COMBINING ABILITY AND GENE ACTION FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN INDIAN MUSTARD (*Brassica juncea* L.)

BY

RAISUL HOQUE

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Approved by:

Azilani

(Dr. Md. Aziz Zilani Chowdhury)
Senior Scientific Officer
Oilseed Research Centre
Bangladesh Agricultural Research Institute
Joydebpur, Gazipur
Supervisor

(Dr. Md. Shahidur Rashid Bhuiyan)
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka -1207
Co-supervisor

Hossain

(Dr. Md. Sarowar Hossain)
Chairman
Examination committee

Oilseed Research Centre
Bangladesh Agricultural Research Institute
Joydebpur, Gazipur-1701

Phone : + 88 02 9252303
PABX : 9261501-5, 9252063,
9252091 Extn. 314
Fax : +88 02 9262713
E-mail : bariorc@dhaka.net

CERTIFICATE

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This is to certify that thesis entitled, **"COMBINING ABILITY AND GENE ACTION FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN INDIAN MUSTARD (*Brassica juncea* L.)"** submitted to the Faculty Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of *bona fide* research work carried out by **MR. RAISUL HOQUE** Registration No. **25254/00366** 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.

Azilani

Dated: 08.02.07
Gazipur, Bangladesh

Dr. Md. Aziz Zilani Chowdhury
Supervisor

Dedicated to
My
Beloved Parents,
Grand parents
&
Late Remu

SYMBOL AND ABBREVIATIONS

FULL WORD	ABBREVIATION
additive genetic effect	A
analysis of variance	ANOVA,
i) regression coefficient (Wr on Vr)	b
ii) dominance effect :-	
mean dominance	b_1
dominance due to array	b_2
residual dominance	b_3
Centimeter	cm
degrees of freedom	d.f
variation due to additive effect	D
expected environmental component of variation	E
the mean of fr values over the arrays	F
first generation offspring from the mating of two parents	F_1
component of variation due to the dominance effect of the genes	H_1
proportion of positive and negative genes in the parents	H_2
dominance effect	h^2
Narrow sense heritability	H^2n
general combining ability	gca
specific combining ability	sca
Gram	g
Hectare	ha
Kilogram	Kg
Metric ton	Mt
Relative humidity	Rh

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Dhaka, Bangladesh *The Author*

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ABSTRACT

A 8 x 8 diallel experiment (excluding reciprocal) on Indian mustard (*Brassica juncea* L.) was conducted to study the nature and magnitude of gene action and combining ability analysis and inheritance for seed yield and other related characters such as days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, 1000-seed weight, seed yield per plant, harvest index and oil content.

There were significant variations among the genotypes for all the characters studied. The components of variance for general combining ability (gca) and specific combining ability (sca) were highly significant for all traits indicating the role of both additive and non-additive components in the genetic system of these characters. The inheritance of secondary branches per plant, length of siliqua, siliquae per plant and seed yield per plant was controlled by non-additive type of gene action. The parental genotype DH-18 (P_1) and DH-11 (P_3) were the best general combiners for seed yield. The parents BARIsar-10 (P_2), Daulat (P_4) and Jun-536 (P_7) were desirable for earliness and dwarfness. Both parents BARIsar-10 (P_2) and BARIsar-11 (P_8) were found suitable for dwarf plant type and higher number of siliquae per plant. The yellow seeded parental genotype BJ-11 (P_6) was found to be the best general combiner for primary branches per plant, seeds per siliqua and oil content. The cross BARIsar-10 x BJ-11 (C_{11}) and DH-18 x BARIsar-10 (C_1) were the best specific combiners for early maturity and dwarfness. The cross DH-18 x Jun-536 (C_6), BARIsar-10 x BJ-17 (C_{10}) and BARIsar-10 x Daulat (C_9) were found best for seed yield per plant and siliquae per plant. Majority of the crosses showed high sca effects for seed yield involving high x low, low x low and high x high gca parents.

Vr-Wr analysis relating to graphical presentation of major genetic features was done for all the twelve characters. Over dominance was observed for primary branches per plant, secondary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, seed yield per plant and harvest index, While partial dominance was recorded for days to 50% flowering, days to maturity, plant height, 1000-seed weight and oil content.

Component of variation and various genetic parameters such as degree of dominance, dominance ratio, narrow sense heritability etc. were estimated. Results showed that positive and negative alleles were in unequal proportion among the parents for all characters. Dominant gene action was predominant in most of the traits except days to 50% flowering, plant height, secondary branches per plant, 1000-seed weight and harvest index. Dominance and recessive genes were unequally distributed in the parents for all characters. High narrow sense heritability was observed for days to maturity, plant height and 1000-seed weight.

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CHAPTER 1

INTRODUCTION

INTRODUCTION

Rape seed and mustard (*Brassica* spp L.) is an important edible oil crop of Bangladesh. Total oil seed crops cover 3.99 lakh hectare of land of Bangladesh and produce about 3.68 lakh Mt oil seeds. However, rape seed and mustard cover 2.97 lakh hectares of land and produce about 2.18 lakh Mt of oil seeds. At present its average yield is 850-900 kg/ha (BBS, 2004a).This crop covers about 74.5% area of the total edible oil crops cultivated in Bangladesh. Oil seed crop covers about 4.04% area of the total cultivable land in Bangladesh (BBS, 2004b).

Various groups of mustard are grown in Bangladesh. Oleiferous *Brassica* belongs to the genus *Brassica* of the family Brassiceae includes three major species viz. *B. campestris* L. (AA, 2n = 20), *B. juncea* Czern and Coss (AABB, 2n = 36) and *B. napus* L. (AACC, 2n = 38). Among the Oleiferous *Brassica* species the varieties of *B. campestris* and *B. napus* are commonly known as rape seed, while those of *B. nigra* (black mustard), *B. carinata* (Ethiopian mustard) and *B. juncea* (Indian mustard/Rai) as mustard (Yarnell, 1965).

Toria (*B. campestris*) is very familier in Bangladesh but comparatively low yielding. It is well fit into any cropping pattern because of its short duration. Rape seed (*B. napus*) is high yielding but it has some limitations like shattering which need to be eliminated before its acceptance to the farmers. This crop is also sensitive to high temperature during siliquae development stage. Indian mustard (*B. juncea*) has comparatively high yield potentiality. The yield of the varieties of Indian mustard (*B. juncea*) is stable when it is late planted. It can tolerate both drought and salinity to some extent. Indian mustard (*B. juncea*) is non shattering type and can grow in boron deficient soil but the duration of this crop is long.

Among the oil seed crops rape seed and mustard is the third highest source of edible oil supply in the world after soybean and palm (FAO 2000, Piazza and Foglia 2001, Walker and Booth 2001). About 13.2% of the world edible oil supply comes from this crop (Downey and Robbelen, 1989). In Bangladesh, rape seed and mustard is the top ranking oil seed crop.

Mustard oil plays a great role as a fat substitute in our daily diet. Fat and oil are vital components of the human diet because they are important sources of energy and act as a carrier of fat soluble vitamins. Low intake of fat and oil limit the availability of fat soluble vitamin and caused dietary imbalance and food wastage. For human health, in a balanced diet 20-25% of calories should come from fats and oils and the average need of fats and oils is about 37g/day (Rahman, 1981). According to the recommendation by Indian Council of Medical Research requirement of fats and oils is 39g/head per day.

Bangladesh is facing a huge shortage in edible oils. Now, Bangladesh requires 0.29 million tons of oil equivalent to 0.8 million tons of oil seeds for nourishing her people, but oil seed production is about 0.254 million ton, which covers only 40% of the domestic need (FAO, 2001). As a result, more than 60% of the requirement of oil and oil seed has been imported every year by spending huge amount of foreign currency involving over 2,500-3,000 crore taka.

The climatic and edaphic factors of Bangladesh are quite favorable for the cultivation of rape seed and mustard (Haque *et al.*, 1987). Although rape and mustard is the most important oil crop in Bangladesh, farmer usually cultivates them in less fertile lands followed by low management with least investment and almost all the cultivars are brown seeded and smaller in size (2-2.5g/1000 seed). Yellow seed contains 1-2% more oil than the same sized brown seeded type due to its thinner seed coat. Bold seeded Indian mustard varieties may increase total production of oil seed in Bangladesh. *Brassica juncea* L. covers about 25% area of the total mustard grown in Bangladesh (Wahhab *et al.*, 2001). High yielding late planting and early mature variety may increase 12-15% of total edible oil seed of Bangladesh when it replaces the local mustard varieties grown in the country. The above scenario indicates the requirement of major qualitative and agronomic modification of this crop. High yielding late planting and early maturity variety should be developed which could be fit into Mustard-Sesame-T. Aman cropping pattern.

The nature and magnitude of gene action is an important factor in developing an effective breeding programme. Among the various mating designs developed for the determination of the genetic architecture of quantitative characters, the diallel cross method, out lined by Jinks (1954, 1955) and Hayman (1954 and 1958) has received considerable attention of the geneticists and plant breeders. Considerable amount of gene action for seed yield and its components in rape seed have been reported by various workers (Duhoon *et al.*, 1980, Yadav and Yadava, 1985, Jindal and Labana, 1986, Singh *et al.*, 2001, Chowdhury *et al.*, 2004.)

The knowledge on the type of genetic variance present in the population is helpful in devising suitable breeding approach in the crop improvement programme. The analysis of combining ability is used to assess the parental genotypes and their crosses on the basis of genetic variation present in them. Varieties good in *per se* performance may not necessarily produce desirable progenies when used in hybridization. Knowledge about the combining ability is, therefore, important in selecting suitable parents for hybridization, proper understanding of inheritance of quantitative traits and also in identifying the promising crosses for further use in breeding programme. About 11 to 82 per cent standard yield heterosis has been reported in F_1 hybrids produced by hybridization in *Brassica juncea* L. (Rai, 1995). Considerable amount of heterosis for seed yield and its components in F_1 hybrids of rapeseed have been reported by various workers (Patnaik and Murty, 1978; Verma *et al.*, 1989). In respect of observation on combining ability in Indian mustard, many workers have found different values of gca, sca and reciprocal effects in parents and hybrids (Katiyar *et al.*, 2000, Verma, 2000, Basudeb and Singh, 2001, Yogeshwar and Sachan, 2003, Acharya and Swain, 2004.) for different characters. Such information almost clearly indicates that the genetic variation is the single most important issue and helps to choose a good parent, good combination and to know the effects. Very little work has, however been done to understand the nature of gene action and the inheritance of yield and yield components in Indian mustard under Bangladesh condition. Selection of the best parents for production of F_1 hybrids has to be based on genetic information and knowledge of combining ability. Therefore, the present work was undertaken with the following objectives:

1. To estimate the nature and extent of combining ability of the parents in crosses and the mode of gene action in governing the characters.
2. To incorporate earliness, yellow and bold seed and other yield contributing traits in recommended varieties of late higher yielding genotype of *Brassica juncea* L.
3. To study the feasibility of exploiting hybrid vigour in Indian mustard.

CHAPTER 2

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Indian mustard (*Brassica juncea* L.) is an important oil seed crop of tropical and sub-tropical agriculture, as it provides available nutrition to human. In Bangladesh the average productivity of mustard is low in comparison to the developed countries. Identification of superior parents, promising cross combination and suitable breeding methodology are the important pre-requisites for development of high yielding genotypes. The combining ability studies are frequently utilized to understand gene effects of yield and yield attributes which helps in formulating proper breeding methodology. The nature and magnitude of gene action is an important factor in developing an efficient breeding programme. It also finds out the breeding potential of parents as well as different cross combinations which helps in the advancement of breeding programme. The diallel analysis provides information of the genetic control of a set of parents in the early generation (Jinks, 1954). Therefore, relevant information available in the literature pertaining to the combining ability and gene action of rapeseed and mustard are reviewed in this section.

2.1 Combining ability

General combining ability is the average performance of a given genotype in hybrid combinations with other genotypes, while the specific combining ability is expressed through average performance of the cross in relation to the genotypes.

Griffing (1956a) proposed a more general procedure for diallel analysis which makes provision for non-allelic interaction. In this approach mean measurement of a cross is partitioned into two major components, a part from a general mean (μ) and an environmental component, (i) the contribution of the parents, the general combining ability (gca) effect analogous to main effect of a factorial designs, and (ii) the excess over and above the sum of the two gca effects called the specific combining ability (sca) effect, analogous to an interaction effect of a factorial design. The diallel approach has been extensively used in cross pollinated crops. Griffing (1958) emphasized the statistical concepts of general and specific combining ability. Variance for general combining ability involves mostly additive gene effects which variance for specific combining ability depends on dominance and epistatic component of variation.

Trivedi and Mukharjee (1986) reported that non additive component in Indian mustard *Brassica juncea* L. is important for all the traits studied except for oil content and days to maturity, for which non additive and additive components were important. Dominance deviation for oil yield, seed yield, 1000 seed weight, seeds per siliqua and days to maturity was due to asymmetrical proportion of genes with positive and negative effects at the loci showing the highest dominance for oil content. The expression of oil content, 1000 seed weight and days to maturity was governed by frequency of dominant alleles where as recessive alleles were preponderant for other traits.

Badwal and Labana (1987) working on seed yield per plant and 8 related traits from a 10 x 10 half diallel cross in *Brassica juncea* L.. They observed that both additive and non additive components of variance controlled the inheritance of seed yield, number of seeds per siliqua, plant height, primary branches and length of siliqua. Only non additive variance was significant for secondary branches.

Gupta *et al.* (1987a) studied combining ability of *Brassica juncea* L. genotype with 8 x 8 diallel cross without reciprocal cross, gca and sca mean squares were significant for all characters studied. Non additive gene effects appeared to be predominant for number of primary and secondary branches, siliqua length, number of seeds per siliqua and seed yield. While additive gene effects were apparently predominant for plant height. Parents with high gca were found the best general combiner for seed yield and the best crosses for future selection were high x high gca parents.

Gupta *et al.* (1987b) performed on analysis in a 13 x 4, line x tester cross in *Brassica juncea* L. Additive gene effects were relatively more important than non additive for seed yield per plant and most of the yield components investigated.

Prakash *et al.* (1987a) evaluated analyzed data of the F_2 of an eight parent diallel cross and showed that gca and sca variances were significant for yield components. sca variance were higher than gca variance for number of seeds per siliqua, 1000 seed weight and seed yield indicating that dominance was possibly the predominant gene action for these traits. The parents DIR 146 and RCL 1017 were good general combiners for most of the characters studied.

Prakash, *et al.* (1987b) observed 8 varieties with their 28 F_2s. the component of variance indicated the importance of additive and dominance components for the character studied.

Rawat (1987) observed 12 females and 5 males line of *Brassica juncea* L. of diverse origin with a line x tester analysis. Variance components of gca and sca were significant for days to 50% flowering, number of primary branch, plant height, seed weight and seed yield per plant. The crosses showed high sca effects for seed yield involving high x low gca parents.

Singh and Chauhan (1987) worked with 60 triple test cross families produced by the crossing of 20 F_2 parents as males to the parents and F_1s. In Varuna x TM 9. additive genetic variance appeard to be predominant for days to maturity, number of primary branch while dominance seemed to be mainly involved in the control of seed yield per plant. In Varuna x RW 75-80-1, additive genetic variance was estimated to be predominant for plant height and dominant for days to maturity, number of seeds per siliqua, 1000 seed weight and yield per plant.

Singh *et al.* (1989) evaluated six *Brassica junceal* L. parents and their resultant 15 F_1 and F_2 population. Significant gca and sca variances were observed for all the 11 characters studied. Majority of the crosses showed high sca effects for seed yield involving low x high gca parents.

Verma *et al.* (1989) evaluated the nature and magnitude of combining ability and heterosis in a set of 7 x 7 diallel crosses (excluding reciprocals) of yellow sarson for yield, yield components and oil content. Predominance of additive gene action was observed for yield, primary and secondary branches per plant, siliquae on main shoot, 1000 seed weight and oil content, while it was non additive for siliquae per plant.

Wani and Srivastava (1989) studied combining ability in seven characters for 23 lines of *Brassica juncea* L. and their F_1 and F_2 hybrids and found that parents with high gca were good general combiners for seed yield.

