030	0.047	-0.202	0.031	0.112	0.177	0.320*

Table 35. Partitioning of genetic correlation into direct (bold) and indirect effects of yield contributing characters on yield of 13 genotypes of *B. juncea* by path analysis

Residual effect =0.3985

** Significant at 1% level of probability

* Significant at 5% level of probability

4.5.4.6 Yield/plant vs. Length of Siliquae (cm)

Length of siliquae had negative direct effect (-0.155) on yield and negative indirect effects through days to maturity, secondary branches/plant and 1000 seed weight. On the other hand, length of siliquae had positive contribution via days to flowering, plant height, primary branches/plant, seed/siliquae and siliquae/plant.

4.5.4.7 Yield/plant vs. Number of Seed/Siliquae

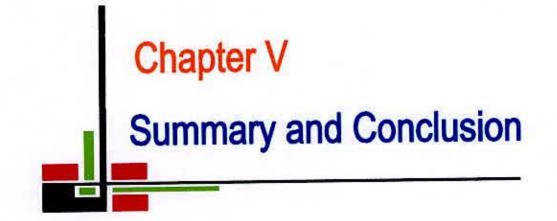
Path analysis showed that number of seed/siliquae had positive direct effect (0.309) on yield/plant (Table 31). It showed negligible negative indirect effect through days to flowering, primary branches/plant, length of siliquae, siliquae/plant, 1000 seed weight and positive indirect effect through days to maturity, secondary branches/plant.

4.5.4.8 Yield/plant vs. Number of Siliquae/Plant

Number of siliquae/plant had positive direct effect (0.425) on yield and negative indirect effects through plant height, seed/siliquae and 1000 seed weight. On the other hand, number of siliquae/plant had positive contribution via days to flowering and maturity, primary and secondary branches/plant and length of siliquae.

4.5.4.9 Yield/plant vs. 1000 Seed Weight (g)

Path analysis showed that 1000 seed weight had positive direct effect (0.177) on yield/plant (Table 31). It showed negligible negative indirect effect through days to maturity, primary branches/plant, length of siliquae and positive indirect effect through days to flowering, plant height, secondary branches/plant, seed/siliquae and siliquae/plant.



Chapter V

SUMMARY AND CONCLUSION

A field experiment was conducted in the Genetics and Plant Breeding experimental field of Sher-e Bangla Agricultural University, Dhaka, Bangladesh to study the morphological characterization and genetic divergence in oleiferous *Brassica*. In this research work, each of the oliferous *Brassica* genotypes was grown in the 2004-2005 cropping season. The 41 genotypes used in this study were not under single mustard rape seed species. They showed wide variation and thus were categorized under three cultivated species – *B. rapa*, *B. napus* and *B. juncea* based on the morphological characteristics. Data on yield and yield contributing characters were recorded. Analytical results of the genotypes have been estimated under different sections of phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic diversity, correlation co-efficient among different important yield contributing characters and also direct and indirect effect of yield related traits on yield.

The genotypes of three different species showed greater diversity. They were grouped into 6 clusters. Many of the groups comprise of the genotypes of the three different species. There is diversity among the genotypes of each species. On the other hand, the inclusion of genotypes of 3 species into the same group showed the close relationships among the genotypes. This closeness was probably due to the presence of AA genome in all the three species as common. Cluster VI was the largest cluster comprising of 6 genotypes followed by cluster IV with 3 genotypes in *B. napus*. Cluster II had the highest intra-cluster distance (0.789) followed by cluster VI (0.666). In *B. rapa* Cluster III and IV was the largest cluster comprising of 4 genotypes followed by cluster II with 2 genotypes. Cluster II had the highest intra-cluster distance (0.901) followed by cluster III (0.666). Inter cluster distance was maximum (8.912) between clusters I and IV, followed by clusters II and III (7.526). In

B. juncea Cluster I had the highest intra-cluster distance (0.779) while cluster II and VI had the lowest (0.00) or no intra cluster distance. Inter cluster distance was maximum (8.912) between clusters I and IV, followed by clusters II and V (8.332).

