GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN *Brassica rapa* L.

MD. AKKAS ALI

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

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GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN *Brassica rapa* L.

BY

MD. AKKAS ALI

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Approved by:

_____
(Prof. Dr. Md. Shahidur Rashid Bhuiyan)
Chairman
Advisory Committee

_____	_____	_____
(Prof. Dr. Md. Sarowar Hossain)	**(Prof. Dr. Naheed Zeba)**	**(Prof. Dr. Md. Hazrat Ali)**
Member	Member	Member
Advisory Committee	Advisory Committee	Advisory Committee

DEDICATED

TO

MY BELOVED PARENTS

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh

Mob: +8801552467945
E-mail: ipbscfc2009@gmail.com

CERTIFICATE

This is to certify that thesis entitled, **"Genetic analysis of yield and its components in Brassica rapa L."** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **MD. AKKAS ALI**, Registration No. **10-04222** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2014
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Shahidur Rashid Bhuiyan)
Chairman
Advisory Committee

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LIST OF SYMBOLS AND ABBREVIATIONS

Abbreviation	Full Words	Abbreviation	Full Words
%	Percentage	MP	Muriate of Potash
CD	Critical Difference	EC	Emulsifiable concentrate
sca, SCA	Specific Combining Ability	@	At the rate of
gca, GCA	General Combining Ability	ml	Milliliter
e.g.	Exempli gratia (by way of example)	RCBD	Randomized Complete Block Design
et al.	and others (at ell)	F_1	Mean of F_1 Individuals or Mean of reciprocal individuals
FAO	Food and Agricultural organization	$\overline{BP}$	Mean of better parent values
cm	Centimeter	$\overline{MP}$	Mean of the mid parent values
Mt	Metric ton	g	Gram
BARI	Bangladesh Agriculture Research Institute	BBS	Bangladesh Bureau of Statistics
SAU	Sher-e-Bangla Agricultural University	ANOVA	Analysis of variances
J.	Journal	Kg	Kilogram
No.	Number	BINA	Bangladesh Institute of Nuclear Agriculture
var.	variety	EMS	Error mean sum of square
viz.	Namely	HBP	Heterosis over better parent
df.	Degrees of freedom	HMP	Heterosis over mid parent
MP	Mid parent	N	North
F_1	The 1^{st} generation of a cross between two dissimilar homozygous parents	E	East
F_2	The 2^{nd} generation of a cross between two dissimilar homozygous parents	pH	Negative logarithm of hydrogen ion concentration (-log [H+])
BP	Better parent	HYV	High yielding varieties
TSP	Triple Super Phosphate	GMA	Generation Mean Analysis