Siddiqe *et al.* (1990) studied a complete diallel cross involving four genotypes of *Brassica campestris* L.and their F_1s for nine characters including seed yield per plant. Both additive and non additive gene action was found in the inheritance of characters except days to flower, plant height and primary branches. Preponderance of additive gene action for days to maturity, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua and non additive gene action for days to flowering, plant height, number of primary branches, length of siliqua were found.

Yadav *et al.* (1992) evaluated 45 F_1 hybrids of Indian mustard together with 10 parents for combining ability with respect to seed yield and its component characters. High gca parents were identified as good combiners for seed yield, early ness, siliqua length, number of seeds per siliqua and 1000 seed weight. Majority of the crosses showed high sca effects for seed yield involving either high x low or low x low general combiners.

Habetinek (1993) worked with *Brassica napus* L. and found higher gca effects than sca for all characters except seed yield per plant. The genotype of Darmor had the highest gca for number of seeds per siliqua, siliqua length and 1000 seed weight, while Sonata had the highest gca for oil content. Sca for seed yield per plant was highest in crosses of high x low gca parents.

Singh *et al.* (1996) worked with combining ability analysis of eight diverse cultivars for ten characters in *Brassica juncea* (L.). They reported high magnitude of σ^2s for most of the characters. However, σ^2g was high only for plant height, siliqua length and 1000-seed weight for which high estimates of $\hat{h}^2$ was also recorded. The parent with high gca effects was best general combiners for seed yield, oil content, 1000-seed weight, plant height, number of primary branches and length of siliqua. Glossy mutant, an early white flowered parent, showed desirable gca for early flowering, reduced plant height and it was involved in crosses with high sca for seed yield, oil content and seeds per siliqua but its per se performance and gca was low. Oil content was positively associated with 1000-seed weight and seed yield indicating the possibility of simultaneous improvement for these characters. Yellow colour of corolla was dominant over white and segregated in 15:1 ratio, indicating control of duplicate genes.

In a study of 8 x 8 diallel analysis (excluding reciprocals), Yadav and Yadava (1996) reported that the presence of both additive and dominance genetic components for seed yield and yield components in Toria (*Brassica campestris* L. var. Toria). But the magnitude of dominance component was larger than the additive component for all the traits including seed yield. Heritability estimates were higher for days to maturity and 1000 seed weight.

Thakur and Sagwal (1997) evaluated combining ability analysis in nine parent diallel analysis of *Brassica napus*. They reported that mean squares due to general and specific combining ability were significant, suggesting the importance of both additive and dominance components. Parents GSL, 8809, HPN-1, GSL 1501 and HNS 8803 were good combiners for seed yield and some of its components and oil content. Estimates of heterosis over better parent (BP) for various traits indicated significant magnitude for seed yield (-14.8 to 82.8%), primary branches (-26.0 to 193.6%) and siliquae per plant (-21.9 to 162.6%). Unidirectional dominance was observed for the most of the traits studied. The cross GSB 7027 x HNS 8803 gave highest positive heterosis for seed yield per plant.

Varshney and Rao (1997) evaluated combining ability, heterosis and inbreeding depression in yellow sarson for 11 quantitative characters. Non additive genetic variance was preponderant for all characters in both F_1 and F_2 generations except for 1000-seed weight in F_2 generation. For seven characters, the best F_2s on the basis of sca involves one parent with high gca effects and the other with poor or average gca effects. The hybrids which exhibited highest heterosis also showed higher inbreeding depression.

Sheikh and Singh (1998) observed combining ability analysis, including reciprocals in Indian mustard for ten characters is preponderance of non additive gene action for most of the characters including seed yield and oil content in 10 x 10 half-diallel. Additive genetic variance was more important for plant height and length of siliqua for which high estimate of heritability was also observed. Majority of the crosses showed high sca effects for seed yield involved high x low gca parents.

Singh *et al.* (1999) studied the combining ability in *Brassica campestris* L. Comparison of sca effects in relation to gca effects of the respective parental lines indicated that crosses with high sca effects involved low x high, high x low and low x low general combiners.

Singh *et al.* (2000) worked with genetic analysis in yellow sarson, *Brassica campestris.* They found significant differences for both sca and gca among the genotypes for all the characters indicating there by that both additive and non additive components were involving in the expression of all the traits. The parents with high gca was showed good general combining ability for seed yield, days to maturity and siliquae per plant in both F_1 and F_2 generation and for primary and secondary branches per plant in F_2 generation only. The cross with high x low gca effects showed significant sca for seed yields.

Mahto and Haider (2001) worked with the magnitude of specific combining ability (sca) effects was much higher than the general combining ability (gca) effects for all the characters studied, except for number of secondary branches per plant. In most of the cases, the crosses showing high sca effects also exhibited high heterosis.

Sarkar and Singh (2001) evaluated ten *Brassica juncea* L. parents and their 45 F_1 population. gca and sca variance were significantly different among parents and crosses for all the characters except for early vigor. The parents with high gca effects was showed good general combining ability for plant height, number of primary and secondary branch, siliquae per plant and seeds per plant. Comparison of sca effects in relation to gca effects of respective parental lines indicated that crosses with high sca effects involved high x low general combiners for yield and seeds per siliqua.

Singh *et al.* (2001) worked with a partial diallel analysis (S=7) involving 20 parents was studied in F_1 and F_2 generations in yellow sarson. The variances for general and specific combining ability were highly significant in both generations. The estimated components of variance revealed that additive gene action was more important for days to flowering, days to maturity and plant height in both generations. Primary branches per plant, secondary branches per plant, siliqua length and siliquae per plant showed additive gene action in F_1 but non additive in F_2. Non additive gene action played a major role in genetic variation for seeds per siliqua and seed yield per plant in both the generations. Parental performances as judged by gca effects indicate that AJL 4, AJL 18, AJL 19, AJL 20, AJL 55, AJL 43 and YID 1 were promising genotypes. These genotypes may be used as potential source in hybridization programme.

In a line x tester analysis involving 29 promising female and seven male parents Indian mustard Ghosh *et al.* (2002) observed high heterosis for seed yield and some of the yield contributing traits. For most the major characters including seed yield both additive and non additive gene action were of prime importance.

Prasad *et al.* (2002) evaluated combining ability of 21F_1 hybrids derived from a diallel cross of seven Indian cultivars along with the parents in a field experiment. The general and specific combining ability were significant for all the traits examined. The cultivar Varuna recorded high general combining ability for most of the characters and *per se* performance. The specific combining ability for early maturity, length of main raceme and yield per plant were observed in the crosses involving high x low gca parents.

Swarnker *et al.* (2002) analyzed combining ability using 36 F_1 hybrids and their parents obtained from a diallel mating for 11 characters. Both the general and specific combining ability variances were highly significant for almost all the traits. Out of 36 crosses, only eight had desirable specific combining ability effects for seed yield.

Achrya and Swain (2004) observed combining ability analysis in 9 x 9 half-diallel set of *Brassica juncea* L. They studied for nine traits revealed the preponderance of additive gene effects for seed yield, secondary branches per plant, siliquae on main stem, siliqua length, seeds per siliqua and 1000 seed weight. Pusa Bahar was best general combiner for seed yield and yield components except days to maturity. Majority of crosses showing high *per se* performance involving parents of high x high or high x low gca effects. Pusa Bold x Pusa Bahar, BM-20-12-3 x JC 26 and Pusa Bahar x JC 26 were promising cross combinations which exhibited high sca effects and high mean performance.

Chowdhury *et al.* (2004a) studied the nature and magnitude of combining ability of parents and crosses (F_1s) were estimated in a 7 x 7 diallel cross analysis in turnip rape for seed yield, its different contributing characters and oil content. Higher magnitudes of gca variances were observed than those of sca variances for all the characters except siliquae per plant, seeds per siliqua and seed yield per plant. Majority of the crosses showed high sca effects for seed yield involving high x low, average x average and average x low gca parents.

2.2 Gene action

Gene action refers to the behaviour of mode of expression of genes in a genetic population. Knowledge of gene action helps in the selection of parents for use in hybridization programmes and also in the choice of appropriate breeding procedures for the genetic improvement of various quantitative characters. Hence insight into the nature of gene action involved in the expression of various quantitative characters in essential to a plant breeder for starting a judicious breeding programme.

Hayman's (1954) graphical and numerical approach to diallel analysis provides information on several valuable aspects of the genetic make up of a quantitative character, such as the adequacy of additive-dominance model, average degree of dominance involved in the action of genes, preponderance of dominant and recessive genes among the parental lines, symmetrical or asymmetrical distribution of genes with positive and negative effects on the attribute, etc. A part from measuring additive and dominance components of variation appropriate model can be used to detect, non-allelic gene interactions by using graphical representation (Vr-Wr) graphs. Hayman (1957) attempted to obtain estimates of certain genetic parameters from statistics involving parents and offspring.

Jindal and Labana (1986) reported epistasis for the inheritance of oil content, mineral content and protein content in Indian mustard. Re-analysis of data after removing certain array points revealed the predominance of additive genetic effects for oil and mineral contents, where as non additive effects were found to be important for protein content. The degree of dominance was partial, but graphical analysis revealed over-dominance for mineral content, a possible effect of confounding with complementary epistasis. Asymmetry of plus and minus genes was indicated for loci showing dominance. Since both additive and non additive effects seemed to be important, they could be exploited to the production of F_1 hybrids or used for population improvement.

Trivedi and Mukharjee (1986) observed the attributes for oil yield of 45 F_1 hybrids and their parents of a 10 x 10 diallel analysis of Indian mustard. They found non additive component to be important for all traits except for oil content and days to maturity for which both non additive and additive components were important. Dominance deviation for oil yield, seed yield, 1000-seed weight, seeds per siliqua and days to maturity was due to asymmetrical proportion of genes with positive and negative effects at the loci showing dominance, which was highest for oil content. The expression of oil content, 1000-seed weight and days to maturity was governed by frequency of dominant alleles, where as recessive alleles were preponderant for other traits.

Yadav and Yadava (1996) worked with 8 x 8 diallel analysis, it was found that both additive and dominance genetic components were important for seed yield components in toria (*Brassica campestris* L. var. Toria). But the magnitude of dominance component was larger than the additive component for all the traits. Heritability estimates were higher for days to maturity and 1000-seed weight. Parent Sangam was the best general combiner for seed yield, primary and secondary branches per plant, siliquae per plant and seeds per siliqua. Another parent T-9 was also found good combiner for seed yield, early ness, 1000-seed weight and seeds per siliqua.

Chowdhury *et al.* (2004b) evaluated a study of the attributes for seed yield of 21 F_1s and their parents in 7 x 7 diallel (excluding reciprocals) of *Brassica rapa*, showed importance of both additive and dominance components. Dominant gene actions were predominant in most of the traits except days to flower, plant height and 1000-seed weight. Highest heritability (89 percent) was observed for days to maturity. The asymmetrical distribution of the positive and negative alleles at all loci was found for most of the characters. The Vr-Wr graphs exhibited dominance effect of genes for all the characters. Plant height was controlled by complete dominant gene actions while primary branches per plant, siliquae per plant, seeds per siliqua, seed yield per plant and oil content were controlled by over dominant gene actions. The graphical analysis indicated wide genetic diversity among the parents.

CHAPTER 3

MATERIALS AND METHODS

MATERIALS AND METHODS

3.1 Experimental site and duration

The experiment was conducted at the experimental farm of Oil Seed Research Center (ORC), Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur, Bangladesh, during November 2005 to March 2006. The land was of medium high and sandy loam soil texture. The site was situated in the subtropical climatic zone, wet summer and dry winter is the general climatic feature of this region. The rainfall at the beginning of the experimental period was very high. Temperature was initially high. During the rabi season the rainfall generally is scant and temperature moderate with short day length.

3.2 Plant materials

Eight diverse genotypes of mustard namely DH-18, BARIsar-10, DH-11, Daulat, BJ-17, BJ-11, Jun-536 and BARIsar-11 were selected as parents based on their performance evaluated in the previous experiments. Code number of parents used in describing results is P_1, P_2, P_3, P_4, P_5, P_6, P_7 and P_8 for DH-18, BARIsar-10, DH-11, Daulat, BJ-17, BJ-11, Jun-536 and BARIsar-11, respectively. The seeds of 28 F_1s obtained from eight parents crossed in all possible combinations excluding reciprocals were the materials of the experiment. Source or place of collection of these materials is shown in Table 1.

3.3 Experimental design and layout

Twenty eight F_1s along with their eight parents were grown on November 16, 2005. The seeds were sown continuously in a randomized block design with 3 replications. Each F_1 line and their parents comprised of single rows of 2.5m long with a spacing of 40 cm between rows and 10 cm between plants. The genotypes were

Table 1: Sources or places of collection of eight Indian mustard genotypes with some important characters

Parent	Origin	Characteristics					
		Seed color	Seed size	Maturity (days)	Siliquae / plant	1000-seed weight(g)	Oil content (%)
DH-18	Netherland	Brown	Bold	115-120	190-235	4.5-5.0	42-43
BARIsar-10	Bangladesh	Brown	Medium	85-95	140-195	3.0-3.2	40-41
DH-11	Netherland	Brown	Bold	115-120	200-240	4.5-5.0	42-43
Daulat	Bangladesh	Brown	Small	95-100	150-200	2.50-3.0	40-42
BJ-17	Bangladesh	Yellow	Small	95-100	140-190	2.50-3.0	41-42
BJ-11	Bangladesh	Yellow	Small	95-100	180-220	2.50-3.0	41-42
Jun-536	Bangladesh	Brown	Medium	95-105	140-190	3.50-4.0	41-42
BARIsar-11	Bangladesh	Brown	Bold	95-105	170-210	3.50-4.0	41-42

randomly distributed to each row within the blocks in the replication. The seedling emerged three to four days after sowing. Plant spacing within the rows was maintained by thinning after 15 days of seedling emergence.

3.4 Land preparation and fertilizer application

The experimental plots were prepared with tractor ploughing followed by harrowing and laddering to bring to the desired tilth. Chemical fertilizers were applied at the rate of 250-170-85-150-10 kg/ha of N-P-K-S-B from Urea, Triple super phosphate (TSP), Muriate of potash (MP), Gypsum and Boric acid, respectively. Cowdung was applied at the rate of 10 ton per ha. Cowdung, 50% Urea and whole amount of TSP, MP, Gypsum and Boric acid were applied during final land preparation. The remaining 50% Urea was applied as top dressing during flower initiation stage.

3.5 Seed sowing

Sowing of seeds was done in the dry soil. Seeds of each genotype were sown in single row on November 16, 2005 by hand uniformly. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.6 Irrigation and drainage

One post sowing irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental field during the growing period.

3.7 Intercultural operation, insect and disease control

Necessary intercultural operations were done during the crop period to ensure normal growth and development of the plants. Thinning of seedlings was done during first weeding after 10 days of germination. The second weeding was done before flowering followed by top dressing of urea. Aphid infestations were found in the crop during the siliquae development stage. To control aphids Diazinon 60 EC at the rate of 1ml per liter was applied. No remarkable disease attack was observed.

3.8 Crop harvesting

The plants of individual block were harvested when 80% of the plants showed symptoms of maturity (straw color of leaves, stem and desirable seed color in the matured siliquae). Ten randomly selected matured plants from each line were cut at the base with the help of sickle and kept separately to avoid seed mixture between lines. Data were collected from these ten plants.

3.9 Data collection

Observations were made on the following quantitative characters:

1. Days to 50% flowering: When more than 50 percent plants had at least one open flower.

2. Days to maturity: Number of days required from sowing to siliquae maturity of 80% plants of each row.

3. Plant height in cm: Mean height in cm measured from top of the soil to the top of the main stem.

4. Number of primary branches per plant: Mean number of branches originated from the main stem from ten randomly selected plants from each F_1's and parents at maturity.

5. Number of secondary branches per plant: Mean number of branches originated from the primary branch from ten randomly selected plants from each F_1's and parents at maturity.

6. Siliquae per plant: Mean number of siliquae obtained from ten randomly selected plants from each F_1's and parents at maturity.

7. Length of siliqua in cm: Mean length of pod in cm measured from bottom of the stalk to the top of the pod.

8. Seeds per siliqua: Mean number of seeds counted from ten randomly selected siliquae.

9. 1000-seed weight (g): Weight in grams of 1000-seed was recorded from ten randomly selected plants of each F_1's and parents.