Maximum days to 50% flowering (51.33) was recorded in genotype *B. napus* BD-7788 and BD-7789 and the minimum days to 50% flowering (38.00) was recorded in the genotypes BD-9102 and BD-7836. The highest yield/plant (8.95 g) was recorded in genotype BD-7789 and the lowest yield/plant (0.92 g) was recorded in the genotypes BD-7788. In *B. rapa data* on yield and yield contributing characters showed significant difference among the genotypes. Maximum and minimum days to flowering were recorded in the genotypes SAU-YC and BD-7102 (44 and 27 days) respectively. The highest yield/plant (7.23 g) was recorded in genotype SAU-YC and the lowest yield/plant (2.31 g) was recorded in the genotype BD-9061. Results of 13 genotypes of *B. juncea* have been predictable under different subdivision. Maximum days to 50% flowering (35.00) was recorded in the genotypes BD-7104. Maximum days to 50% flowering (35.00) was recorded in the genotypes BD-8884 and the minimum days to maturity (78.00 days) were obtained from the genotype BD-7132. The highest yield/plant (8.09 g) was recorded in genotype BD-8884 and the lowest yield/plant (8.09 g) was recorded in genotype BD-8884 and the lowest yield/plant (4.01 g) was recorded in the genotypes BD-7138.

The phenotypic variance of each of characters was higher than respective genotypic variance showing the minimum role of environment on these characters. High heritability with low genetic advance was observed for the characters days to 50% flowering, days to maturity, primary branches/plant, 1000-seed weight and yield/plant. In *B. napus* the phenotypic variance for days to 50% flowering (25.56) was slightly higher than the genotypic variance (16.99) which was supported by slender difference between phenotypic (11.38%) and genotypic (9.28%) co-efficient of variation. The phenotypic variance for 1000 seed weight

(0.159) was considerably higher than the genotypic variance (0.099) and the phenotypic and genotypic co-efficient of variations were 13.41% and 10.59%, respectively. Days of 50% flowering showed high heritability (66.51%) with genetic advance (8.88%) and genetic advance in percentage of mean (19.97). High heritability (89.02%) coupled with low genetic advance (4.853%) and high genetic advance in percentage of mean (250.41) was recorded in respect of yield/plant.

In *B. rapa* the phenotypic variance for days to 50% flowering (48.35) was slightly higher than the genotypic variance (43.385) which was supported by narrow difference between phenotypic (18.753%) and genotypic (17.766%) co-efficient of variation. Days of 50% flowering showed high heritability (89.729%) with genetic advance (16.471%) and genetic advance in percentage of mean (44.423). High heritability (49.16%) coupled with low genetic advance (2.19%) and high genetic advance in percentage of mean (44.72). High heritability (49.16%) was recorded in respect of yield/plant.

On the other hand in *B. juncea* the phenotypic variation for days to flowering (24.58) was slightly higher than the genotypic variance (14.89) and phenotypic (12.56%) and genotypic (9.77%) co-efficient of variation. The phenotypic variance (3.393) was higher than the genotypic variance (0.964) and narrow difference between phenotypic (33.30%) and genotypic (17.75%) co-efficient of variation for yield/plant. Days of 50% flowering showed high heritability (60.59%) with genetic advance (7.930%) and genetic advance in percentage of mean (20.084). High heritability (28.41%) coupled with low genetic advance (1.382%) and high genetic advance in percentage of mean (24.98) was recorded in respect of yield/plant.

Days to 50% flowering showed significant positive association with days to maturity (0.663), plant height (0.678), seed/siliqua (0.595), 1000 seed weight (0.438) and yield/plant (0.415). Yield/plant confirmed highly significant positive association with days to flowering (0.415),

plant height (0.570) and seed/siliqua (0.361) but insignificant association with days to maturity (0.123), primary branches/plant (0.27). Days to 50% flowering showed significant positive association with days to maturity (0.725), plant height (0.689) and siliqua/plant (0.383). Yield/plant confirmed highly significant positive association with days to flowering (0.395), plant height (0.610), seed/siliqua (0.396) siliqua/plant (0.679) and 1000 seed weight (0.320). Days to 50% flowering showed significant positive association with days to maturity (0.742) and plant height (0.362). Days to maturity confirmed highly significant positive association with days to maturity (0.742) and plant height (0.534) and primary branches/plant (0.391) and yield/plant but insignificant association with siliqua/plant (0.188). Yield/plant confirmed highly significant positive association with days to maturity (0.373) plant height (0.439) and primary branches/plant (0.466), length of siliqua (0.352), seed/siliqua (0.595), siliqua/plant (0.689) and 1000 seed weight (0.458). In *B. napus* Path analysis revealed that days to 50% flowering had positive direct effect (-0.245) on *B. juncea* yield/plant. Path analysis revealed that days to 50% flowering had positive direct effect (0.391) on *B. rapa* yield/plant.