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ABSTRACT

The experiments were carried out at Sher-e-Bangla Agricultural University from October, 2010 to March, 2013 to perform genetic analysis of yield and its components of *Brassica rapa* genotypes generated through half diallel crosses and back crossing. No parent showed significant positive gca for yield per plant. SAU Sarisha 2 and SAU Sarisha 3 showed significant negative gca for days to maturity. In case of hybrids, the lowest days to the maturity of 79.33 days was observed in SAU Sarisha 3 × TORI 7. The highest yield per plant and 1000 seed weight were observed in the hybrids BARI Sarisha 6 × SAU Sarisha 2 and BARI Sarisha 6 × SAU Sarisha 1 respectively. The life span of the parent SAU Sarisha 3 was the lowest but the yield was moderate in comparism to other parents. The highest yield and 1000-seed weight were noticed in TORI 7 and its 80% maturity was achieved in 81 days. No hybrid showed significant higher yield over better parent. Three hybrids showed significant negative heterosis for days to maturity. Significant additive and dominant, additive × additive, additive × dominant and dominant × dominant gene interaction were present in Tori 7 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 2, and SAU Sarisha 2 × SAU Sarisha 3.For numbers of siliqua per plant, number of seed per siliqua and length of siliqua, Vr-Wr graph indicated over dominance gene action for controlling these traits. However, partial dominance gene action was found for controlling the yield per plant. The D and H components were significant for all the traits under study suggesting the importance of both additive and dominance components for the inheritance of all the traits in *B. rapa*. The ratios of H2/4H1 provide an estimate of the average frequency of positive and negative alleles in all the parents. Regression line intersected the Wr-axis below the origin for all the characters except yield per plant indicating the presence of over dominance. There was no evidence of non-allelic interaction for the character plant height which agreed with the conclusion from individual scaling test results. For the remaining crosses at least one of the two (i and l) interaction parameters were significantly different from zero. The dominance × dominance effects were greater in magnitudes that additive × additive and additive × dominance in all cases which recorded non-allelic interaction in case of plant height. The highest heritability was recorded for days to maturity (99.99%) in the hybrid P1 (TORI 7) × P3 (SAU Sarisha 2). In the cross P1 (TORI 7) × P2 (SAU Sarisha 1), length of siliqua showed high narrow sense heritability (58.06%) with very low genetic gain (0.65). High narrow sense heritability with high genetic gain showed better selection in early segregating generations leading to substantial improvement of the character. In this hybrid P2 (SAU Sarisha 1) × P6 (BARI Sarisha 15), yield per plant showed high broad sense heritability but the narrow sense heritability was poor which might be due to presence of non allelic interaction for this character. High values for heritability and genetic advance for various traits indicated good genetic potential for selection.

CHAPTER 1
INTRODUCTION

The oleriferous *Brassica* represented by rapeseed and mustard plays an important role in vegetable oil production of the world and contributes approximately 10% of the world's vegetable and 12% of the worldwide edible oil supply (USDA, 2014).The genus *Brassica* belongs to the family Brassicaceae is an important genus of plant kingdom consisting of 3200 species with high diverse morphology. It has generally been divided into three groups namely rapeseed, mustard and cole (Yarnell *et al*., 1956). The component species of rapeseed are *Brassica campestris* L. (turnip rape) now *Brassica rapa* and *Brassica napus* L. (rape) while mustard group includes *B. nigra* Koch, *B. carinata* Braun and *B. juncea* Czern Coss (Yarnell *et al*., 1956). The cole includes the vegetables like cabbage, cauliflower etc. The primary center of origin for *B. rapa* is near the Himalayan region and the secondary center of origin is located in the European–Mediterranean area and Asia.

Brassica is one of the most important annual oil and protein rich crops in the world. Seed provides oil both for industrial and culinary purpose to meet up the demand of mankind. Vegetable oils and fats (lipids) constitute an important component of human diet. Oils of plant origin are nutritionally superior to that of animal origin (Singh, 2000). Rapeseed and mustard is the second most important edible oil source in the world after soybean (FAO, 2014). Total area of mustard and rapeseed in the world is 34.33 million hectares (FAO, 2013). In 2012-2013, the edible oil production from major oilseed crops in the world is 497.9 million tons where rapeseed contributes 64.3 million tons (FAO, 2014). Vegetable oils are used mostly for edible purpose and a part finds industrial application. Bangladesh produces good number of oil seed crops like rapeseed and mustard, sesame, groundnut, linseed, niger, safflower, sunflower, soybean, castor etc. of which rapeseed and mustard is considered as the major one (Razzaque and Karim. 2007).

The utilization of oil seed in Bangladesh is 1.8 million tons where 1.6 million tons is

imported (FAO, 2013). In Bangladesh, *B. rapa* is the main oil yielding species of *Brassica* (FAOSTAT, 2013). It is the top ranking oil seed crop in Bangladesh that covers about 60% of the total acreage of land (BBS, 2010). That is why *B. rapa* is grown widely in the country (Islam, 2013). It occupies the first position in oil crops with cultivated area 252238.13 ha which produced 0.246494 million tons seed and average yield was 0.99 t/ha during 2010-2011 (BBS, 2011a).