10. Seed yield per plant (g): Mean seed weight in grams of ten randomly selected plants from each F_1's and parents after harvest.

11. Oil content: Percentage of oil in the seed sample was determined by extracting the oil with petroleum ether at 40-60°C in a soxhelt's extraction apparatus. A random seed sample of approximately 40 g was taken from the bulk yield of each of the line. The seeds of individual genotype were grand to a fine powder in a porcelain mortar and pestle. The powder was then transferred into a Whatman's filter paper. The mortar and pestle were washed with petroleum ether to collect the traces of oil and powder sticking to them and the solution was transferred to the thimble in the socket. Approximately 125 ml of petroleum ether was taken into the distillation flask and the extraction set was fixed on an electrical water bath. Ten extraction sets were used so as to extract oil from the sample simultaneously for 5.5 hours. The distillation flask was later separated and the petroleum ether was distilled off. Last traces of it were removed by suction pressure. The extract or oil remain in the flask was accurately weighed and the percentage of extract in seed material was calculated.

12. Harvest index: Mean of ratio of seed weight (g) to the total plant weight (g) obtained from ten randomly selected plants of each F_1's and parents after harvest expressed in percentage.

3.10 Statistical analysis

All the observations reordered were subjected to Analysis of variance (ANOVA). The total variances of each character were partitioned into block, genotype and error differences. The genotypic variances were also partitioned into parent, F_1 and parent x F_1 variances. The differences within the classes of effects were tested by F-test.

Combining ability analysis of the traits with significant genotypic differences was done according to the Model 1 and Method 2 of Griffing (1956a and 1956b). This analysis partitioned the variation due to genotypic differences into general combining ability (gca) and specific combining ability (sca) effects.

The mathematical model used in the analysis was as follows:

$$Yij = m + gi + Sij + \frac{1}{bc} \Sigma\Sigma\, eijKl$$

Where,

Yij = mean of i x jth genotype over k and l.

i,j = 1,.....p k = 1,.....b l = 1,.....c

m = population mean.

gi = gca effects of the ith parent.

gj = gca effects of the jth parent.

Sij = sca effects for the cross between ith and jth parent.

eijkl = environmental effects.

$\frac{1}{bc} \Sigma\Sigma\, eijkl$ = mean error effect.

The variance components due to gca and sca were calculated according to Singh and Choudhary (1995) as follows:

3.10.1 gca and sca variances

a. Components due to gca

$$\text{gca variance} = \frac{1}{(n-1)} \sum_i gi^2 = \frac{(MSg - Mse)}{(n+2)}$$

b. Components due to sca

$$\text{sca variance} = \frac{2}{n(n-1)ij} \text{ Sij}^2 = \text{MSs} - \text{Mse}$$

$$\text{The ratio of gca variance to sca variance} = \frac{gca\ \text{var}\ iance}{sca\ \text{var}\ iance}$$

3.10.2 gca and sca effects

The gca and sca effects were estimated according to Sharma (1998) by the following formulae:

$$\text{gca effects (gi)} = \frac{1}{n+2} \sum[(Yi. + Yii) - \frac{2}{n} (\text{Y..})] \qquad \text{Restricted to } \sum_i^n gi = 0$$

$$\text{sca effects (Sij)} = \text{Yij} - \frac{1}{n+2}[\text{Yi.+Yii+Yj.+Yjj}] + \frac{2}{(n+1)(n+2)}[\text{Yii}]\ (\text{i} < \text{j})$$

3.10.3 gca and sca variances associated with the parents

gca and sca variances associated with the parent were estimated according to Sharma (1998) as follows:

$$\sigma^2\text{gi} = (\text{gi})^2 - [\frac{n-1}{n(n-1)}]\ \text{Mse}$$

$$\sigma^2\ \text{si} = \frac{1}{n-2}\ [\sum_j^n Sij^2] - [\frac{n-3}{n-2}\ \text{Mse}]$$

3.11 Graphical diallel analysis

Diallel analysis for the components of genetic variances and Wr-Vr graphs for all the characters studied were done according to Hayman (1954a,b). A diallel table was prepared from the averages over all the three replications and the following statistics were estimated.

Vr = Variance of all the progenies in each parental array (an array is a group of crosses involving a particular parents)

Wr = Covariance between parents and their offspring in each array

V_{0L0} = Variance of parents

V_{0L1} = Variance of the means of array

Wr^2 = The Wr for constructing the limiting parabola

bwr.vr = Regression of Wr on Vr

a = the Y- intercept

V_1L_1 = Mean of all the Vr values

W_{0L01} = Mean of all the Wr values

Yr' = Standardized mean for each parent

$(Wr + Vr)'$ = Standardized (Wr + Vr) values for each parent

$ry_{r\text{-}(Wr+Vr)}$ = Correlation between parental order of dominance

$(M_{L1} - M_{L0})^2$ = Dominance relationship

r^2 = Possible limit of selection of parents showing dominance

The validity of Hayman's hypothesis was tested for all the characters studied by the equations.

3. 11.1 Test of homogeneity of Wr-Vr variances

$$t^2 = \frac{n-2}{4}\left[\frac{(VarVr - VarWr)2}{(VarVrXVarWr) - Cov2(Vr,Wr)}\right]$$

Where,

Var Vr = Variance of the array variance

Var Wr = Variance of the parent and array covariance

Cov (Vr, Wr) = covariance of the variance and covariance

n = Number of parents involved in the diallel crosses

t = equivalent to a F-test with 4 and (n-2) degrees of freedom

3.11.2 Test of deviation of regression slope from unity

i. Deviation from 0

$t_1 = (b-0)/SE_b$ (at n-2 df)

ii. Deviation from unity

$t_2 = (1-b)/SE_b$ (at n-2 df)

Where,

b = regression co-efficient of Wr on Vr

SE_b = standard error

3.12 Numerical diallel analysis

After testing the validity of hypothesis that epistasis was absent, graphical analysis was performed followed by the determination of genetic variance components (additive and dominance variances) together with allied parameters.

3.12.1 Computation of variance components in F_1 diallel

Using the values of different statistics computed earlier the variance components and allied parameters were calculated according to Sharma (1998) as follows:

Variance components	Formulae
D (additive variance)	$V_{OLO} - E$
F (Mean co-variance of additive and dominance)	$2v_{OLO}-4W_{OLOI} -2(n-2). (E/n)$
H_1 (Dominance variance)	$V_{OLO} + 4V_{ILI} - 4W_{OLOI} - (3n-2). (E/n)$
H_2 (Proportion of positive or negative genes)	$4V_{ILI} - 4V_{OLO} - 2E$
h^2 (Dominance effects)	$4(M_{LI} - M_{LO})^2 - 4(n-1). (E/n^2)$
E (Environmental variance)	$1/r[Rss + ESS]/[(r-1)+(c-1)(r-1)]$

Where,

n = Number of parents

r = Number of replications

V_{OLO} = Variance of parents

V_{OLI} = Variance of array means

W_{OLOI} = Average Wr

V_{ILI} = average Vr

$(M_{LI} - M_{LO})^2$ = 1/n [(Grand total/n) – Parental total]

3.12.2 Computation of standard error (SE) and t values for each of the main components

SE was calculated to test the significance that is the accuracy of the above components according to Sharma (1998) by the following formula :

Standard error (SE) = $(Cs^2/n)^{0.5}$

Where,

$s^2 = 1/2[\text{MSS } (Vr-Wr)]$, n = Number of parents and

C = Multiplier of each of the main component

Main components	Multipliers	t-values
D	$C(D) = (n^5 + n^4)/n^4$	$T(D) = D/SE(D)$
F	$C(F) = (4n^2 + 20n^4 - 16n^3 + 16n^2)/n^5$	$T(F) = F/SE(F)$
H_1	$C(H_1) = t(n^5 + 41n^4 - 12n^3 + 4n^2)/n^5$	$T(H_1) = H_1/SE(H_1)$
H_2	$C(H_2) = 36n^4/n^5 = 36/n$	$T(H_2) = H_2/SE(H_2)$
H^2	$C(h^2) = (16n^4 + 16n^2 - 32n + 16)/n^5$	$T(h^2) = h^2/SE(h^2)$
E	$C(E) = n^4/n^5 = 1/n$	$T(E) = E/SE(E)$

3.12.3 Computation of allied genetic parameters

After computation of main components the following allied genetic parameters were calculated by the respective formulae

Mean degree of dominance = $(H_1/D)^{0.5}$

Proportion of dominant genes with positive or negative effects = $H_2/4H_1$

Proportion of dominant and recessive genes = $(4D\,H_1 + F)^{0.5}/(4D\,H_1 - F)^{0.5}$

Number of gene blocks exhibiting dominance = h^2/H_2

h^2n (Heritability in narrow sense) = $[D/4]/[D/4 + H_1/4 + E - F/4]$

CHAPTER 4

RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

4.1 Analysis of variance (ANOVA), general combining ability (gca) and specific combining ability (sca) variances

The variances due to general and specific combining ability were estimated for assessing the contribution of the additive and non-additive type of gene action involved in the inheritance of different characters. The analysis of variance indicated highly significant differences among parents and hybrids for twelve characters (Table 2). The components of variance for general combining ability (gca) and specific combining ability (sca) were highly significant for all traits indicating that both additive and non-additive gene actions were important for expression of these traits. The results showed the agreement with the findings of Acharya and Swain (2004). Similar findings were also reported by Tamber *et al.* (1991) in Indian mustard, Labana *et al.* (1978) in Yellow sarson, Malik *et al.* (1995) and Thakur and Sagwal (1997) in rape seed.

The higher magnitude of gca variance was observed than that of sca variance for all the characters except secondary branches per plant, length of siliqua, siliquae per plant and seed yield per plant. In an earlier study of Verma (2000), also reported sca variance was higher than gca variance (non-additive type) for primary branches per plant, siliquae per plant and seed yield per plant. Verma *et al.* (1989) and Labana *et al.* (1978) reported non-additive type of gene action for siliquae per plant, seed yield per plant in yellow sarson.

4.2 General combining ability (gca) effects

The gca effects represent the additive nature of gene action. The nature and magnitude of both are considered. Besides *per se* performance of the parent was also considered together with gca effects since the former offers authenticity to gca effects as guidance to select the parent. A parent with higher positive significant gca effects is

Table 2. Analysis of variance for general and specific combining ability for yield and yield components in *Brassica juncea* L. genotypes

Source of variation	Characters												
	df	Days to flower (50%)	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Length of siliqua (cm)	Siliquae per plant	Seeds per siliqua	1000-seed weight (g)	Seed yield per plant (g)	Harvest index	Oil content
Genotypes	35	46.44**	48.66**	1212.74**	1.05**	22.43**	0.357**	16603.95**	13.79**	1.06**	26.10**	22.37**	0.40*
Gca	7	60.68**	65.95**	1623.24**	0.509**	3.98**	0.094**	2893.95**	6.49**	1.43**	3.23**	14.85**	0.139*
Sca	28	4.15**	3.78**	99.49**	0.312**	8.35**	0.125**	6194.82**	4.12**	0.085**	10.07**	5.61**	0.132*
Error	70	0.99	0.399	20.59	0.025	0.165	0.016	253.56	0.176	0.008	0.265	0.705	0.054
gca/sca		14.52	17.42	16.31	1.63	0.476	0.751	0.467	1.57	16.77	0.321	2.65	1.05

* Significant at P = 0.05; ** Significant at P = 0.01

considered as a good general combiner. A parent showing high gca and sca variances is a better parent for creating high yielding specific combination.

The estimates of gca effects are given in Table 3. The magnitude and direction of the significant effects for the eight parents provide meaningful comparisons and would give clue to the future breeding programme. The results of gca effects of different characters are presented below:

Days to (50%) flower

Highest negative significant gca effects (-3.30) was provided by BARIsar-10 (P_2) for days to 50% flower. Hence the parent BARIsar-10 (P_2) was desired as general combiner in crosses aimed at promoting earliness in *Brassica juncea* L. (Table 3). Singh *et al.* (2000) obtained earliness in YSK-8501 in *Brassica campestris/rapa*. Verma (2000) observed earliness in RC 832 in *Brassica juncea* L. Chowdhury *et al.* (2004a) found earliness in Din-2 in *Brassica rapa* L.

Days to maturity

Parent BARIsar-10 (P_2) showed highest significant and negative gca effects (-2.35) followed by Daulat (P_4 = -2.08) and hence these two cultivars BARIsar-10 (P_2) and Daulat (P_4) were the best general combiners for early maturity in *Brassica juncea* L. The parent DH-18 (P_1) provided highest significant positive gca effects for days to maturity (5.58) followed by DH-11 (P_3 = 1.45), and hence these two parents were undesirable general combiners to promote the earliness in *Brassica juncea* L. (Table 3). Singh *et al.* (2000) found earliness in YSC-68 in *Brassica campestris* L. Acharya and Swain (2004) obtained earliness in JC 26 in *Brassica juncea* L. Chowdhury *et al.* (2004a) observed earliness in Din-2 in *Brassica rapa* L.

Plant height

The higher significant and negative effects (-21.37) for the parameter was found in BARIsar-10 (P_2) followed by Daulat (P_4 = -9.74). Thus, both BARIsar-10 (P_2) and Daulat (P_4) are good general combiners for breeding dwarf plant type. The highest significant and positive gca effect (18.69) was observed in DH-18 (P_1) followed by DH-11 (P_3 = 10.72) for the trait (Table 3). Singh *et al.* (1996) observed dwarfness in glossy mutant in *Brassica juncea* L. Singh *et al.* (2000) obtained dwarfness in YSK-8501 in *Brassica campestris* L. Chowdhury *et al.* (2004a) found dwarfness in Din-2 in *Brassica rapa* L.

Primary branches per plant

All the parents showed low values for this parameter. DH-18 (P_1) provided significant and positive gca effects (0.246) followed by BJ-17 (P_5 = 0.230). The parents BARIsar-11 (P_8), BARIsar-10 (P_2) and Daulat (P_4) showed the significant but negative effects (-0.391, -0.181 and -0.125 respectively). Thus, DH-18 (P_1) and BJ-17 (P_5) were found good for using in the breeding programme for more primary branches (Table 3). Sheikh and Sing (1998) found more primary branches in poorbijayr in *Brassica juncea* L. Singh *et al.* (2000) observed maximum number of primary branches on YSP-842 in *Brassica campestris* L. Chowdhury *et al.* (2004a) obtained more primary branches on sampad in *Brassica rapa* L.

Secondary branches per plant

This parameter showed low values for all the parents. Significant positive value of gca effects for the characters were revealed by BARIsar-10 (P_2 = 0.851) followed by BJ-11 (P_6 = 0.532), BJ-17 (P_5 = 0.345) and Daulat (P_4 = 0.333) and significant negative values by DH-18 (P_1 = -0.966) followed by BARIsar-11 (P_8 = -0.745). Thus, BARIsar-10 (P_2) was good to use in the breeding programme for more secondary branches in *Brassica juncea* L. (Table 3). Singh *et al.* (1996) obtained highest secondary branches in BJ-1235 in *Brassica juncea* L. Singh *et al.* (2000) found maximum number of secondary branches on SS-1 in *Brassica campestris* L. Chowdhury *et al.* (2004a) observed more secondary branches in Din-2 in *Brassica rapa* L.

Siliquae per plant

The highest significant and positive effects for the character was indicated by BARIsar-10 (P_2 = 29.07) followed by BARIsar-11 (P_8 = 22.59). The other parents showed insignificant or negative significant values for the trait. Thus, BARIsar-10 (P_2) was the best general combiner to use in hybridization programme to improve number of siliquae in *Brassica juncea* L. (Table 3). Singh and Murty (1980) obtained maximum number of siliquae per plant in SS-1 in *Brassica campestris* L. Acharya and Swain (2004) observed more siliquae in Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) found highest number of siliquae in Din-2 in *Brassica rapa* L.

Length of siliqua

Significantly highest and positive gca effects (0.074) was observed in both the parents Daulat (P_4) and BJ-17 (P_5). The other parents showed insignificant or negative significant effects for the trait. Hence Daulat (P_4) and BJ-17 (P_5) was the good general combiner to use in crossing for improves length of siliqua (Table 3). Sheikh and Singh (1998) and Acharya and Swain (2004) obtained maximum siliqua length in glossy mutant and Pusa Bahar respectively in *Brassica juncea* L.