Considering the situation of the present experiment, further studies in the following areas may be suggested:

- Such study is needed in different agro-ecological zones (AEZ) of Bangladesh for regional adaptability and other performance
- Wide crossing should be possible between different group and intra specific crossing should be possible between same group
- If we select the parents from cluster II & IV then maximum heterosis will be manifested





REFERENCES

- Abraham, V. (1994). Rate of out-crossing in Indian mustard, Brassica juncea. Cruciferae Newsl., 16: 69-70.
- Alam, M. S., Rahman, A. R. M. S. and Khair, A. B. M. A. (1985). Genetic variability and character association in groundnut (*Arachis hypogaea* L.). Bangladesh J. Agric., 10 (4): 9-16.
- Alam, M., Begum, D. and Khair, A. B. (1986). Study of genetic parameters and character interrelationship in groundnut. *Bangladesh J. Agric. Res.*, 10 (2): 111-117.
- Allard, R. W. (1960). Principles of Plant Breeding. John Willey and Sons, Inc, New York. p. 36.
- Anand, I. J. and Rawat, D. S. (1984). Genetic diversity, combining ability and heterosis in brown mustard. Indian J. Genet. 44 (2): 226-234.
- Andrahennadi, C. P., Weerasena, L. A. and Aberyratne, M. D. R. S. (1991). Evaluation of brown mustard germplasm in Srilanka. *Cruciferae News letter*. 14-15: 62-63.
- Ariyo, O. J. (1987). Multivariate analysis and choice of parents for hybridization in Okra. *Theor. Appl. Genet.*, **74** : 361-363.
- Ashana, A. N. and V. K. Pandey. (1980). Genetic divergence in linseed. Indian J. Gent., 40: 247-250.
- Azad, M. A. K. and Hamid, M. A. (2000). Genetic variability, character association and path analysis in groundnut (Arachis hypogaea L.) Thai J. Agric Sci., 33 (3-4): 153-157.
- Badignnavar, A. K., Kale, D. M. and Murty, G. S. S. (2002). Genetic variability and diversity in groundnut genotypes. *Plant Breeding*. 121: 4, 348-353.

- Balasch, S., Nuez, F. Palomares, G. and Cuartero. (1984). Multivariate analysis applied to tomato hybrid production. *Theor. Appl. Genet.*, 69: 39-45.
- Banerzee, H. T., Bhattacharjee, H. and Das, M. (1968). A note on the relationship between growth and yield of the yellow sarson var. Prain. Indian J. Agron., 13: 203-04.
- Baydar, H. and Bayraktar, N. (1994). Correlation and path coefficient analysis among quantitative characters on Virginia type peanut (Arachis hypogaea L.) cultivars. Ankara Universities Ziraat Fakiiltesi Yilligi. 44 (1/2): 59-64.
- BBS. (2005). Monthly Statistical Bulletin of the Bangladesh Bureau of Statistics (August). Administration and MIS Wing, Bangladesh Secretariat, Dhaka. p. 280.
- Behl, N. R., Rangopal, K., Ghetin, N. R. and Bhalodia, P. K. (1992). An analysis of correlation of principal agronomic characters in Virginia bunch peanut germplasm. Groundnut News. 5 (1): 4-5.
- Bengtsson, P. P., Basu, M. S. and Reddi, P. S. (1972). Genetic variability, character association and path coefficient of quantitative traits of groundnut. Indian J. Agric. 41 (2): 215-284.
- Bhardwaj, R. P. and Singh, R. R. (1969). Morphological and genetic variability in brown sarson (B. campestris var. Brown sarson). Madras Agric. J., 56 (1): 28-31.
- Bhatt, G. M. (1973). Significance of path co-efficient analysis determining the nature of character association. *Euphytica*, 22: 338-343.
- Biswas, K. P. (1989). Performance evaluation of 18 genotypes of oleriferous *Brassica*. Proceeding of the 14th Annual Bangladesh Sci., Conf., p. 70.
- Burton, G. W. (1952). Quantitative inheritance in grass pea. Proceedings of the 6th International Grassland Congress. 1: 277-283.