Although a huge amount of oilseed is utilized in Bangladesh, the production is not sufficient to meet the requirement (Razzaque and Karim, 2007). As the population of Bangladesh is increasing and economic prosperity has been growing fast, it is now a challenge for accelerating the production of oils. It is essential to reduce the import dependence of it to insulate the domestic market from the volatility of the world market (Hossain, 2013). The production of oilseed is very low compared to its requirement in Bangladesh (BBS, 2011b). To fulfill this lacking the country imports 0.89970 million tons of mustard oil that costs 371.8457000 million in taka (BBS, 2011c).

The area for rapeseed and mustard is reduced from 0.784730 million acres to 0.5780208 million acres in 2001 to 2009 due to increasing Boro rice cultivation (BBS, 2010). The reduction of area for the crop is 26.32% (Bhuiyan, 2012). On the other hand, the area as well as production was increased in 2013-14 compared to the 2012-13. In 2012-13 and 2013-14, the production was 1.10 and 1.12 ton per hectare considering the occupied land area was 0.518 and 0.532 million hectares, respectively (MoA, 2014).

In Bangladesh, per capita consumption of edible oil is one of the lowest in the world (11kg/head/day) which is one fifth of the recommended requirement for a balance diet (FAO, 2014). In spite of being a major oil producing crop, *Brassica sp.* has lower yield per hectare than the other developing countries. As *B. rapa* is well suited in cropping pattern with rice variety i.e. Aman-Mustard-Boro, farmers rely mainly on short durable mustard varieties (Karim *et al.*, 2014). In this context, farmers of Bangladesh still use the low yielding varieties with smaller seed size and lower seed wt. such as 2-2.5g/1000seeds. The

leading short durated variety of *B. rapa* in Bangladesh is Tori-7 but it has lower yield potentiality 1.1-1.3 t ha^{-1} (Karim *et al.,* 2014). There is no improved short durated and high yielding variety to replace the variety at present in Bangladesh.

The targeted yield of oil seed in 2015-2020, 2020-2025 and 2025-2030 is 1.73, 2.14 and 2.57 t ha^{-1} in Bangladesh that is now 1.18 t ha^{-1} only. In present status, there are total 14 varieties of *B. rapa* in the county. Among them 8 are released from Bangladesh Agricultural Research Institute (BARI), 3 from Bangladesh Institute of Nuclear Agriculture (BINA), 2 from Sher-e-Bangla Agricultural University (SAU) and 2 from Bangladesh Agricultural University (BAU) (Rahman and Chowdhury, 2010). There are many varieties and hybrids being developed in different parts of the world. In Bangladesh the crop has got importance and a few varieties have been developed by Sher-e-Bangla Agricultural University, Bangladesh Agriculture Research Institute, Bangladesh Institute of Nuclear Agriculture and Bangladesh Agricultural University.

Grain yield and oil content of mustard and rapeseed groups ranged between 600 and 3000 kg/ha and 30 and 45 percent, respectively depending upon the species, the variety and climatic conditions under which they are grown (Kakroo and Kumar, 1991). Breeding for yield improvement usually practiced through selection indices based on yield and yield contributing characters.

Information on the nature and magnitude of variability present in the existing material and association among the various morphological characters is a prerequisite for any breeding programme to be initiated by the breeders for high yields. However, yield, a complex character, is usually controlled by non-additive gene action and it is not only influenced by a number of other morphological characters which are governed by a large numbers of genes, but also environment to a great extent. Thereby, the heritable variation creates difficulty in a selection programmed. Therefore, it is necessary to partition the overall variability into heritable and non-heritable components which enable the breeders to adopt suitable breeding procedure for further improvement of genetic stocks.