Seeds per siliqua

Higher significant and positive gca effects were observed in Daulat (P_4 = 1.28), BJ-11 (P_6 = 0.577) and BARIsar-10 (P_2 = 0.371). Thus three parents were found best general combiners to increase the number of seeds in *Brassica juncea* L. (Table 3). Singh and Murty (1980) obtained more seeds per siliqua in YPS-842 in *Brassica Campestris* L. Acharya and Swain (2004) observed highest seeds per siliqua in

Table 3. Estimation of gca effects and mean performance of parents for 12 characters in a diallel cross of *Brassica juncea* L. genotypes

Parents	Characters											
	Days to flower (50%)	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Length of siliqua (cm)	Siliquae per plant	Seeds per siliqua	1000 seed weight (g)	Seed yield per plant (g)	Harvest index	Oil content
DH-18 (P_1)	4.47** 47.00	5.58** 105.67	18.69** 166.67	0.246** 5.20	-0.966** 7.08	0.023 5.37	8.61* 207.67	-0.767** 11.24	0.466** 3.98	0.933** 8.33	1.12** 29.67	-0.099 41.0
BARIsar-10 (P_2)	-3.30** 37.67	-2.35** 93.67	-21.37** 100.00	-0.181** 3.96	0.851** 9.05	-0.209** 5.27	29.07** 175.67	0.371** 13.92	-0.166** 3.03	0.212 4.13	2.22** 32.33	-0.026 41.81
DH-11 (P_3)	2.40** 43.67	1.45** 103.67	10.72** 152.00	-0.041 4.54	-0.207* 9.29	0.035 5.31	-16.39** 220.67	-0.981** 12.05	0.567** 3.68	0.352** 7.36	-0.441* 28.33	0.019 41.11
Daulat (P_4)	-2.23** 36.33	-2.08** 92.33	-9.74** 113.33	-0.125** 4.12	0.333** 7.59	0.074* 5.36	-3.99 178.00	1.28** 14.31	-0.466** 2.16	-0.798** 4.87	-0.275 31.67	-0.168** 41.51
BJ-17 (P_5)	-0.067 38.33	-1.22** 94.33	5.52** 134.33	0.230** 5.34	0.345** 9.06	0.074* 5.69	-9.69 165.67	0.120** 13.96	-0.289** 2.69	-0.753** 5.53	-1.57** 28.00	0.030 41.72
BJ-11 (P_6)	-0.233 38.33	-0.816** 94.667	6.22** 143.33	0.181** 5.08	0.532** 8.66	0.066* 5.77	14.74** 194.00	0.577** 14.62	-0.316** 2.52	0.118 5.98	-1.14** 30.33	0.207** 42.13
Jun-536 (P_7)	-0.90** 38.33	-0.883** 95.67	-4.64** 128.00	0.080* 4.55	-0.142 7.59	0.004 4.98	0.242 160.00	0.273** 11.54	0.017 3.15	-0.015 4.85	-0.208 30.67	0.102 41.59
BARIsar-11 (P_8)	-0.133 39.67	0.316* 99.33	-5.41** 127.33	-0.391** 3.94	-0.745** 7.83	-0.069* 5.18	22.59** 189.33	-0.882** 10.59	0.186** 3.31	-0.047 5.78	0.291 31.33	-0.066 41.01
SE (gi) SE (gi-gi)	0.233 0.352	0.148 0.224	1.06 1.60	0.037 0.056	0.095 0.144	0.030 0.045	3.72 5.63	0.098 0.148	0.021 0.032	0.120 0.182	0.196 0.297	0.054 0.082

Upper line GCA effects;
Lower line mean performance

*Significant at P= 0.05;
**Significant at P= 0.01

Varuna in *Brassica juncea* L. Chowdhury *et al.* (2004a) found maximum seeds per siliqua in Dhali in *Brassica rapa* L.

1000-seed weight

The highest significant and positive gca effects for 1000-seed weight was observed in DH-11 (P_3 = 0.567) followed by DH-18 (P_1 = 0.466). The other parents showed insignificant or negative significant effects for the trait. Hence DH-18 (P_1) and DH-11 (P_3) was the good general combiner to use in crossing for improved seed size (Table 3). Singh *et al.* (2000) observed more seed weight in YSC-68 in *Brassica campestris* L. Acharya and Swain (2004) obtained maximum seed weight in Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) found highest seed weight in Dhali in *Brassica rapa* L.

Seed yield per plant

The highest significant and positive gca effects for seed yield per plant was observed in DH-18 (P_1 = 0.933) followed by DH-11 (P_3 = 0.352). The other parents showed insignificant or negative significant effects for the character. Hence DH-18 (P_1) and DH-11 (P_3) was the good general combiner to use in crossing programme for improved seed yield per plant in *Brassica juncea* L. (Table 3). Singh *et al.* (2000) obtained more seed yield per plant in SS-2 in *Brassica campestris* L. Acharya and Swain (2004) found highest seed yield in Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) observed maximum seed yield in PT-303 in *Brassica rapa* L.

Harvest index

The highest significant and positive gca effects for harvest index was observed in BARIsar-10 (P_2 = 2.22) followed by DH-18 (P_1 = 1.12). The other parents showed insignificant or negative significant effects for the character (Table 3). Singh *et al.* (2000) obtained maximum harvest index in YSP-842 in *Brassica campestris* L.

Oil content

The yellow seeded parent BJ-11 (P_6) showed significant and positive gca effects (0.207) and hence it was found good general combiner to improve the oil content in Indian mustard (Table 3). Singh *et al.* (1996) and Sheikh and Singh (1998) obtained maximum oil content in PR-1108 and Pusa Bold respectively. Chowdhury *et al.* (2004a) observed highest oil content on Dhali in *Brassica rapa* L.

High additive gene action observed for only days to 50% flower, days to maturity, plant height and 1000-seed weight, while moderate additive gene action was observed in primary branches per plant, seeds per siliqua, harvest index and oil content. Non-additive type of gene action was predominant for secondary branches per plant, length of siliqua, siliquae per plant and seed yield per plant (Table 2). Similar results were also reported by several workers including Verma (2000) and Acharya and Swain (2004) in Indian mustard.

The estimates of gca indicated that the parents P_1 (DH-18) and P_3 (DH-11) were good general combiners for seed yield per plant. Parents P_2 (BARIsar-10) and P_6 (BJ-11) were good general combiners for secondary branches per plant and siliquae per plant. Parents P_1 (DH-18) and P_3 (DH-11) was good general combiner for 1000-seed weight. BARIsar-10 (P_2), Daulat (P_4) and Jun-536 (P_7) were desirable for earliness as well as dwarfness. Only BJ-11 (P_6) was found good general combiner for oil content. Most of the characters showed both additive and non-additive gene actions and found important in the expression of the characters. For exploitation of non-additive gene action in order to recover transgressive segregants by breaking undesirable linkage, releasing concealed variability and changing linkage equilibrium, it is necessary to follow modified breeding methods, viz., bi-parental cross or triple test cross or recurrent selection.

4.3 Specific combining ability effects

The specific combining ability effects signify the role of non-additive gene action in the expression of the characters. It denotes the highly specific combining ability leading to highest performance of some specific cross combinations. For this reason it relates to a particular cross. The specific combining ability effects are also seen in relation to their size. High sca effects may arise not only in cross involving high x high combinations, but also in those involving low x high and also from low x low. Thus in practice, some of the low combiners should also be accommodated in hybridization programme. The specific combining ability effects of twenty eight F_1 crosses for twelve different characters studied are presented in Table 4. The magnitude and direction of the significant effects for the eight parents provide meaningful comparisons and would give clue to the future breeding programme. The results of sca effects of different characters are given below:

Days to (50%) flower

Highest significant and negative value from the parameter was obtained from BARIsar-10 x BARIsar-11 (C_{13} = -2.12) for days to 50% flower. Significant and positive sca effects was observed in the cross combinations, BJ-17 x BARIsar-11 (C_{25} = 2.97) followed by DH-18 x BJ-11 (C_5 = 2.54). Thus, the cross combinations, BARIsar-10 x BARIsar-11 (C_{13}) provides opportunity for earliness in *Brassica juncea* L. (Table 4). Singh *et al.* (1996) observed earliness in PR-1108 x BJ-1235 in *Brassica juncea* L. Singh *et al.* (2000) obtained earliness on YSK-8501 x SS-2 in *Brassica campestris/rapa* .

Days to maturity

The cross combination DH-11 x BARIsar-11 (C_{18}) showed highest significant and negative sca effects (-1.82) while significant and positive value form the parameter was obtained from DH-18 x BJ-17 (C_4 = 3.57). Hence the cross combination DH-11 x BARIsar-11 (C_{18}) provides opportunity for early maturity in *Brassica juncea* L. (Table 4). Singh *et al.* (2000) obtained earliness in SS-3 x SS-1 in *Brassica campestris* L. Acharya and Swain (2004) found early maturity in JC 26 x Jai kisan in *Brassica juncea* L. Chowdhury *et al.* (2004a) observed earliness in M-27 x Din-2 in *Brassica rapa* L.

Plant height

The F_1 of crosses, BARIsar-10 x BJ-11 (C_{11}) and DH-18 x BARIsar-10 (C_1) showed higher significant and negative sca effects (-7.08 and -6.55, respectively) for plant height. The highest significant and positive sca effects was observed in the cross combination, DH-18 x BJ-17 (C_4 = 19.21) followed by Daulat x BJ-11 (C_{20} = 17.28). Thus, the cross combinations BARIsar-10 x BJ-11 (C_{11}) and DH-18 x BARIsar-10 (C_1) could be used for dwarfness of the crop (Table 4). Acharya and Swain (2004) obtained dwarfness in Varuna x Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) observed dwarfness in PT-303 x Tori-7 in *Brassica rapa* L.

Primary branches per plant

The cross combinations BARIsar-10 x DH-11 (C_8 = 0.792) were found best specific combiner to improve plants with more number of primary branches as they showed significant positive sca effects for this trait (Table 4). Sheikh and Singh (1998) observed best positive effect in Pusa x Barani in *Brassica juncea* L. Singh *et* *al.* (2000) obtained maximum number of primary branches per plant in YSK-8501 x SS-1 in *Brassica campestris* L. Chowdhury *et al.* (2004a) found more primary branches in Sampad x Tori-7 in *Brassica rapa* L.

Secondary branches per plant

Highest significant positive values of sca effects for the character were revealed by Daulat x BARIsar-11 (C_{22} = 3.55) and BJ-17 x BJ-11 (C_{23} = 3.41). On the other hand the highest significant and negative sca effects was provided by DH-11 x Daulat (C_{14} = -2.08) followed by BJ-17 x BARIsar-11 (C_{25} = -0.884). Thus, Daulat x BARIsar-11 (C_{22}) and BJ-17 x BJ-11 (C_{23}) was best specific combiner to improve plants with more number of secondary branches and DH-11 x Daulat (C_{14}), BJ-17 x BARIsar-11 (C_{25}) were best specific combiner to obtained plants with minimum secondary branches (Table 4). Singh *et al.* (2000) observed highest secondary branches in YSC-68 x SS-2 in *Brassica campestris* L. Acharya and Swain (2004) obtained more secondary branches in BM 20-12-3 x JC 26 in *Brassica juncea* L. Chowdhury *et al.* (2004a) found maximum secondary branches in Sampad x Din-2 in *Brassica rapa* L.

Length of siliqua

Among the cross combinations, BJ-17 x BARIsar-11 (C_{25} = 0.655) showed highest significant and positive sca effects followed by Daulat x BJ-11 (C_{20}) and Daulat x Jun-536 (C_{21}), (0.523 and 0.498 respectively). On the other hand, the remaining combinations showed significant but negative sca effects or insignificant effects for the trait (Table 4). Sheikh and Singh (1998) and Acharya and Swain (2004) observed maximum siliqua length in Pusa Barani x Glossy mutant and BM 20-12-3 x Pusa Bahar respectively in *Brassica juncea* L.

Table 4. Estimation of sca effects for 12 characters in a diallel cross of *Brassica juncea* L. genotypes

Crosses	Characters											
	Days to flower (50%)	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Length of siliqua (cm)	Siliquae per plant	1000- seed weight (g)	Seeds per siliqua	Seed yield per plant (g)	Harvest index	Oil content
DH-18 x BARIsar-10 (C_1)	0.277	-0.955*	-6.55*	0.058	2.77**	0.456**	17.77	-0.072	2.33**	0.231	0.233	-0.346*
DH-18 x DH-11 (C_2)	0.578	0.578	9.35**	-0.135	-0.181	0.378**	-54.43**	0.534**	0.362	0.161	5.56**	0.025
DH-18 x Daulat (C_3)	0.211	-1.22**	-4.85	0.282**	0.602*	-0.274**	75.84**	-0.558**	-2.21**	-0.545	1.73**	0.226
DH-18 x BJ-17 (C_4)	2.37**	3.57**	19.21**	0.226**	1.75**	0.059	41.20**	0.271**	-0.872**	2.12**	0.366	0.115
DH-18 x BJ-11 (C_5)	2.54**	3.17**	10.85**	0.632**	1.29**	-0.482**	51.77**	-0.448**	-0.128	1.24**	-5.4**	0.055
DH-18 x Jun-536 (C_6)	-0.122	1.57**	3.38	0.676**	1.23**	0.059	66.94**	0.211**	-0.725**	4.02**	-0.667	0.043
DH-18 x BARIsar-11 (C_7)	1.77**	2.37**	-0.848	-0.561**	-0.739**	-0.023	5.77	0.065	0.397	0.497	0.833	0.207
BARIsar-10 x DH-11 (C_8)	1.01	0.511	10.42**	0.792**	2.15**	-0.066	46.77**	0.061	-1.81**	1.60**	-1.20*	0.372*
BARIsar-10 x Daulat (C_9)	-1.35*	1.71**	2.88	0.487**	3.36**	-0.125	107.37**	0.088	0.189	3.83**	0.967	-0.401**
BARIsar-10 x BJ-17 (C_{10})	-1.85**	0.178	0.285	0.655**	1.73**	-0.352**	83.74**	-0.229**	0.791**	3.85**	1.93**	-0.489**
BARIsar-10 x BJ-11 (C_{11})	-1.68**	-0.889*	-7.08*	-0.422**	-0.696**	0.246**	72.30**	-0.212**	2.58**	3.41**	1.50**	-0.249
BARIsar-10 x Jun-536 (C_{12})	0.977	-0.156	5.12	0.538**	1.19**	-0.252**	65.80**	-0.068	-1.08**	1.38**	-0.767	0.389**
BARIsar-10 x BARIsar-11 (C_{13})	-2.12**	0.978*	-1.45	-0.163	-0.446	-0.465**	43.03**	-0.195**	-4.66**	-0.535	-0.933	-0.263
DH-11 x Daulat (C_{14})	0.944	-0.088	-3.88	0.129	-2.08**	-0.363**	-40.83**	0.101	-0.758**	-1.98**	-3.03**	-0.693**
DH-11 x BJ-17 (C_{15})	0.778	-0.956*	6.85*	-0.012	-0.015	-0.219**	9.87	0.026	-1.04**	-0.082	0.600	-0.107
DH-11 x BJ-11 (C_{16})	1.27**	-1.35**	2.48	0.300**	2.37**	-0.108	28.44**	-0.126*	-1.13**	1.16**	-1.16*	-0.057
DH-11 x Jun-536 (C_{17})	0.944	-0.288	4.02	0.264**	1.005**	0.357**	54.27**	0.023	-0.261	2.41**	-0.767	0.527**
DH-11 x BARIsar-11 (C_{18})	0.511	-1.82**	-1.21	0.012	2.08**	0.354**	34.77**	0.381**	1.33**	3.51**	-0.933	0.515**
Daulat x BJ-17 (C_{19})	2.07**	2.24**	2.65	0.195	1.78**	0.061	56.80**	0.137*	-1.63**	0.687*	-1.56**	0.090
Daulat x BJ-11 (C_{20})	1.91**	1.51**	17.28**	0.264**	1.49**	0.523**	36.04**	0.098	1.93**	2.63**	-1.66**	0.110
Daulat x Jun-536 (C_{21})	-0.089	0.578	-1.18	-0.141	2.18**	0.498**	-28.46**	0.015	0.820**	0.519	-1.93**	-0.672**
Daulat x BARIsar-11 (C_{22})	-1.52**	0.378	10.58**	0.640**	3.55**	0.072	7.04	0.022	2.87**	2.58**	-1.43**	0.376*
BJ-17 x BJ-11 (C_{23})	-0.256	0.311	-0.315	-0.271**	3.41**	-0.607**	-17.93	0.220**	-4.05**	-0.968**	-1.7**	-0.201
BJ-17 x Jun-536 (C_{24})	0.744	0.044	6.22*	-0.163	0.219	0.138	6.57	-0.283**	1.34**	0.678	-1.63**	0.019
BJ-17 x BARIsar-11 (C_{25})	2.97**	-0.822*	7.65**	0.191	-0.884**	0.655**	35.40**	-0.589**	2.73**	0.277	-2.8**	-0.012
BJ-11 x Jun-536 (C_{26})	0.578	2.31**	1.52	0.125	1.15**	0.223**	55.47**	-0.156**	1.93**	0.489	0.266	-0.173
BJ-11 x BARIsar-11 (C_{27})	1.81**	0.444	2.62	0.514**	0.535*	-0.263**	30.64**	0.411**	-3.36**	1.20**	0.433	-0.195
Jun-536 x BARIsar-11 (C_{28})	0.478	-0.822*	-4.52	0.508**	2.01	-0.148	46.12**	0.128*	0.689*	1.38**	0.833	-0.066
SE (Sij)	0.622	0.395	2.83	0.099	0.254	0.080	9.95	0.056	0.263	.322	.525	0.146