- Chandola, R. F., Dixit, P. K., Sharina, K. N. and Saxena, D. K. (1977). Variability in *B. juncea* under three environments. *Indian J. Agric. Sci.*, 47 (9): 680-683.
- Chandra, S. (1977). Comparison of Mahalanobis's method and meterglyph technique in the study of genetic divergence in *Linum usitatissimum*. L. germplasm collection. *Euphytica*. 26: 141-148.
- Chaturvedi, G. S., Singh, B. B. and Chauhan, Y. S. (1988). Physiological analysis of yield in Indian mustard under irrigated condition. *Indian J. of plant physiology*, **31** (1): 38-44.
- Chaudhari, L. B. and Prasad, B. (1968). Genetic variation and heritability of quantitative characters in Indian mustard. *Indian J. Agric. Sci.*, 38 (5): 820-825.
- Chaudhary, M. A. Z., Mai, M. F. U., Afzal, M. A. and Ali, M. M. (1990). Comparative study of D² and metrogylph analysis in groundnut. *Thai. J. Agric. Sci.*, **31**: 3, 436-443.
- Chauhan, J. and Singh, P. (1985). Association of some morphological determinates with seed yield in Toria (*B. campestris* L. var. Toria). Thesis Abstract, XI-I: 42-43.
- Chauhan, R. M., Kumar, A. and Shukla, P. T. (1985). Variability, heritability and genetic advance in bunch and spreading types of groundnut. *Indian J. Agric. Sci.*, 55 (2): 71-74.
- Chay, P. and Thurling, N. (1989). Identification of genus controlling pod length in spring rapeseed and their utilization for yield improvement. Plant Breeding, **103** (1): 5462.
- Chen, C., Hau, K. K., Liu, C. P. and Lin, M. S. (1983). Selection criteria for yield improvement in rape. Journal of the Agricultural association of China, 124: 63-73.
- Choudhary, B, R. and Joshi, P. (2001). Genetic diversity in advanced derivatives of *Brassica* interspecific hybrids. Kluwer Academic Publishers. the Netherlands. **121**: 1-7.

- Chowdhury, M. A., Miah, A. J., Rahman, L. and Rahman, A. (1987). Correlation and path coefficient analysis of nine important characters of Mustard (*Brassica juncea L. Czern and Coss.*). *Bangladesh J. Agric.*, 12 (3): 149-154.
- Comstock, K. and Robinson, P. R. (1952). Estimation of genetic advance. Indian J. Hill. 6 (2): 171-174.
- Dabholkar, A. R. 1992. Elements of Biometrical genetics. Concept publishing Company. New Delhi, India. 25 pp.
- Das, M. L. and Rahman, A. K. (1989). Character association and path analysis in improved groundnut varieties. Indian J. Agric. Sci. 56: 300-302.
- De, R. N., Seethara, R., Sinha, M. K. and Banarjee, S. P. (1988). Genetic divergence in rice. Indian J. Genet., 48: 189-194.
- Deshmukh, S. N., Basu, M. S. and Reddi, P. S. (1986). Genetic variability, character association and path coefficient of quantitative traits in Virginia bunch varieties of groundnut. *Indian* J. Agric. 56 (12): 816-821.
- Dewery, D. R. and Lu, K. H. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J. 51: 515-518.
- Dhillon, M. M. Deshmukh, D. D. and Dev, D. V. (1990). Association of physiological traits with productivity and regression analysis in groundnut (Arachis hypogaea L.). Annals Pl. Physiol. 7 (1): 123-125.
- Digby, P., N. Galway and P. Lane. (1989). Genstat 5, A Second Course. Oxford Science Publications, Oxford. pp. 103-108.

- Dorn, L. A. and Mitchell, T. (1991). Genetics of B. campestris. Genetic constraints on evolution of life history characters. Evolution, 45 (2): 371-379.
- Edris, K. M., Islam, A. T. M. T., Chowdhury, M. S. and Haque, A. K. M. M. (1979). Detailed Soil Survey of Bangladesh Agricultural University Farm, Mymensingh, Dept. Soil Survey, Govt. People's Republic of Bangladesh. 118 p.
- Ghosh, K. and Chatarzee, D. (1988). Variability studies in Spanish groundnut. Madras Agron. J. 82 (5): 395-397.
- Golakiya, P. R. and Makne, V. G. (1991). Genetic diversity in Spanish bunch groundnut. J. Maharastra Agric. Univ. 16 (3): 337-339.
- Gomez, K. A. and Gomez, A. A. (1984). Statistical Procedure for Agricultural Research (2nd edn.). Int. Rice Res. Inst., A Willey Int. Sci., Pub., pp. 28-192.
- Grosse, C. and Geisler, G. (1988). Variability in the physiological yield characteristics and assortment of water rape cultivars yield components. Milteilungen der pflangen baurissenschaften, 1: 67-69.
- Gupta, M. L., Labana, K. S. and Badwal, S. S. (1987). Correlation and path co-efficient of metric traits contributing towards oil yield in Indian mustard. In the International rapeseed congress, Poznan, Poland, 107.
- Gupta, S. K. and Labana, K. S. (1989). Triple test cross analysis for some physiomorphological traits in oil seed rape. Indian J. Genetics and Plant Breeding, 49 (3): 365-367.