Hybridization at the inter-varietal level is a common method to combine desirable genes, creating genetic variability and to develop new varieties. Intra-specific or inter varietal hybridization is a good way of improving the existing varieties of different natures by combining desired traits followed by selection. The most important aspect for hybridization is the choice of parents and the selection of best genotypes for hybrid progenies. Information on yield and its components of hybrid progenies at its early generation are very useful for the purpose of selection criteria. Information regarding genetic variability is necessary for initiating a successful breeding program. The experiment will be carried out to study genetic parameters such as heterosis, heritability, genetic advance and genetic advance in percentage of mean, genetic diversity, combining ability and direct and indirect effect of genes of different traits on yield and its components.

Combining ability studies are reliable as they provide useful information for the selection of parents in terms of performance of the hybrids and elucidate the nature and magnitude of various types of gene action involved in the expression of quantitative traits. Genetic information helps in the selection of suitable parents for hybridization and in isolating the promising early generation hybrids for further exploitation in breeding programs. Information on heterosis and combining ability of hybrid progenies at its early generation are very useful for the purpose of selection criteria.

Generation mean analysis, a biometrical method developed by Mather and Jinks (1982), is a useful technique for determining gene effects for polygenic traits. Gene action of each quantitative trait such as yield and its yield component can be evaluated by generation mean analysis. One of the best methods for the estimation of genetic parameters is generation mean analysis, in which epistatic gene effect such as additive×additive, additive×dominance and dominance ×dominance interaction could also be estimated. Therefore, generation mean analysis study was designed to (1) determine gene action (2)

estimate components of variance (3) estimate broad and narrow sense heritability's (4) test the adequacy of simple additive dominance model.

The understanding of the relative contribution of the genetic components i.e, additive, dominance, epistasis and linkage that control the variation is of great importance for any improvement in a trait under a breeding program. Information regarding additive genetic variance, dominance variance, environmental component of variation, proportion of positive and negative genes, distribution of genes among the parents, ratio of dominant and recessive genes and average degree of dominance can be obtained through the diallel analysis (Hayman's approach). Specific combining ability and general combining ability can provide information about the type of gene action controlling a trait. Variance for general combining ability (GCA) is the additive portion while specific combining ability (SCA) is the non-additive portion of total variance (Malik *et al*., 2004). It is important to have information about the desirable parental combinations which can represent a high degree of heterotic response. By exploiting heterosis in the F_1 hybrids, production cost could be reduced by increasing yield level and enhancing input use efficiency (Pingali, 1997). Information regarding relative importance of average effect of genes, dominance deviation and effect due to epistasis, in determining genotypic values of individuals and consequently, mean genotypic values of families and generations can be derived through generation mean analysis.

The present investigation is an attempt to generate genetic variation in *B. rapa* genotypes through hybridization and genetic information on yield and yield components for selection in different generations. In the present studied, different generations of *B. rapa* were obtained which were evaluated through different years with the following objectives:

- Performance of the rapeseed genotypes for yield and yield contributing characters.
- To estimate the nature, extent and magnitude of gene action for the yield and yield contributing traits.

- To estimate heterosis and inbreeding depression for different yield contributing characters of rapeseed.
- To identify the potential parents and promising cross combinations to utilize them in developing high yielding short durated varieties.

CHAPTER 2
REVIEW OF LITERATURE

Rapeseed is the most important oil crops of Bangladesh and many countries of the world. The crops have received much attention by a large number of researchers on various aspects of its production and utilization. Identification of suitable parental lines on the basis of their genetic parameters, nature and magnitude of genetic variability and the correlation of different yield attributing characters is important for successful rapeseed breeding programs. Yield in rapeseed is associated with many yield contributing characters and in addition there are other characters plant height, days to maturity, raceme length, number of siliquae per plant etc. which also contribute to rapeseed yield. Reviewing the information and knowledge on performance of different genotypes, variation for genetic divergence, relationship between yield and yield contributing characters, heritability and genetic advance for yield and yield contributing characters in rapeseed is important for future breeding programme.

2.1 The Combining ability analysis

The concept of combining ability (CA) is very important. Combining ability is the ability to produce superior hybrids in combination with other inbreeds. In crop breeding for hybrid varieties, general and specific combining ability effects are important indicators of the potential of inbred lines in hybrid combination. General combining ability (GCA) is the average performance of a line in hybrid combination and specific combining ability (SCA) is the deviation of certain cross from the average performance of the lines (Sprague and Tatum, 1942).