* Significant at P= 0.05;   ** Significant at P= 0.01

Siliquae per plant

Among the cross combinations, BARIsar-10 x Daulat (C_9 = 107.37) showed highest significant and positive sca effects followed by BARIsar-10 x BJ-17 (C_{10}) and DH-18 x Daulat (C_3), (83.74 and 75.84) respectively. On the other hand, the cross DH-18 x DH-11 (C_2 = -54.43) showed highest significant but negative sca effects for the trait followed by DH-11 x Daulat (C_{14} = -40.83) and Daulat x Jun-536 (C_{21} = -28.46), (Table 4). Singh and Murty (1980) observed more siliquae per plant in YSP-842 x SS-3 in *Brassica campestris* L. Acharya and Swain (2004) obtained highest siliquae per plant in Pusa Bahar x JC 26 in *Brassica juncea* L. Chowdhury *et al.* (2004a) found maximum siliquae in Sampad x Din-2 in *Brassica rapa* L.

Seeds per siliqua

Among the cross combinations, Daulat x BARIsar-11 (C_{22} = 2.87) exhibited highest significant and positive sca effects followed by BJ-17 x BARIsar-11 (C_{25} = 2.73) for seeds per siliqua. Significant and positive moderate values for the parameter were showed by BARIsar-10 x BJ-11 (C_{11}), DH-18 x BARIsar-10 (C_1) and Daulat x BJ-11 (C_{20}). The other cross combinations showed insignificant or negative sca effects. Hence Daulat x BARIsar-11 (C_{22}) was the best specific combiner to increase the number of seeds in the siliqua for yield improvement (Table 4). Singh *et al.* (2000) obtained more seeds per siliqua in YSP-842 x YSK-8501 in *Brassica campestris* L. Acharya and Swain (2004) observed maximum seeds per siliqua in BM 20-12-3 x Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) found height seeds per siliqua in Dhali x Sampad in *Brassica rapa* L.

1000-seed weight

The cross combinations C_2, C_{27}, C_{18}, C_4, C_{23}, C_6, C_{19} and C_{28} provided significant and positive sca values for 1000-seed weight indicated considerable heterosis for the trait. The cross combination DH-18 x DH-11 (C_2 = 0.534) and BJ-11 x BARIsar-11 (C_{27} = 0.411) showed significant positive sca effects for this trait and seems to be the best combinations regarding seed size (Table 4). Singh *et al.* (2000) observed more seed weight in YSC-68 x SS-2 in *Brassica campestris* L. Acharya and Swain (2004) found highest seed weight in Pusa Bold x Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) obtained maximum seed weight in Dhali x Sampad in *Brassica rapa* L.

Seed yield per plant

The cross combinations C_6, C_{10}, C_9, C_{18}, C_{11}, C_{20}, C_{22}, C_{17}, C_4, C_8, C_{12}, C_{28}, C_5, C_{27}, C_{16} and C_{19} exhibited significant and positive sca effects of which DH-18 x Jun-536 (C_6) and BARIsar-10 x BJ-17 (C_{10}) provided maximum effects (4.02 and 3.85 respectively) for seed yield per plant. The other combinations showed either significant negative or insignificant sca effects. Thus, DH-18 x Jun-536 (C_6) and BARIsar-10 x BJ-17 (C_{10}) were the best specific combinations for the improvement of seed yield per plant in *Brassica juncea* L. (Table 4). Singh *et al.* (2000) observed more seed yield per plant in YSP-842 x YSK-8501 in *Brassica campestris* L. Acharya and Swain (2004) found maximum seed yield in Pusa Bold x Pusa Bahar in *Brassica juncea* L. Chowdhury *et al.* (2004a) obtained highest seed yield in M-27 x Din-2 in *Brassica rapa* L.

Harvest index

Among the cross combinations, only four crosses DH-18 x DH-11 (C_2), BARIsar-10 x BJ-17 (C_{10}), DH-18 x Daulat (C_3) and BARIsar-10 x BJ-11 (C_{11}) showed significant and positive sca effects for harvest index. The cross DH-18 x DH-11 (C_2 = 5.56) had the highest value for the trait. The remaining combinations showed either insignificant or negative significant effects (Table 4). Singh *et al.* obtained highest positive value for harvest index in SS-1 x SS-2 in *Brassica campestris* L.

Oil content

Among the F_1 hybrids only five crosses BARIsar-10 x DH-11 (C_8), BARIsar-10 x Jun-536 (C_{12}), DH-11 x Jun-536 (C_{17}), DH-11 x BARIsar-11 (C_{18}) and Daulat x BARIsar-11 (C_{22}) revealed significant and positive sca values for oil content. The cross DH-11 x Jun-536 (C_{17}) had the highest value (0.527) in this regard and this cross combination might improve the oil content in *Brassica juncea* L. The remaining combinations showed either insignificant or negative significant effects (Table 4). Singh *et al.* (1996) and Sheikh and Singh (1998) obtained highest oil content in Glossy mutant x BJ-1257 and poorbijaya x BJ-38 respectively in *Brassica juncea* L. Chowdhury *et al.* (2004a) found maximum oil content in Tori-7 x Din2 in *Brassica rapa* L.

Some of the crosses showed superior specific combination for seed yield and 1000-seed weight. However, DH-18 x JUN-536 (C_6), BARIsar-10 x BJ-17 (C_{10}) and BARIsar-10 x Daulat (C_9) showed significant sca effects for seed yield. DH-18 x DH-11 (C_2) and BJ-11 x BARIsar-11 (C_{27}) showed significant sca effects for 1000-seed weight. The cross DH-18 x JUN-536 (C_6) also showed significant effects for primary branches per plant, secondary branches per plant, siliquae per plant, 1000-seed weight and seed yield per plant. DH-18 x BARIsar-10 (C_1) and BARIsar-10 x BJ-11 (C_{11}) showed significant effects for earliness and dwarf plant type. It was interesting to note that the parents BARIsar-10 (P_2), Daulat (P_4), Jun-536 (P_7) and BARIsar-11 (P_8) were poor general combiners for seed yield and 1000-seed weight. While DH-18 was good general combiner for seed yield and highly significant value for seed yield was observed in the cross DH-18 x JUN-536 (C_6), in which the DH-18 parent were good combiners for seed yield but Jun-536 were poor combiners for seed yield and also had poor mean performance. Such results could be due to the presence of different genes or gene groups separately in both the parents.

The above results indicated that the cross with superior sca effects involving high x low gca parents could be expected to yield positive heterosis in higher frequencies. Earlier study of Sheikh and Singh (1998) and Chowdhury *et al.* (2004a) also pointed similar trend for the improvement of seed yield in mustard.

4.4 Diallel analysis following Jones approach

Result on Jones analysis of variance and Haymans Vr-Wr analysis including graphical presentation for 12 plant characters are provided as follows:

Days to (50%) flowering

Jones analysis (Table 5) showed that both additive (a) and dominance (b) genetic components were significant, which indicated they were important in the regulation of flowering data. The results were similar to Griffing's combining ability analysis (Table 2). Mean dominance (b_1) and dominance due to array (b_2) and residual dominance effect (b_3) were highly significant for the character.

The regression of Wr on Vr gave the slope b = 0.578±0.128 (Fig: a), which was not significantly different from unity. These results therefore clearly suggested that simple additive dominance genetic model was adequate without any complication of non-allelic interaction.

Days to maturity

Jones analysis showed both additive (a) and dominance (b) genetic components were significant for days to maturity (Table 5). Griffing's combining ability analysis suggested the same result (Table 2). Other dominance fractions viz. mean dominance (b_1), dominance due to array (b_2) and residual dominance effect (b_3) were significant for this trait.

From the regression of Wr on Vr, which yielded b value of 0.645±0.211 (Fig: b) was close to unity. The results, therefore suggested an additive-dominance situation without any complication of non-allelic interaction.

Plant height

Both additive (a) and dominance (b) effect were highly significant ($P< 0.01$) for this character (Table 5). Similar result was obtained in Griffing's combining ability analysis (Table 2).

The Vr-Wr analysis yielded b value of 0.451±0.123 (Fig: c), which was statistically equal to one. It likes that the additive-dominance nature of gene action was involved in the genetic background.

Primary branches per plant

Jones analysis shows both additive (a) and dominance (b) genetic components were involved in the inheritance of the trait (Table 5). The result found similar to Griffing's combining ability analysis. Dominance component such as mean dominance (b_1), dominance due to array (b_2) and residual dominance effect (b_3) were significant at different levels ($P< 0.05$-0.01).

The regression of Wr on Vr gave the slope b value of 0.564±0.059 (Fig: d), which was not significantly different from unity. These result therefore, clearly suggested that simple additive-dominance genetic model was adequate without any complication of non-allelic interaction.

Secondary branches per plant

Both additive (a) and dominance (b) component (Table 5) were significant for the secondary branches per plant. This result was similar to Griffing's combining ability analysis (Table 2).

The regression of Wr on Vr gave the slope b = 0.384±0.158 (Fig: e), which is close to unity. The results, therefore suggested an additive-dominance situation without any complication of non-allelic interaction.

Siliquae per plant

Mean square for the item (a) and (b) were significant for siliquae per plant (Table 5) suggesting that both additive and dominance gene action were important for the character of siliquae per plant. The result is similar to the Griffing's combining ability analysis (Table 2).

The regression of Wr on Vr gave the slope b value of 0.124±0.117 (Fig: f), which is statistically equal to one. It likes that the additive-dominance nature of gene action was involved in the genetic background.

Length of siliqua

Jones analysis showed the variance due to additive (a) and dominance (b) genetic components were significant (Table 5). ANOVA further showed out the mean dominance (b_1) is not significant, dominance due to array (b_2) and residual dominance effect (b_3) were significant for the character.

Table 5. Jones analysis of variance for 12 characters in Indian mustard, *Brassica juncea* L.

Source of variation	df	Mean square											
		Days to flower (50%)	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Length of siliqua (cm)	Siliquae per plant	Seeds per siliqua	1000-seeed weight (g)	Seed yield per plant	Harvest index	Oil content
a	7	113.47**	111.93**	2844.68**	0.753**	8.16**	0.194**	7639.95**	10.54**	2.59**	6.38**	31.94**	0.238**
b_1	1	45.01**	31.08**	1514.34**	5.72**	196.74**	0.021	131257.4**	1.41**	0.0003	232.92**	27.50**	0.172*
b_2	7	8.22**	7.38**	76.95**	0.089*	2.03**	0.122**	3802.33**	2.65**	0.115**	3.08**	7.71**	0.217**
b_3	20	47.28**	48.57**	1289.14**	1.58**	28.97**	0.691**	6169.22**	21.54**	1.02**	34.4**	31.46**	1.10**
Error	70	0.99	0.04	20.59	0.025	0.169	0.016	253.56	0.229	0.01	0.263	0.70	0.054

* Significant at P = 0.05; ** Significant at P = 0.01

The regression of Wr on Vr, gave the slope b value of 0.414±0.348 (Fig: g), which was close to unity. The results, therefore suggested an additive-dominance situation without any complication of non-allelic interaction.

Seeds per siliqua

Jones analysis (Table 5) shows the variation due to additive (a) and dominance (b) genetic components were significant for seeds per siliqua. Griffing's combining ability analysis suggested the same result (Table 2). The dominance component such as mean dominance (b_1), dominance due to array (b_2) and residual dominance effect (b_3) were also significant.

The regression of Wr on Vr, gave the slope b = 0192±0.158 (Fig: h), which was not significantly different for one. It likes that the non-additive interaction was not involved and the genetic system governing the character was of simple additive-dominance model.

1000-seed weight

Result demonstrated (Table 5) that both additive (a) and dominance (b) genetic effects were significant and important for the expression of this trait. ANOVA further showed out the mean dominance (b_1) was not significant, dominance due to array (b_2) and residual dominance effect (b_3) were significant for the character.

The Vr-Wr analysis yielded b value of 0.638±0.094 (Fig: i), which was not significantly different from unity. This indicates that simple additive-dominance genetic model was adequate without any complication of non-allelic interaction.

Seed yield per plant

The analysis of variance following Jones approach (Table 5) demonstrated that both additive (a) and dominance (b) genetic components were highly significant (P<

0.01) for this trait. Results of Griffing's combining ability analysis also suggested the same (Table 2).

The regression of Wr on Vr, gave the slope b = 0562±0.182 (Fig: j), which was not significantly different for one. It likes that the non-additive interaction was not involved and the genetic system governing the character was of simple additive-dominance model.

Harvest index

Jones analysis showed the variance due to additive (a) and dominance (b) genetic components were significant (Table 5). The fraction of dominance component such as, mean dominance (b_1), dominance due to array (b_2) and residual dominance effect (b_3) were significant for the character. The result was similar to the Griffing's combining ability analysis (Table 2)

From the regression of Wr on Vr, which yielded b value of 0.169±0.147 (Fig: k), which was close to unity. The results, therefore suggested an additive-dominance situation without any complication of non-allelic interaction.

Oil content

The variation due to additive (a) and dominance (b) item were significant (Table 5) that is both the component was important for the expression of this character. Dominance component such as mean dominance (b_1), dominance due to array (b_2) and residual dominance effect (b_3) were significant at different levels ($P< 0.05-0.01$).

The regression of Wr on Vr gave the slope b = 0.087±0.056 (Fig: l), which was not significantly different from unity. These results there fore clearly suggested that simple additive dominance genetic model was adequate without any complication of non-allelic interaction.

4.5 Genetic component analysis

4.5.1 Genetic components

The components of variation along with the derived genetic ratios for different traits (Table 6) showed that the D and H component which measure additive and dominance variation respectively were significant for all the traits. This indicated the importance of both additive and dominance components for the inheritance of all the traits in *Brassica juncea* L. However, the magnitude of dominance was higher than the additive component for all the traits except days to maturity, plant height and 1000-seed weight which indicated that dominance component had a predominant role in the inheritance of these traits. These results agreed with Chowdhury *et al.* (2004b) for days to flower and days to maturity in *Brassica rapa* L., Trivedi and Mukharjee (1986) and Yadav and Yadava (1996) found same result for Indian mustard and yellow sarson respectively.

The H_2 representing dominance deviation due to relative frequency of positive and negative genes was significant for all the characters. These results agree with Chowdhury *et al.* (2004) for *Brassica rapa* L., Trivedi and Mukharjee (1986) for *Brassica juncea* L., Yadav and Yadava (1996) for *Brassica campestris* L.