Han, J. X. (1990). Genetic analysis of soil content in rape (B. napus). Oil crops of China, 2: 1-6.

- Hossain, K. G. (1988). Genetic variability and character association in groundnut. M. Sc. (Ag) Thesis. Department of Henetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh.
- Hossain, K. G. and Alam, M. S. (1989). Genetic variation and character association in groundnut (Arachis hypogaea L.). Bangladesh J. Pl. Breed. Genet. 2 (1): 27-30.
- Islam, M. S. and Islam, M. O. (2000). Genetic diversity in rapeseed and mustard (Brassica sp.). Bangladesh J. Plant Breeding and Genetics. 13 (2): 25-30.
- Islam, M. S. and Rasul, M. G. (1998). Genetic parameters, correlation and path coefficient analysis in groundnut (Arachis hypogaea L.). Bangladesh J. Sci. and Ind. Res., 33 (2): 250-254.
- Islam, M. S. and Rasul, M. G., Bhowmik, A. and Akbar, M. A. (1995). Genetic parameters, correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.). *Bangladesh J. Sci. and Ind. Res.* 38 (1): 211-284.
- Jain, A. K., Tiwari, A. S. and Kushwah, V. S. (1988). Genetics of quantitative traits in Indian mustard. Indian J. Genetics and Plant Breeding, 48 (2): 117-119.
- Jeger, M. I., D. G. Jones and E. Griffiths. (1983). Components of partial resistance of wheat seedlings to Septoria nodorum, Euphytica. 32: 575-584.
- Joel, A. J. and Mylsamy, V. 1998. (1998). Genetic divergence in groundnut. Madras Agril. J. 85 (2): 134-135.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.

- Johnson, K. F., Robinson, H. F. and Comstoc, R. E. (1995). Genotypic and phenotypic correlation in soybean and their implications in selection. Agron. J., 47 (10): 477-483.
- Kakroo, P. and Kumar, S. (1991). Genetic determination of seed yield through its components in Indian mustard. Thesis Abstract, XVII-I: 82.
- Katule, B. K., Patil, F. B. and Thombare, M. V. (1991). Genetic divergence in semi-spreading groundnut. J. Maharashtra Agric. Univ. 16 (3): 450.
- Khanna, K. R. and Chaudhary, R. C. (1974). The nature of gene action and combining ability for some vegetative characters in tomato. *Euphytica*. 23 : 159-165.
- Khera, M. K. and Singh, P. (1988). Sensitivity and performance of some *Brassica napus* genotypes in stress and non stress environments. Crop improvements, **15** (2): 209-211.
- Krug, H. and Liebig, H. P. (1989). Production planning main growth period (radish). Acta Horticulture. 248 : 181-186.
- Kudla, B. (1994). Estimation of variability and heritability for quantitative traits in groundnut. Sarad J. Agric. 14 (6): 575-579.
- Kudla, M. (1993). Comparative analysis of winter swede rape genotypes. Biuletyn Instytutu Hodowli Roslin, 190: 99-107.
- Kumar, C. H. M. V., Arunchalam, V. and Rao, P. S. K. (1996). Ideotype and relationship between morphological characters and yield in Indian mustard (*B. juncea*). Indian J. Agric. Sci., 66 (11): 14-17.
- Kumar, N., Bisht, J. K. and Josh, M. C. (1988). Correlation and discriminate function analysis in Indian mustard. *Indian J. Agric. Sci.*, 58 (1): 51-52.