Many investigators used diallel techniques to study the genetics of *Brassica* species particularly *B. juncea* and *B. napus*. To perform a successful investigation for the improvement of various characters of crop plants, diversity in germplasm i.e., phenotypic and genotypic variations, is basic requirement. Paul (1978) reported wide range of

variations in yield contributing components viz. number of primary branches, number of secondary branches, siliquae per plant and seed size in F_1 and F_2 populations. He studied five inter-varietal crosses of mustard. In a study, Singh *et al*. (1987) evaluated 179 *B. juncea* genotypes and found considerable genetic variability for 15 traits. High genotypic and phenotypic variations were found for seed yield and number of siliquae per plant by Chowdhury and Goswami (1991) as they analyzed 40 genotypes of *B. juncea* for 14 yield related characters. Rabbani *et al*. (1999) classified 52 accessions of Indian mustard mostly collected from Pakistan, for different morphological traits. He suggested that oilseed mustard had a narrow genetic base in Pakistan.

After evaluation of 1708 genotypes from twenty *Brassica* species by near infrared reflectance spectroscopy (NIRS), Velasco and Becker (2000) reported very high variability for seed glucosinolates content and profile. A diallel analysis was carried out with nine inbred lines of Indian mustard by Thakral *et al*. (2000) showing the presence of both additive and non-additive genetic components. Results revealed that additive component of variation were more important for 1000-seed weight and length of main shoot. The H1/D1/2 ratio indicated presence of over dominance for all the traits.

Tyagi and Singhal (2001) investigated twelve Indian mustard/rape cultivars, i.e, Raya RH 781, Raya RH 2859, Raya RC 781, Toria Shyamgarh, Toria TH 83, Toria Sangram, Toria Kranti, Toria TH 109, B 054, B Bold, *B. carinata* and *B. napus* for proximate composition, cell wall constituents and total glucosinolate content. The highest values were detected for oil (38.96%), crude protein (46.23%) and glucosinolate content for Toria Kranti, Toria Shyamgarh and Toria Sangram, respectively. No significant relationship was found between oil and glucosinolate content. Similarly, in a study Shalini *et al*. (2001) estimated different genetic parameters to assess the magnitude of genetic variation in 81 diverse Indian mustard genotypes. For all the studied 10 characters, the results for analysis of variance showed that sufficient genetic variation was present among the genotypes. In another investigation, forty-five hybrids of Indian mustard obtained from crossing of 10 cultivars (Varuna, PR 9625, HUM 9512, BIO 772, PCR 7, RH 9511, Ronini, Seeta, RH

9401 and PSR 30) were investigated for seed yield and its components by Tyagi *et al*. (2001). For plant height of parents and their hybrids, variations were maximum however, seed yield per plant showed maximum coefficient of variation (41.1%).

After studying morphological characters and patterns of variability for fatty acid profiles of 14 low erucic accessions of rapeseed and mustard, Chauhan *et al*. (2002) found that erucic acid content of 5 accessions, 3 from Indian mustard and 2 from rapeseed, was consistently zero however, it varied from 0 to 1.6% in remaining accessions. The study also revealed that Indian mustard accessions were taller (214.1 cm.) and matured earlier (125 days) than rapeseed accessions. However, higher oil content (40.6-40.9%) were found in rapeseed accessions than the Indian mustard accessions (33.0-38.4%). Protein content ranged between 19.6 to 25.7% irrespective of the crops. Noshin *et al*. (2003) evaluated F_1 generation of brown mustard (*Brassica juncea* L.) through a 6x6 diallel experiment to examine the inheritance pattern of various yield related components. Analysis of variance indicated that highly significant differences were present for parents and their hybrids for all the characters studied in F_1 generation except seed yield per plant. The genetic analysis indicated that additive effects were prominent for plant height, primary branches, siliqua per main inflorescence and seed yield per plant. Dominant gene effects were found to be important in controlling inheritance of number of secondary branches. Regression line deviated non-significantly and thus, supporting the absence of epistasis.