The net dominance effect, obtained by the estimate h^2 expressed as the algebraic sum over all loci in heterozygous condition in all crosses, was significant for all the character studied. This revealed that substantial contribution of dominance effects was due to heterogeneity of loci in all characters. In an earlier study Chowdhury *et al.* (2004b) obtained significant for days to maturity, plant height, siliquae per plant and seed yield per plant in *Brassica rapa* L., Trivedi and Mukharjee (1986) observed significant for days to maturity, 1000-seed weight and seed yield per plant in *Brassica juncea* L. The positive and negative estimation of h^2 indicated mean direction of dominance and respective genes towards positive and negative sides, respectively. The results showed that eight characters viz. days to flower, days to maturity, plant height, primary branches per plant, secondary branches per plant, length of siliqua, siliquae per plant and seed yield per plant possessed positive effects, indicating the mean direction of dominance as well as important of excess of dominant genes in the expression of these traits. On the other hand 1000-seed weight, seeds per siliqua, harvest index and oil content exhibited the values in negative direction, showing the excess of recessive gene for these traits. These findings agreed with Yadav and Yadava (1996) in *Brassica campestris* L.

The proportion of positive and negative effects as indicated by F value was significant for all the characters. Positive F value for days to maturity, primary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, seed yield and oil content, suggesting great frequency of dominant alleles governing these characters. Negative F value for days to flower, plant height, secondary branches per plant, 1000-seed weight and harvest index exhibited a preponderance of recessive alleles (Table 6). These findings agreed with Chowdhury *et al.* (2004b) for days to maturity and plant height in *Brassica rapa* L., Trivedi and Mukharjee (1986) found negative F value for seed yield per plant, seeds per siliqua and siliquae per plant in *Brassica juncea* L., Yadav and Yadava (1996) observed negative F value for secondary branches per plant and siliquae per plant in *Brassica campestris* L.

The environmental component E, exhibited significant values for all the traits indicating influence of environmental factors in the expression of those traits. Chowdhury *et al.* (2004b) obtained significant value for plant height, primary branches

Table 6: Estimates of genetic components of variation and their ratios for 12 characters in Indian mustard, *Brassica juncea* L.

Source of variation	Characters											
	Days to flower (50%)	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Length of siliqua (cm)	Siliquae per plant	1000-seed weight	Seeds per siliqua	Seed yield per plant (g)	Harvest index	Oil content
D	11.81** ±0.009	24.01** ±0.009	423.42** ±0.171	0.290** ±0.0002	0.446** ±0.006	0.051** ±0.0002	142.52** ±7.16	0.354** ±0.0002	1.98** ±0.012	1.59** ±0.006	1.69** ±0.015	0.116** ±0.0003
H_1	15.15** ±0.022	15.66** ±0.023	280.98** ±0.393	0.894** ±0.0005	23.12** ±0.014	0.509** ±0.0004	17887.67** ±16.47	0.345** ±0.0005	17.59** ±0.027	27.93** ±0.013	22.44** ±0.036	0.470** ±0.0007
H_2	9.74** ±0.019	10.42** ±0.018	241.68** ±0.342	0.849** ±.0004	21.79** ±0.012	0.430** ±0.0003	15308.37** ±14.33	0.267** ±0.0004	15.77** ±0.024	25.87** ±0.011	17.18** ±0.032	0.347** ±0.0006
h^2	8.43** ±0.013	7.2** ±0.012	40.74** ±0.229	3.15** ±.0003	18.44** ±0.008	0.180** ±0.0002	334.48** ±9.61	-0.025** ±0.0003	-1.67** ±0.016	20.04** ±0.008	-7.24** ±0.021	-0.573** ±0.0004
F	-10.89** ±0.022	1.368** ±0.023	-242.31** ±0.404	0.154** ±0.0006	-0.199** ±0.014	0.085** ±0.0004	898.12** ±16.93	-0.213** ±0.0005	1.23** ±0.028	2.14** ±0.014	-0.859** ±0.037	0.192** ±0.0007
E	1.006** ±0.003	0.392** ±0.003	24.55** ±0.056	0.029** ±0.00008	0.261** ±0.002	0.016** ±0.00006	319.32** ±2.38	0.010** ±0.00007	0.224** ±0.004	0.331** ±0.002	0.701** ±0.005	0.053** ±0.00009
$(H_1/D)^2$	1.132	0.807	0.814	1.75	7.19	3.17	11.38	0.986	2.98	4.19	3.64	2.01
$H_2/4H_1$	0.161	0.166	0.215	0.237	0.235	0.211	0.214	0.193	0.224	0.231	0.191	0.185
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$	0.421	1.073	0.480	1.36	0.939	1.72	1.78	0.533	1.23	1.38	0.869	2.39
Heritability(b)	0.90	0.96	0.90	0.89	0.96	0.87	0.93	0.96	0.95	0.95	0.89	0.65
H^2 (ns)	0.282	0.762	0.505	0.253	0.018	0.093	0.007	0.472	0.103	0.055	0.061	0.191

* Significant at P = 0.05; ** Significant at P = 0.01

per plant, seeds per siliqua, seed yield per plant and oil content in Turnip rape. Jindal and Labana (1985) found significant value for oil content in Indian mustard However, the magnitude of E for each character was much lower than the respective value of D and H_1 except siliquae per plant. This indicated that the characters were influenced less by the environment. These findings agreed with the earlier findings of Trivedi and Mukharjee (1986) for seed yield per plant, 1000-seed weight, length of siliqua and siliquae per plant in *Brassica juncea* L.

The average degree of dominance as indicated by the proportion $(H_1/D)^{1/2}$ was more than unity, suggesting that over dominance was operating in the expression for most of the components of oil yield. Trivedi (1980), Trivedi and Mukharjee (1986) also found over-dominance in graphic analysis of oil yield attributes in Indian mustard. These findings also agreed with Chowdhury *et al.* (2004b) for turnip rape, Yadav and Yadava (1996) for toria.

The ratio of $H_2/4H_1$ provides an estimate of the average frequency of positive and negative alleles in all the parents. A value of this ratio smaller than 0.25 for all the characters studied suggested asymmetrical distribution of only the negative alleles. Most of the characters studied indicating unequal distribution of positive and negative alleles. However, the value of primary branches per plant (0.237), secondary branches per plant (0.235) and seed yield per plant (0.231) was closer to 0.25 suggesting equal distribution of positive and negative alleles (Table 6). These findings agreed with Chowdhury *et al.* (2004b) for *Brassica rapa* L., Trivedi and Mukharjee (1986) found symmetrical distribution for length of siliqua and siliquae per plant.

The ratio of $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ estimates the relative proportion of dominant and recessive alleles in the parents. In the present study the ratio for all the characters except days to flower, plant height, secondary branches per plant, 1000-

seed weight and harvest index were greater than unity suggesting excess of dominant alleles and minority of recessive alleles i.e., asymmetrical distribution for dominant and recessive alleles in the parents for seven characters. These findings also agreed with Chowdhury *et al.* (2004b) for days to flower, plant height and 1000-seed weight in turnip rape.

The estimated number of effective factors (h^2/H_2) was less than unity for all yielding attributes except for primary branches per plant and oil content. The proportion of genes or group of genes showing dominance was thus very less, which could be owing to the predominant concealing effects of positive and negative effects of genes or to non-isodirectional distribution of polygene (Cooke and Mather, 1962). These findings also agreed with Chowdhury *et al.* (2004b) for plant height and siliquae per plant in *Brassica rapa* L., Trivedi and Mukharjee (1986) for days to maturity in *Brassica juncea* L.

Heritability in narrow sense was higher for days to maturity, plant height and 1000-seed weight, indicating these characters was highly heritable. For the remaining traits it ranged from low to moderate and very low for seed yield. The results agree with Chowdhury *et al.* (2004) in turnip rape, Yadav and Yadava (1996) in toria, Trivedi and Mukharjee (1986) in Indian mustard.

4.5.2 Vr-Wr graph

Vr-Wr graphs, the two dimensional depiction made based on the parental variance (Vr) and parent offspring co-variance (Wr) are presented in the Fig. a to Fig. l. The ANOVA due to diallel progenies indicated significant differences among themselves (Table 2). Hayman's graphic approach to diallel analysis is based on monogenic additive model. The regression coefficient differ significantly from zero and approaching to unity for all the traits studied except primary and secondary branches per plant suggesting that there was no epistasis for most of the traits indicated the validity of such type of analysis. Vr-Wr graphs for the ten characters are described below:

Days to (50%) flowering

The regression line intersected above the point of origin suggesting partial dominance gene action for controlling the trait (Fig: a). The distribution of array points indicated two parents DH-11 (P_3) and DH-18 (P_1) contained most dominant alleles as they fell closer to the point of origin. Whereas rest of the parents fallen far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) observed partial dominance for the character in *Brassica rapa* L.

Days to maturity

The regression line intersected above the point of origin suggesting partial dominance gene action for controlling the trait (Fig: b). The parents BARIsar-10 (P_2), DH-18 (P_1) and Daulat (P_4) contained maximum dominant alleles as they fell closer to the point of origin. The parents Jun-536 (P_7) and BARIsar-11 (P_8) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. The parent BJ-17 (P_5) and BJ-11 (P_6) fell far from the origin and thus it contained maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) observed partial dominance in *Brassica rapa* L., Trivedi and Mukharjee (1986) found over dominance in *Brassica juncea* L.

Plant height

The regression line intersected above the point of origin suggesting partial dominance gene action for controlling the trait (Fig: c). The distribution of array points indicated three parents BARIsar-10 (P_2), DH-11 (P_3) and BARIsar-11 (P_8) contained most dominant alleles as they fell closer to the point of origin. Whereas rest of the parents fallen far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) obtained nearly complete dominance in *Brassica rapa* L.

Primary branches per plant

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance gene action for controlling the trait (Fig. d). The parent BJ-17 (P_5) fell closer to the origin means they contained maximum frequencies of dominant alleles. The parent BARIsar-10 (P_2) fallen far from the origin and thus it contained maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) observed nearly complete dominance for the character in *Brassica rapa* L., and Yadav and Yadava (1996) found over dominance in *Brassica campestris* L. respectively.

Secondary branches per plant

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance gene action for controlling the trait (Fig: e). The parents DH-11 (P_3) and Jun-536 (P_7) fell closer to the point of origin suggesting they contained maximum number of dominant alleles. The parents BJ-17 (P_5), BARIsar-10 (P_2), BARIsar-11 (P_8) and DH-18 (P_1) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. The parent Daulat (P_4) fell far from the origin indicating the presence of maximum frequency of

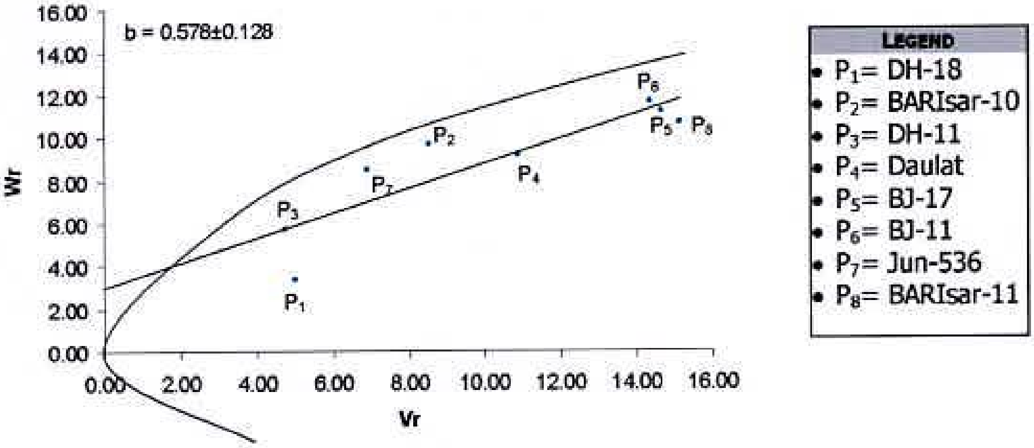

Fig a: Vr-Wr graph for days to (50%) flowering in *Brassica juncea* L.

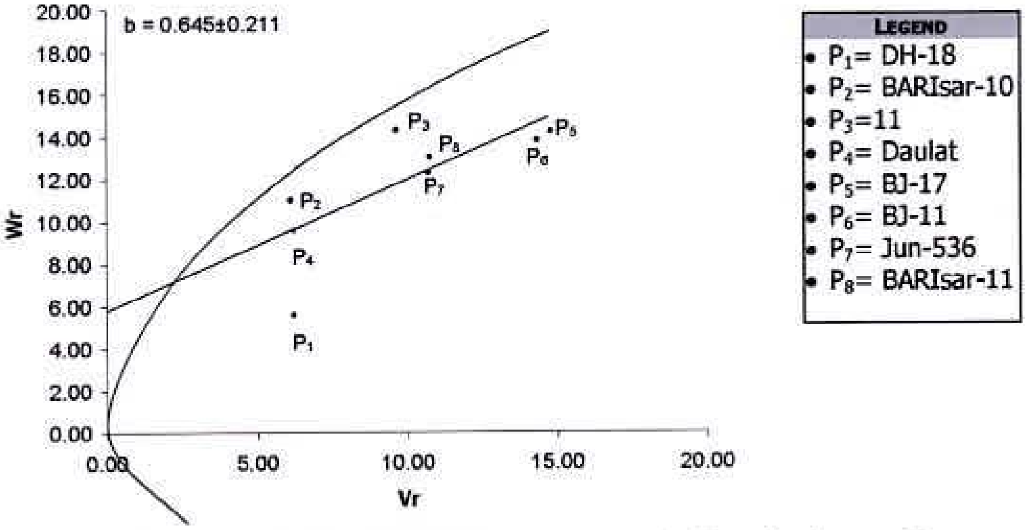

Fig b: Vr-Wr graph for days to maturity in *Brassica juncea* L.

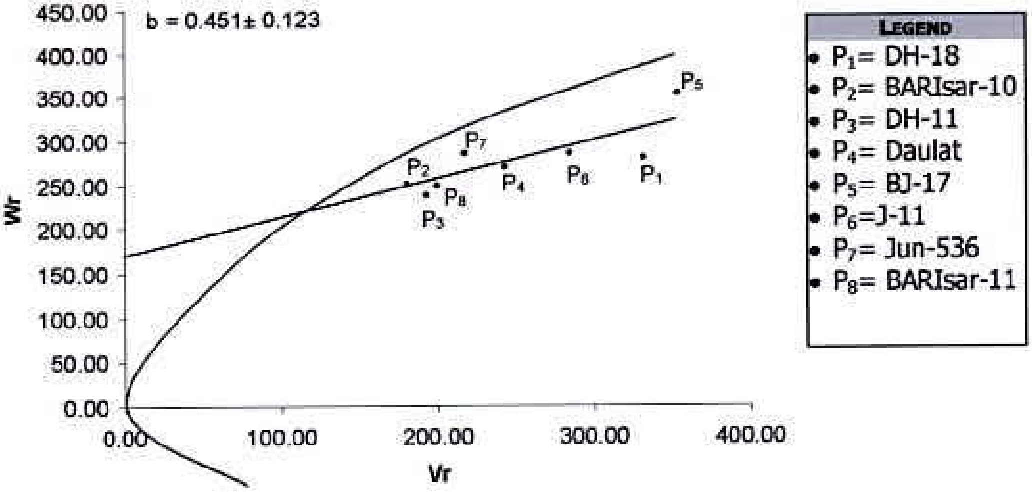

Fig c: Vr-Wr graph for plant height in *Brassica juncea* L.

recessive alleles in that parent. Chowdhury *et al.* (2004b) obtained partial dominance in *Brassica rapa* L., Yadav and Yadava (1996) observed over dominance in *Brassica campestris* L.

Siliquae per plant

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance gene action for controlling the trait (Fig: f). The parents BARIsar-11 (P_8) and DH-11 (P_3) contained maximum number of dominant alleles as they fell closer to the point of origin. The parents BJ-11 (P_6), DH-18 (P_1) and BJ-17 (P_5) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. The parents Daulat (P_4) and BARIsar-10 (P_2) fell far from the origin indicating the presence of maximum frequency of recessive alleles in that parent. Chowdhury *et al.* (2004b) and Trivedi and Mukharjee (1986) observed over dominance in *Brassica rapa* L. and *Brassica juncea* L. respectively.

Length of siliqua

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig: g). The parents DH-18 (P_1) and DH-11 (P_3) contained maximum dominant alleles as they fell closer to the point of origin. The parent BARIsar-10 (P_2) and Daulat (P_4) fallen at the nearly middle portion means they contained nearly equal frequencies of dominant and recessive alleles. The parent BARIsar-11 (P_8) fell far from the origin and thus it contained maximum frequency of recessive alleles. Trivedi and Mukharjee (1986) found over dominance in *Brassica juncea* L.