- Kumar, P. and Yadava, T. P. (1982). Character association in bunch group of groundnut (Arachis hypogaea L.). Indian J. Agric Res. 16: 61-64.
- Kumar, P., Yadava, T. P. and Yadav A. K. (1991). Association of seed yield and its component traits in the F₂ generation of Indian mustard. *Indian J. Agril. Sci.*, 54 (7): 604-607.
- Kumar, R., Dhable, M. V. and Ranwar, B. B. (1984). Genetic variability and divergence analysis. SABRAO J. 10 (1): 1-4.
- Kumar, R., Ghosh, J. and Sah, J. N. (1998). Variability and correlation studies in mutant cultures of groundnut. J. Appl. Biol., 8 (2): 20-23.
- Kumar, V. and Singh, D. (1994). Genetics of yield and its components in Indian mustard (B. juncea L. Czern & Coss). Crop Research. 7 (2): 243-246.
- Kuriakose, K. P. and Joseph, C. A. (1986). Path analysis and selection index in groundnut. Agric, Res. J. Kerala. 24 (2): 111-117.
- Labana, K. S., Ahuja, K. L. and Banga, S. S. (1987). Evaluation of some ethiopian mustard (B. carinata) genotypes under Indian conditions. In 7th International rapeseed congress, poznan, Poland, 115.
- Labana, K. S., Chaurasia, B. D. and Singh, B. (1980). Genetic variability and inter-character associations in the mutants of Indian mustard. *Indian J. Agric. Sci.*, 50 (11): 803-806.
- Lebowitz, R. J. (1989). Image analysis measurements and repeatability estimates of siliqua morphological traits in *B. campestries. Euphytica*, 43 (1-2): 113-116.
- Lederle, E. (1989). Simulation of plant growth based on methods of plant growth analysis exemplary for radish. Acta Horticulture. 248 : 243-246.

- Li, J. N., Qiu, J. and Chen, L. (1990). Correlation analysis of the major yield and quality characters in oilseed rape (*B. napus*). Oil crops of China, 1: 11-16.
- Li, J. N., Qiu, J. and Tang, Z. L. (1989). Analysis of variability of some genetic parameters in segregation hybrid generations of *B. napus*. Hereditas Beijing, 11 (6): 4-7.
- Malik, A. R., Aki, I., Yoshie, M. Tohru, S. and Kenji, T. (1997). Phenotypic variation and the relationships among mustard germplasm from Pakistan. Kluwer Academic Publishers. Netherlands. 101 : 357-366.
- Malik, V., Singh, H. and Singh, D. (1995). Gene action of seed yield and other desirable characters in rapeseed. Annals of Biology (Ludhiana), 11 (1/2): 94-97.
- Mishra, L. K. and Yadav, R. K. (1992). Genetic variability and correlation studies in summer groundnut. Adv. Plant Sci., 5 (1): 106-110.
- Mishra, R. M., Kouth, G. K. and Bilaiya, S. K. (1987). D² and metrogylph analysis in soybean. J. Oilseeds Res. 4 (1): 103-107.
- Naidu, N. V. and Satanarayana, A. (1991). Studies on the genetic divergence over environments in Mungbean *Tigna radiata* (L) Wilczek. *Indian J. Genet.*, 51 (4): 454-460.
- Nanda, R., Bhargava, S. C. and Tomar, D. P. S. (1995). Rate and duration of siliqua and seed filling and their relation to seed yield in *Brassica* species. *Indian J. Agric. Sci.*, 64 (4): 227-232.
- Nazzar, A., Mallik, S. N., Khurram, B. and Mirza, M. Y. (2000). Genetic variability, heritability and correlation studies in groundnut. Sarhad J. Agric. 16 (5): 533-536.
- Oleagineux, 1983. Selection criteria for improving yield in groundnut (Arachis hypogaea L.). Indian J. Agric. 38 (11): 607-613.

Olsson, G. (1990). Rape yield production components. Sversk Frotidning, 59 (9): 194-197.