An experiment was carried out by Khan and Khan (2003) to evaluate the genetic potential of eight *Brassica* accessions sown under RCBD in four replications, in Faisalabad, Pakistan in 2001-02. Genetic differences were significant among all the accessions for different traits. They suggested that improvement in plant height, number of primary and secondary branches, siliquae per plant and seed index would result in improvement in seed yield. A 6x6 diallel experiment on F_1 generation of Brown mustard was performed by Iqbal *et al*. (2003) to study the genetic control of some important agronomic and quality characters. Highly significant differences among parents and their hybrids in F_1 generation were revealed by analysis of variance, for all the characters except for days to maturity.

The genetic analysis indicated that days to flowering and erucic acid were under the control of additive gene action, while glucosinolates content, oil percentage and days to maturity were governed by over dominance. Non-significant deviation of regression line from the unit slope inferred that epistasis was absent.

A line x tester experiment was carried out by Rai *et al*. (2005). 60 F_1 Indian mustard genotypes were analyzed. Siliqua length, 1000-seed weight and oil content showed over-dominance. Partial dominance was identified for days to 50% flowering and days to maturity, number of primary and secondary branches, siliquae on main raceme, seeds per siliqua, plant height and seed yield per plant. Narrow-sense heritability was high for days to flowering and maturity, number of secondary branches, plant height, oil content and seed yield while low estimates were observed for siliquae length. PCR-20, RK-9301, DIR-612, NDR-119, RL-962, KBJ-39 and Kranti showed desirable general combining ability effects. Significant positive specific combining ability was found for 76.92% of the crosses for seed yield. An experiment was undertaken by Alemayehu and Becker (2005) to estimate the level of natural variation for oil, protein and total glucosinolates, in Ethiopian mustard cultivars through diallel cross of six inbred lines. Significant differences were indicated through analysis of variance among the parental lines as well as their hybrids. To estimate genetic parameters and interactions, Hayman's method of diallel analysis and a mixed linear model were used. The results showed that for all the traits, additive, dominance and cytoplasmic effects were highly significant. The additive variance was twice the dominance component which was also approximately twice the cytoplasmic component of variance. Total glucosinolate contents were governed by partial dominance however, some indications of over dominance were also detected.

Khan *et al*. (2005) evaluated eight genotypes of *Brassica juncea* L. and found considerable variability for siliqua length, seed yield, number of primary branches 1000-seed weight, oil content and plant height indicating good potential for selection. In another study Bhutto *et al*. (2006) studied various yield contributing characters in eight commercial cultivars of

Brassica species and their eight F_1 hybrids. Considerable variability among all the entries was determined by analysis of variance.

Ten Indian mustard parents were mated in diallel pattern excluding reciprocals by Shweta *et al*. (2007a). The results derived from analysis showed the frequency of dominant genes for all 10 yield related traits except days to flowering. For plant height, seed yield and days to flowering, symmetrical proportions of negative and positive genes were detected. For the remaining characters, negative and positive genes were found in asymmetrical proportions. More than one group of major genes was found to be present in governing the inheritance of most of the traits. Predominance of non-additive gene action was identified for seed yield and its attributes. Heterosis breeding was proposed for improvement of seed yield and its component by exploiting non-additive gene action. In another experiment, Shweta *et al*. (2007b) carried out a study on Indian mustard using diallel crossing technique consisting of 10 parents and 90 crosses. Number of siliquae on main raceme in both the generations, secondary branches in F_1 and primary branches and oil content in F_2 showed over dominance with presence of non-additive gene effects while remaining traits showed partial dominance.