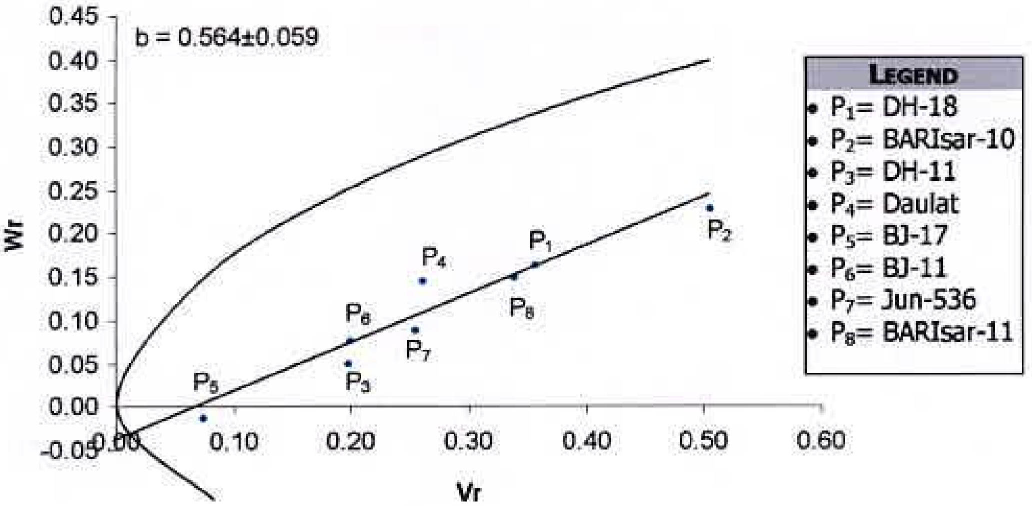

Fig d: Vr-Wr graph for primary branches per plant in *Brassica juncea* L.

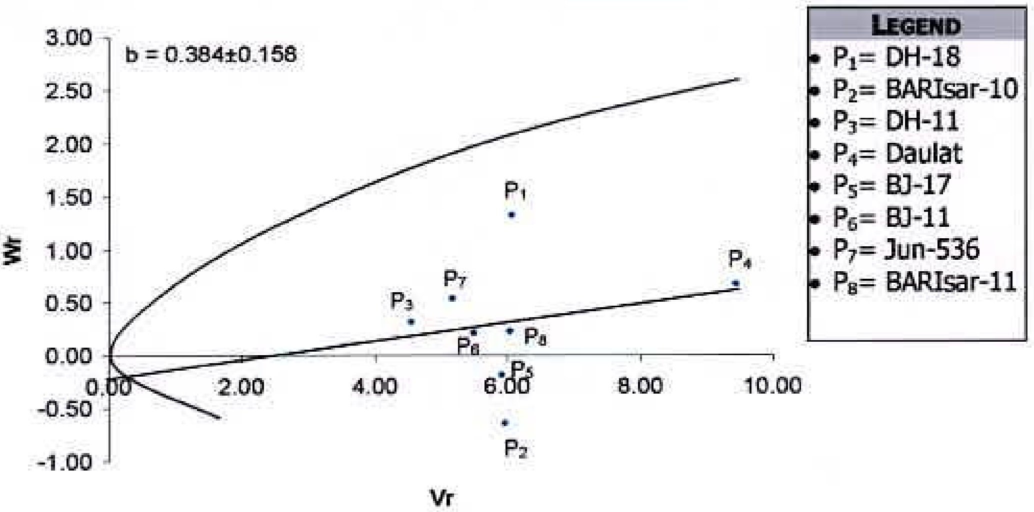

Fig e: Vr-Wr graph for secondary branches per plant in *Brassica juncea* L.

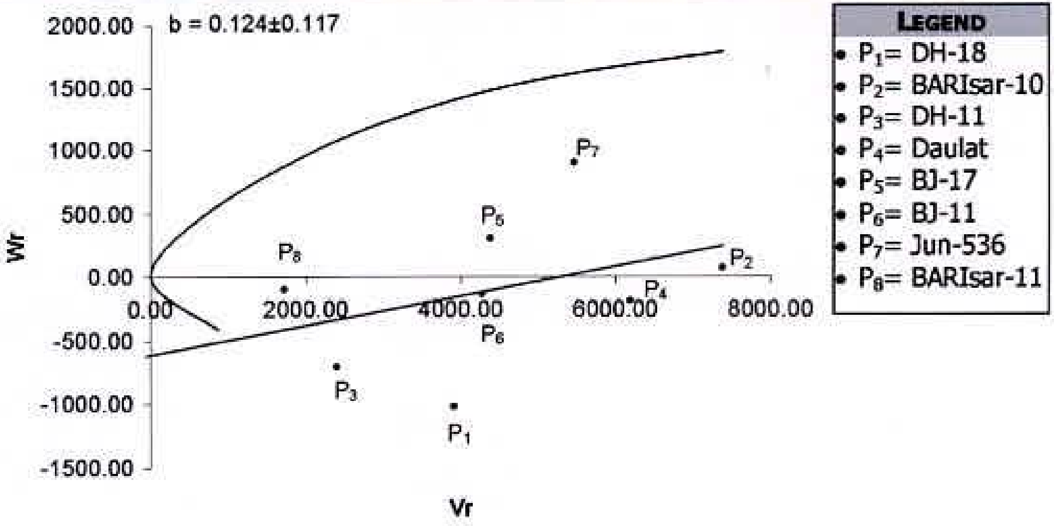

Fig f: Vr-Wr graph for siliquae per plant in *Brassica juncea* L.

Seeds per siliqua

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig: h). The parents DH-11 (P_3) and DH-18 (P_1) contained maximum dominant alleles as they fell closer to the point of origin. The parents BJ-17 (P_6) fallen far from the origin indicating the presence of maximum frequency of recessive alleles in those parents. Chowdhury *et al.* (2004b) observed over dominance in *Brassica rapa* L., Trivedi and Mukharjee (1986) found over dominance in *Brassica juncea* L.

1000-seed weight

The regression line intersected the Wr axis above the point of origin suggesting partial dominance gene action for controlling the trait (Fig: i). The distribution of array points indicated two parents Daulat (P_4) and BJ-11(P_6) contained most dominant alleles as they fell closer to the point of origin. The parents DH-11 (P_3) and Jun-536 (P_7) follen at the middle portion suggesting they contained equal frequencies of dominant and recessive alleles. The parent DH-18 (P_1) fell far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) found partial dominance in *Brassica rapa* L., Trivedi and Mukharjee (1986) observed over dominance in *Brassica juncea* L.

Seed yield per plant

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig: j). The parent DH-18 (P_1) fell closer to the point of origin indicating that it contained maximum dominant alleles. The parents DH-11 (P_3), BARIsar-11 (P_8), BJ-17 (P_5) and BJ-11 (P_6)

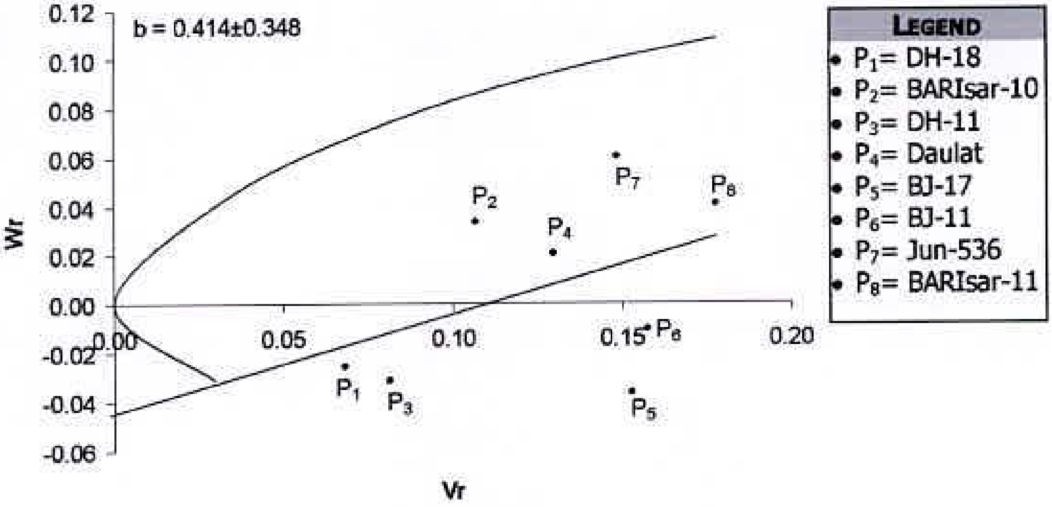

Fig g: Vr-Wr graph for length of siliqua in *Brassica juncea* L.

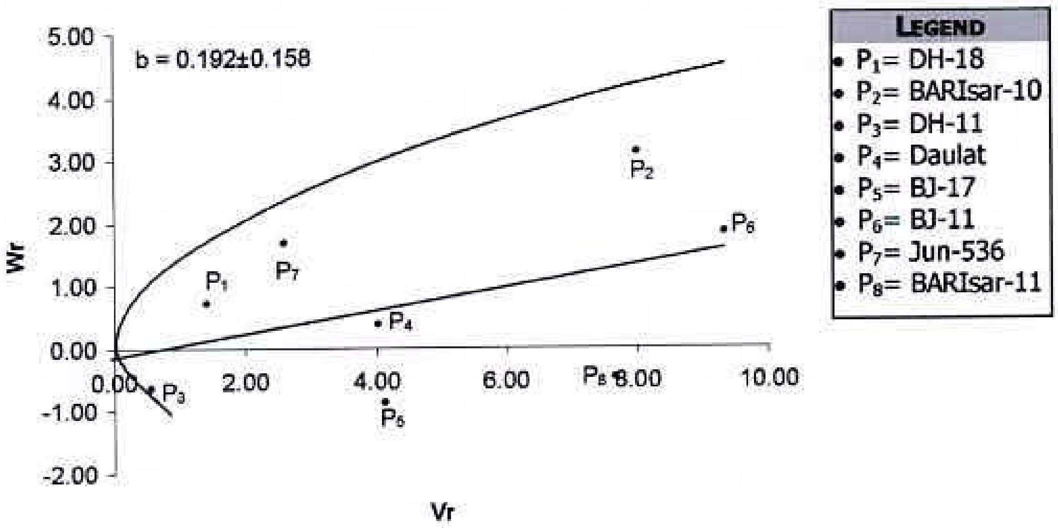

Fig h: Vr-Wr graph for seeds per siliqua in *Brassica juncea* L.

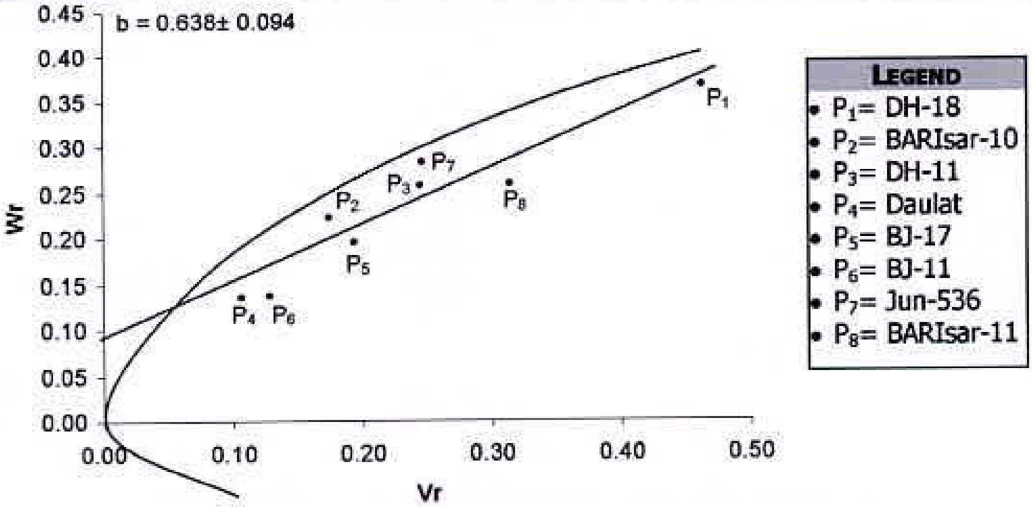

Fig i: Vr-Wr graph for 1000-seed weight in *Brassica juncea* L.

fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parents Jun-536 (P_7) and BARIsar-10 (P_2) fell far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) obtained over dominance in *Brassica rapa* L., Trivedi and Mukharjee (1986) observed over dominance in *Brassica juncea* L. respectively.

Harvest index

The regression line intersected the Wr axis above the point of origin suggesting partial dominance gene action for controlling the trait (Fig: k). The parent BARIsar-10 (P_2) fell closer to the point of origin indicating that it contained maximum dominant alleles. The parent BJ-17 (P_5) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parent DH-18 (P_1) fell far from the origin indicated that they possess maximum frequency of recessive alleles.

Oil content

The regression line intersected the Wr axis above the point of origin suggesting partial dominance gene action for controlling the trait (Fig: l). The parent DH-18 (P_1) and BJ-17 (P_5) contained maximum dominant alleles as it fell nearer to the point of origin. The parent DH-11 (P_3) fallen farthest from the origin indicating it possesses maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) found over dominance in *Brassica rapa* L. Trivedi and Mukharjee (1986) and Jindal and Labana (1985) observed partial dominance in Indian mustard.

Regression line intersected the Wr-axis below the origin for all the characters except days to flower, days to maturity, plant height, 1000-seed weight and oil content indicating the presence of over dominance. Such serious inflation of dominance has been postulated by Hayman (1954) and Jinks (1955). A further support to the existence

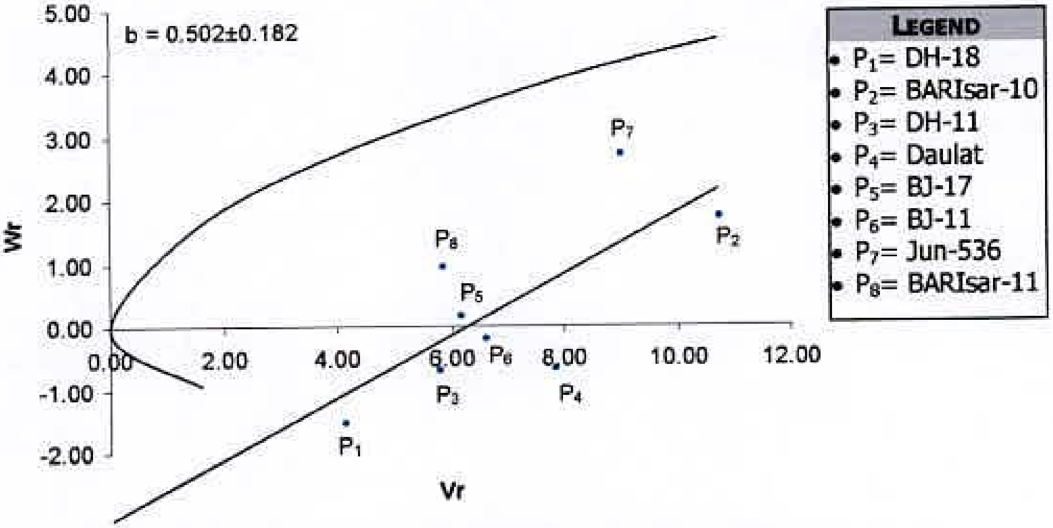

Fig j: Vr-Wr graph for seed yield per plant in *Brassica juncea* L.