- Patil, F. B., Thombre, M. B. and Sindde. W. M. (1987). Genetic diversity in relation to geographic diversity in Maize. *Indian J. Agric. Sci.*, 58 (1): 4-6.
- Paul, N. K., Joarder, O. I. and Eunus, A. M. (1976). Genotypic and phenotypic variability and correlation studies in *B. juncea* L. Zeitschrift für pflazenzuchtung, 77 (2): 145-154.
- Prakash, B. G., Khanure, S. K. and Sajjanavar, G. M. (2000). Karnataka J. Agril. Sci. 13 (4): 988-990.
- Rakow, G. and Woods, D. L. (1987). Outcrossing in rape and mustard under Saskatchewan prairies conditions. Can. J. Plant Sci., 67: 147-151.
- Reddy, V. R. G., Singh, B. N. and Rai, B. (1987). Analysis of genetic divergence in spreading varieties of groundnut. Crop Impro. 14 (2): 149-152.
- Saini, R. and Kumar, T. (1995). Correlation and path analysis in F₃ and F₄ generation of intraspecific crosses in groundnut. *Madras Agric. J.* 75 (3): 95-98.
- Shabana, A. S. Sanjeev, K. and Aravind, K. (1990). Production potential of various Spanish and Virginia groundnut (Arachis hypogaea L.). Cultivars in mid-western plains of Uttar Prodesh. Indian J. Agril. Sci. 69 (7): 519-520.
- Sharma, S. K. (1984). Variation and correlation studies in Indian mustard (*B. juncea*). Thesis Abstract, **10** (2): 146-147.
- Shivahare, M. D., Singh, A. B., Chauhan, Y. S. (1975). Path co-efficient analysis of yield component in Indian mustard. Indian J. Agric. Sci., 45 (9): 422-425.

- Singh, P., Khera, M. K. and Gupta, V. P. (1991). Variability and correlation studies for oil and seed yield in gobhi sarson. Crop Improvement, 18 (2): 99-102.
- Singh, H., Yadav, A. K. and Yadava, T. P. (1989). Morphophysiological attributes in relation to seed yield in Indian mustard. *Haryana Agricultural University J. Res.*, 15 (3): 295-299.
- Singh R. P., Singh, D. P. and Chaudhury, B. D. (1987). Morphological variation in Indian mustard. Annals of Biology, 3 (1): 26-31.
- Singh, P. Sangha, A. S. and Sandhu, R. S. (1985). Genetic variability and correlation studies in groundnut (Arachis hypogaea). Crop improvement. 25 (1): 122-123.
- Singh, D. N., Sharma, V. K. and Varshney, S. K. (1978). Path action in groundnut rays in combined mutagensis of groundnut (*Arachis hypogaea* L.). *Annals Agril. Res.* 19 (1): 49-53.
- Singh, S. B. and Singh, J. P. (1999). Correlation analysis of growth and yield components in groundnut. J. Maharahtra Agric. Univ., 17 (2): 224-226.
- Singh, R. K. and Chaudhury, B. D. (1985). Biometrical Method in Quantitative Genetics Analysis (rev. ed.). Kalyain Publishers, New Delhi, India, pp. 78-85.
- Singh, B. D. (1993). Plant Breeding in Biometrical Techniques. In: Plant Breeding. Kaylani Publishers. pp. 100-125.
- Singh, H. (1986). Genetic variability, heritability and drought Indices analysis in Brassica species. J. Oilseed Res., 3 (2): 170-177.
- Singh, P. (1983). Studies on genetic variability and diversity of rice. Madras Agric. J., 70 (7): 436-440.



- Srivastava, P. P. Salara, B. S. and Gowda, M. V. C. (1983). Variability and correlation studies in groundnut (Arachis hypogaea). Crop Impro. 25 (1): 122-123.
- Tak, G. M. and Patnaik, M. C. (1977). Genetic variation and heritability on the 3 forms of B. campestris. Indian J. Agric. Res., 11 (2): 89-93.
- Thakral, N. K. (1982). To study the association of some morphophysiological attributes with yield of toria. Thesis Abstract, 8 (11): 66-67.
- Thurling, N. (1974). An evaluation of an index method of selection for high yield in turnip rape, B. campestris L spp. Euphytica, 23 (2): 321-331.
- Thurling, N. (1983). Variation in pod length in spring rape (B. napus) and its relationship to yield. In proceedings, Australian Plant Breeding conference, Adelaide, South Australia. pp. 14-18.
- Tomooka, N. (1991). Genetic diversity and landrace differentiation of mungbean, Vigna radiata (L.) Wilczek, and evaluation of its wild relatives (The subgenus Ceratotropics) as breeding materials. Tech. Bull. Trop. Res. Center, Japan No. 28. Ministry of Agr. Forestry and Fisheries, Japan. 1.
- Uddin, M. J. (1994). Genetic divergence in mustard. Bangladesh J. Plant Breeding and Genetics, 7 (2): 23-27.
- Uddin, M. J., Chowdhury, M. A. Z., Sultan, M. K. and Mitro, B. N. (1995). Genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.) *Bangladesh J. Sci. and Ind. Res.*, **30** (2-3): 235-241.
- UNDP. (1988). Land Resources Appraisal of Bangladesh for Agricultural Development. Report 2: Agro-ecological Regions of Bangladesh, FAO, Rome. pp. 212, 577.