Fifty-six advanced breeding lines of Indian mustard selected for superior oil quality (low erucic acid in oil) along with 3 controls, i.e, Kranti, Pusa Karisma and PRQ-2005-1 were evaluated for fatty acid composition and yield performance by Singh and Singh (2008). Considerable genotypic variation for 1000-seed weight, days to maturity and total oil content was present among the 56 advanced lines. Low erucic acid and high oleic acid contents were noticed in many advanced breeding lines and this potential might be explored for developing new cultivars with improved oil quality. In a field experiment, Iqbal *et al*. (2008) evaluated ten genotypes each of *Brassica napus* and *Brassica juncea* under semi-arid conditions. Great variability was shown by genotypes of both *Brassica* species for yield, days to flowering and maturity, primary branches, plant height and other yield related traits. *B. juncea* showed much better estimates for yield and related attributes than *B. napus* genotypes. Oil content was higher while erucic acid and glucosinolates contents were lower in *Brassica napus* than *Brassica juncea*.

Singh *et al*. (2008) evaluated thirty-three families of Indian mustard (*Brassica juncea*) to determine additive, dominance and epistatic component of variation. Epistasis was present for all of the characters. The results showed that additive x additive (i type) of interaction was important for all the characters except for primary branches, secondary branches and seeds per siliquae. j and l types interactions were prominent for all the characters. Prominence of both additive and dominance components for all the characters indicated that both the additive and dominance components were significant in genetic control of the characters. Therefore, in advance generation, selection would help to improve the seed yield. The selection must not be carried out in early generations due to presence of epistasis. However, in advanced segregating generations, biparental mating could be effective to enhance seed yield.

Eighty-five accessions (with three controls) of Indian mustard (*Brassica juncea*) were investigated by Misra *et al*. (2008) for morphological, yield and quality characters under irrigated condition. For all the traits, considerable variability was noticed. The highest values were reported for seed yield (CV 48.4%) and 1000-seed weight (CV 27.6%), respectively and lowest variability estimates were noticed for protein content (CV 5.7%). Significant positive correlation was observed for seed yield, number of primary branches, number of secondary branches plant, shoot length, plant height and harvest index. Genotype IC-342777 was found to be a useful contributor for main shoot length, siliquae on main shoot, number of secondary branches and seed yield per plant and IC-248995 was recognized to be useful for improvement in early flowering and more number of siliquae on main shoot. Malviya *et al*. (2009) examined thirty six crosses and for days to maturity and siliquae on main raceme, epistasis was detected.

Understanding of the genetic control of agronomic characters and its expression is the basic requirement of the purposeful management of genetic variability. In addition, the choice of a suitable breeding method depends to a large extent on the nature of gene action involved. Wright (1921,1935) defined three types of variance as additive genetic variance,

variance due to dominance deviations and epistatic variance resulting from the interaction of non-allelic genes. Among the various mating designs developed for the determination of the genetic architecture of quantitative characters, the Line x Tester method, has received considerable attention of the geneticist and plant breeders.

Apart from measuring additive and dominance components of variation, appropriate model can be used to detect, though not measure, non-allelic gene interactions by using graphical representation (Vr-Wr graphs). The diallel approach has been extensively used in cross pollinated crops. Griffing (1956, 1958) emphasized the statistical concepts of general and specific combining ability. Hayman (1954,1957) attempted to obtain estimates of certain genetic parameters from statistics involving parents and off-springs. Variances for general combining ability, involves mostly additive gene effects while variance for specific combining ability depends on dominance and epistatic component of variation.