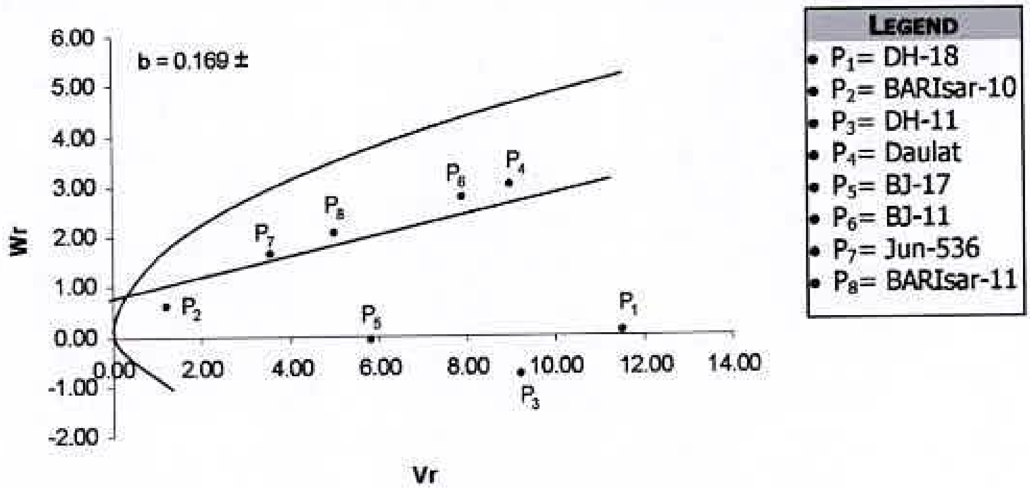

Fig k: Vr-Wr graph for harvest index in *Brassica juncea* L.

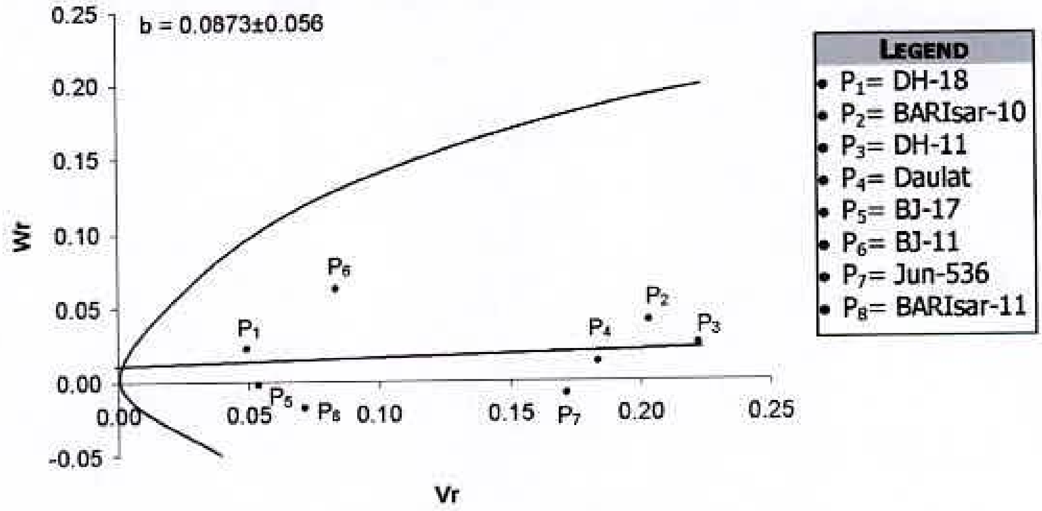

Fig l: Vr-Wr graph for oil content in *Brassica juncea* L.

of pseudo-over dominance was visualized in the estimates of D and H components and relative magnitude of gca and sca in variance component analysis for these traits. This was supported by the earlier findings reported by Chowdhury *et al.* (2004b) in turnip rape, Trivedi and Mukharjee (1986) in Indian mustard. The over dominance might not be an index of real over-dominance at gene level, since particular combination of positive and negative genes or a complementary type of gene interaction of simply correlated gene distribution could have caused serious inflation in particular combinations of unidirectional dominance which might have resulted in over-estimation of partial dominance (Comstock and Robinson, 1952; Hayman, 1954; Grafius, 1959). The presence of over dominance in the various components of oil yield and seed yield in the present study has also been substantiated by the findings of Singh *et al.* (1970, 1971) in *B. campestris* L., Rawat (1975) in *B. juncea* L., and Trivedi and Mukharjee (1985) in *B. juncea* L., Chowdhury *et al.* (2004b) in *B. rapa* L.

As non-fixable variation was high for all the attributes except days to maturity plant height and 1000-seed weight, considerable improvements of these traits might be possible by transferring complementary gene into non-epistatic high-dominance crosses or by eliminating duplicate genes from some of high-dominance crosses. A study of epistatic components would be helpful in formulating an efficient breeding programme.

The results obtained from both Griffing and Hayman's analysis indicated the importance of both additive and dominance genetic variances, the later being more important to utilise simultaneously both additive and dominant genetic variances.

CHAPTER 5

SUMMARY AND CONCLUSION

SUMMARY AND CONCLUSION

8 x 8 half-diallel cross analysis (excluding reciprocals) in Indian mustard (*Brassica juncea* L.) was carried out during November, 2005 to March, 2006 with the aim of obtaining various genetic information on seed yield and important quantitative traits and also of identifying the best parents and specific crosses of mustard.

The parental genotypes used in the study are DH-18, BARIsar-10, DH-11, Daulat, BJ-17, BJ-11, Jun-536 and BARIsar-11 which were chosen for their genetic differences and diverse origin. The characters studied are days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, 1000-seed weight, seed yield per plant, harvest index and oil content.

Analysis of combining ability following Griffing's approach showed significant gca and sca variances ($P< 0.05-0.01$) for all the characters studied, indicating the role of both additive and non-additive components in the genetic system controlling these characters. The higher magnitude of gca variance was observed than that of sca variance for all the characters except secondary branches per plant, length of siliqua, siliquae per plant and seed yield per plant, which indicated the preponderance of additive component in their expression. Estimates of gca effects for different characters suggested that parent BARIsar-10 (P_2) was the best general combiner for earliness and dwarfness. Daulat (P_4) was also good general combiner for early maturity and dwarf ness. BARIsar-11 (P_8) showed desirable gca for plant height, siliquae per plant and 1000-seed weight. Jun-536 (P_7) showed desirable gca for days to flower, plant height and seeds per siliqua. BJ-11 (P_6) showed desirable gca for days to maturity, secondary branches per plant and oil content. Both the parent DH-18 (P_1) and DH-11 (P_3) showed desirable gca for 1000-seed weight and seed yield per plant.

The sca estimates of various characters revealed that cross BARIsar-10 x BARIsar-11 (C_{13} = -2.12) was the best specific cross for days to flowering followed by BARIsar-10 x BJ-17 (C_{10} =-1.85). The best specific crosses were DH-11 x BARIsar-11 (C_{18} = -1.82) and BARIsar-10 x BJ-11 (C_{11} = -0.889) for days to maturity and which was also reflected the mean performance (Appendix-I). BARIsar-10 x BJ-11 (C_{11} = -7.08) for dwarf plant type. BARIsar-10 x DH-11 (C_8 = 0.792) for primary branches per plant, Daulat x BARIsar-11 (C_{22} = 3.55) for secondary branches per plant and seeds per siliqua (C_{22} = 2.87), BJ-17 x BARIsar-11 (C_{25} = 0.655) for length of siliqua, BARIsar-10 x Daulat (C_9 = 107.37) for siliquae per plant, DH-18 x DH-11 (C_2 = 0.534) for 1000-seed weight and harvest index (C_2 = 5.56), DH-18 x Jun-536 (C_6 = 4.02) for seed yield per plant and DH-11 x Jun-536 (C_{17} = 0.527) for oil content.

Mean square for additive and dominance components in Hayman ANOVA following Jones modification suggested that both additive and dominance components played role in the expression of studied characters. The additive components were generally more important in most of the characters except primary branches per plant, secondary branches per plant, siliquae per plant and seed yield per plant. Dominance was predominant in these four characters.

The components of variation revealed that both additive and dominance genetic components were important for all the studied characters. The components of variation due to dominance effect of the genes (H_1) was greater than (H_2) component for almost all the characters, indicating the presence of unequal proportion of positive and negative alleles in the loci governing the characters. The dominant alleles were predominant for all characters except days to maturity, plant height and 1000-seed weight.

An asymmetrical distribution of positive and negative alleles was found for all the characters studied. Dominant and recessive genes were unequally distributed in the parental genotypes for all the characters studied. High narrow senses heritability was observed for days to maturity, plant height and 1000-seed weight.

Result showed that simple additive-dominance genetic model to be adequate without presence of non-allelic interaction. Over dominance was observed for primary branches per plant, secondary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, seed yield per plant and harvest index. Partial dominance was noticed for days to flower, days to maturity, plant height, 1000-seed weight and oil content.

The parental genotype DH-18 (P_1) contained more dominant gene for seed yield per plant, oil content and length of siliqua. BARIsar-10 (P_2) contained more dominant gene for days to maturity, plant height and harvest index.

In the present study both additive and non-additive gene actions were found important in the expression of the characters. For exploitation of non-additive gene action in order to recover transgressive segregants by breaking undesirable linkage, releasing concealed variability and changing linkage equilibrium, it is necessary to follow modified breeding methods, viz., bi-parental cross or triple test cross or recurrent selection. The crosses such as DH-18 x Jun-536 (C_6), BARIsar-10 x Daulat (C_9), BARIsar-10 x BJ-17 (C_{10}), BARIsar-10 x BJ-11 (C_{11}) and DH-11 x BARIsar-11 (C_{18}) which exhibited high sca effects for seed yield and different yield components such as secondary branches per plant, siliquae per plant and 1000-seed weight might throw desirable or transgressive recombination in the subsequent generations.

Both additive and dominant genetic components were important for seed yield and yield components in Indian mustard (*Brassica juncea* L.). But, the magnitude of dominant component was higher than the additive components for all the traits except days to maturity, plant height and 1000-seed weight which indicated that dominance component had a predominant role in the inheritance of these traits. Non-additive type of gene action was found to be predominant for secondary branches per plant, siliquae per plant, seeds per siliqua, seed yield per plant and harvest index.

The Vr-Wr graph indicate over dominance for primary branches per plant, secondary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, seed yield per plant and harvest index. Partial dominance was observed for days to flowering, days to maturity, plant height, 1000-seed weight and oil content. The graphical analysis also indicates wide genetic diversity among the parents.

The parent BARIsar-10 was found good combiner for earliness based on the gca effects and *per se* performance. The good general combiners could be effectively used in future hybridization programme for developing high yielding and short duration varieties of Indian mustard (*Brassica juncea* L.).

CHAPTER 6

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CHAPTER 7

APPENDICES

Appendix I: Mean performance of 28 cross combinations of Indian mustard along with their parents during rabi 2005-2006

	Crosses & parents	DF	DM	PH (cm)	PBR	SBR	S/P	LS (cm)	S/S	SW	Y/P (g)	HI	OIL content
C-1	**DH-18** x BARIsar-10	43	101	135	5.4	15.03	348	5.68	14.3	3.28	11.7	32	40.9
C-2	x DH-11	49	107	183	5.4	11.02	260	5.85	11	4.62	11.6	35	41.3
C-3	x Daulat	44	101	149	5.7	12.35	373	5.23	10.7	2.49	9.9	31	41.3
C-4	x BJ-17	49	107	188	6	13.51	333	5.57	10.8	3.5	12.6	28	41.4
C-5	x BJ-11	49	107	180	6.3	13.23	368	5.02	12.1	2.75	12.6	23	41.5
C-6	x Jun-536	45	105	162	6.3	12.5	368	5.5	11.1	3.75	15.2	29	41.4
C-7	x BARIsar-11	48	107	157	4.6	9.93	284	5.34	11.1	3.77	11.7	31	41.4
C-8	**BARIsar-10** x DH-11	42	99	144	5.8	15.16	352	5.17	9.9	3.51	12.5	29	41.7
C-9	x Daulat	35	96	116	5.5	16.92	425	5.15	14.2	2.51	13.7	32	40.8
C-10	x BJ-17	37	96	129	6.0	15.3	396	4.92	13.6	2.37	13.7	31	40.9
C-11	x BJ-11	37	95	122	4.9	13.06	409	5.51	15.9	2.36	14.2	31	41.3
C-12	x Jun-536	39	96	123	5.7	14.27	388	4.95	11.9	2.83	12.1	30	41.8
C-13	x BARIsar-11	36	98	116	4.6	12.03	256	4.67	7.2	2.88	10.1	30	41.0
C-14	**DH-11** x Daulat	43	98	141	5.2	10.42	231	5.16	11.9	3.25	7.8	25	40.5
C-15	x BJ-17	45	98	167	5.5	12.5	276	5.3	10.5	3.36	9.7	27	41.3
C-16	x BJ-11	45	98	164	5.7	15.07	319	5.4	10.8	3.18	11.9	26	41.5
C-17	x Jun-536	44	99	154	5.6	13.03	331	5.8	11.4	3.66	12.9	27	42.0
C-18	x BARIsar-11	45	99	148	4.9	13.51	288	5.73	11.8	4.19	14	27	41.8
C-19	**Daulat** x BJ-17	42	98	143	5.6	14.84	336	5.62	12.1	2.43	9.4	25	41.3
C-20	x BJ-11	41	98	158	5.6	14.73	339	6.07	16.1	2.37	12.3	26	41.5
C-21	x Jun-536	39	97	129	5.1	14.75	260	5.98	14.7	2.62	10	26	40.6
C-22	x BARIsar-11	38	98	140	5.4	15.51	273	5.48	15.6	2.79	12	27	41.5
C-23	**BJ-17** x BJ-11	41	97	156	5.4	16.67	280	4.94	9	2.67	8.7	24	41.4
C-24	x Jun-536	42	97	151	5.4	12.8	290	5.63	14	2.5	10.3	25	41.5
C-25	x BARIsar-11	45	97	152	5.3	11.09	296	6.07	14.3	2.36	9.8	26	41.3
C-26	**BJ-11** x Jun-536	41	100	147	5.6	13.92	363	5.70	15.1	2.6	10.9	28	41.5
C-27	x BARIsar-11	43	99	148	5.6	12.7	315	5.14	8.7	3.33	11.6	28	41.3
C-28	**Jun-536**x BARIsar-11	41	98	123	5.4	13.5	316	5.2	12.4	3.38	11.9	30	41.2
P-1	DH-18 (P_1)	47	106	167	5.2	7.08	207	5.37	11.2	3.98	8.33	30	41.0
P-2	BARIsar-10 (P_2)	38	94	100	4.0	9.05	175	5.27	13.9	3.03	4.3	32	41.8
P-3	DH-11 (P_3)	44	104	152	4.5	9.29	220	5.31	12	3.69	7.4	28	41.1
P-4	Daulat (P_4)	36	92	113	4.1	7.6	178	5.36	14.3	2.17	4.9	32	41.5
P-5	BJ-17 (P_5)	38	94	134	5.3	9.06	165	5.69	13.9	2.7	5.4	28	41.7
P-6	BJ-11 (P_6)	38	95	143	5.1	8.66	294	5.77	14.6	2.53	6.0	30	42.1
P-7	Jun-536 (P_7)	38	96	128	4.5	7.6	160	4.98	11.5	3.15	4.9	31	41.6
P-8	BARIsar-11 (P_8)	40	99	127	3.9	7.83	189	5.18	10.6	3.32	5.8	31	41.0
	Mean	**41.8**	**99**	**145.8**	**5.3**	**12.38**	**293**	**5.41**	**12.3**	**3.02**	**10.7**	**28.5**	**41.3**
	Max	49	107	188	6.5	16.92	425	6.07	16.1	4.62	15.2	35	42.1
	Min	36	94	122	3.9	7.08	178	4.67	7.2	2.17	4.3	23	40.5

Note: DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PBR = Primary branches per plant, SBR = Secondary branches per plant, S/P = Siliquae per plant, LS = Length of siliquae (cm), S/S = Seeds per siliquae, SW = 1000-seed weight, Y/P = Yield per plant (g), HI = Harvest index, OIL % = Oil content

Appendix II: Mean monthly weather data during the crop growing periods, BARI, Joydebpur, Gazipur, Bangladesh

Month	Characters			
	Temperature		Rh (%)	Rain (mm)
	Min	Max		
November 1-15	19.4	30.0	90	Nil
November 16-30	16.8	28.1	89	Nil
December 1-15	13.9	27.4	83	Nil
December 16-31	14.3	26.8	86	Nil
January 1-15	11.7	24.2	84	Nil
January 16-31	12.5	26.6	83	Nil
February 1-14	15.6	29.3	79	Nil
February 15-28	20.9	34.4	86	Nil

Source: Agronomy division, BARI.