- Varshney, M. A. (1986). Character association and path analysis in virginia runner groundnut (Arachis hypogaea L.). Madras Agril J. 79 (9): 500-504.
- Varshney, S. K., Rai, B. and B. Singh. (1986). Component analysis of harvest index in *Brassica* oilseeds. *Indian J. Agric. Res.*, 20 (3): 129-134.
- Venkatramana, P., Sheriff, R. A. and Janakiraman, N. (2001). Assessment of groundnut germplasm and isolation of elite genotypes for improvement. J. Soils and Crops. 11 (2): 156-160.
- Verma, O. P., Kushwaha, G. D. and Singh, H. P. (2000). Heterosis in relation to genetic diversity in Indian mustard. Cruciferae News., 2000 (22): 93-94.
- Wan, Y. L. and Hu, G. C. (1983). Studies on heritability, genetic correlations and genetic advances of the major characters in rape. Chinese oil crops. 1: 1-7.
- Whan, B. R., Carlton, G. P. and Anderson, W. K. (1991). Potential for increasing early vigour and total biomass in spring Wheat. Identification of genetic improvements. Aust. J. Agric. Res., 42: 347-361.
- Yadav, A. K. and Singh, H. (1988). Selection indices for seed yield in Indian mustard based on Physiological attributes. *Indian J. Genetics and Plant Breeding*, 48 (1): 103-106.
- Yadav, T. P., Kumar, P. and Thakral, S. K. (1982). Association of pod yield with some characters in groundnut. Haryana. Agric. Univ. J. Res. 14 (1): 75-88.
- Yadav, Y. P., Singh, H. and Singh, D. (1993). Gene action for seed yield and its attributes under two environments in Indian mustard. Crop Research, 6 (1): 168-172.
- Yadava, C. K. (1983). Studies on genetics of yield and its components in Indian mustard (Brassica juncea L, Czern & Coss). Thesis Abstract, 9 (2): 186-187.

- Yadava, N. (1975). Correlation coefficients and selection indices in brown sarson (Brassica campestris L.). Thesis Abstract, 8 (2): 184.
- Yadava, N., Kumar, P. R. and Behl, R. K. (1985). Genetic variability and selection indices in brown sarson. Cruciferae Newsletter, 10: 62-63.
- Yadava, T. P. (1973). Variability and correlation studies in B. juncea (L.) Czern and Coss. Madras Agric J., 60: 1508-1511.
- Yadava, T. P., Kumar, P., Thakral, S. K. and Yadava, A. K. (1989). Association of seed yield with different physiological traits in Indian mustard. In 4th International SABRAO congress, 1981 at Kebagsaan, Malaysia, 40.
- Yadava, T. P., Yadav, A. K. and Singh, H. (1978). A concept of "Plant Ideotype" in Indian mustard B. juncea (L.) Czern and Coss. 5th International Rapeseed Conf., June, 1978; 7.
- Yin, J. C. (1989). Analysis on Ecological, Physiological and Production characteristics of high quality rapeseed cultivars. Acta Agriculture Shanghai, 5 (4): 25-32.
- Yogendra, P., Verma, A. K., Haider, Z. A., Mahto, J., Prasad. Y. and Mahto, J. (2002). Variability studies in Spanish bunch groundnut. J. Res. 14 (1): 91-93.



APPENDIX

Appendix I.	Monthly average temperature, relative humidity and total rainfall of the
19.250	experimental site during the period from November 2005 to March 2006

Month	Air ten	perature (°C)	RH (%)	Total rainfall	Sunshine (hrs/day) 208,9	
	Maximum	Minimum	Mean	9 am	(mm)		
October 05	30.97	23.31	27.14	75.25	208		
November 05	29.45	18.63	24.04	69.52	00	233.2	
December 05	26.85	16.23	21.54	70.61	00	210.5	
January 06	24.52	13.86	19.19	68,46	04	194.1	
February	28.88	17.98	23.43	61.04	03	221.5	
March	29.55	18.25	23.90	61.51	24	225.4	

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