Some researchers used combining ability analysis to determine the selection procedure for different traits in Indian mustard. A diallel cross excluding reciprocals in *B. juncea* was conducted by Sharma and Singh (1994) to evaluate combining ability for percentage germination, seedling vigor index, root length, shoot length, seed volume and 1000-seed weight. Among parents and treatments, F_1s, F_2s, parents x (F_1 + F_2) and F_1 vs. F_2, significant variations were indicated for all the traits by analysis of variance. In both generations, significant general combining ability variance and specific combining ability variance were detected for all the characters. High heritability along with predominance of additive gene effects was reported for seed volume and for rest of the traits prevalence of non-additive gene action with low heritability estimates was identified. Singh *et al*. (1996) conducted combining ability analysis for ten characters of eight diverse cultivars in *Brassica juncea*. The best general combining ability for primary branches and secondary branches, 1000-seed weight, seed yield, plant height, length of siliqua and oil content was shown by parent variety PR-1108 which also participated in the best cross combinations for number of branches, seed yield, 1000-seed weight and oil content. In PR-1108 x BJ-679 and BJ-1257 x Glossy mutant, better parent heterosis estimates of 77.6% and 13.1%

was noticed for seed yield and oil content, respectively. Positive association of oil content with seed weight and yield declared the possibility of simultaneous improvement for these traits. After studying the combining ability analysis of eight *Brassica juncea* parents and their 28 F_1 hybrids evolved through diallel mating, Khulbe *et al*. (1998) detected the prevalence of additive and non-additive gene effects in governing various yield related attributes. For seed yield, predominance of non-additive gene effects was apparent.

Sheikh and Singh (1998) conducted combining ability analysis of a 10X10 diallel set of crosses in Indian mustard (*Brassica juncea*). For many studied traits including oil contents and seed yield, non-additive gene action was detected. Additive gene effects with higher estimate of heritability were reported for siliqua length and plant height. The best was shown by Pusa Barani for days to flowering, seed yield, plant height, 1000-seed weight, oil content and length of siliqua. The other good general combiners for seed yield and several other characters were Varuna and RH-30. For plant height, desirable GCA was identified from Poorbi raya and Glossy. Desirable SCA effects were reflected by Pusa Barani x Glossy mutant for number of primary branches, seed yield, plant height and oil contents. It was also concluded that when high x low GCA parents were involved, high specific combining ability effects were shown by most of the crosses for seed yield. After performing diallel crossing, the combining ability analysis of eight *Brassica juncea* parents and their 28 F_1s by Khulbe *et al*. (1998) showed that significant differences existed for general and specific combining ability for all the traits under study. For all the characters, general and specific combining ability variances were important showing that both type of gene effects i.e, additive and non additive were prominent in controlling of various characters. Three parents reflected high estimates for GCA while 13 crosses showed good SCA for seed yield and some attributes. Predominance of non-additive gene effects was found to be playing an active role in governing yield. The researchers concluded that the crosses with good SCA did not always have parents with high GCA, reflecting the importance of epistasis. Desirable transgressive sergeants were expected to be produced if the parents with additive gene action had good GCA and the complementary epistatic effect of F_1 would act in the same direction for the improvement of yield attributes.

Information on combining ability was collected by Yadav and Kumar (1999a) from data on oil content in 10 Indian mustard genotypes and their 45 F_1 hybrids. The best general combiner for oil content was RH781, followed by RH8311, RH839, RH848 and Varuna. The best specific combination was RH781 x Varuna. Verma and Kushwaha (1999) evaluated parents and 45 F_1 hybrids of Indian mustard for seed weight, oil content and seed yield. Significant differences for SCA and GCA were detected for all the characters. Values for specific combining ability variance were higher than values for general combining ability variances, pointing out predominant role of non-additive gene action in the expression of these characters. In another investigation by Yadav and Kumar (1999b), ten Indian mustard genotypes and their hybrids were studied for earliness. The best specific combiner was RH838 x RH30 while RH30 showed best general combining ability for earliness.

Rao and Gulati (2001) estimated combining ability of F_1 and F_2 diallel crosses in Indian mustard and found predominant role of non additive gene action for most of the yield attributes. Combining ability for 13 traits was estimated by Sarkar and Singh (2001) using ten Indian mustard cultivars. Significant GCA and SCA variances were discovered for seed yield, days to 50% flowering and maturity, early vigour, plant height, length of siliqua, number of primary and secondary branches, number of siliqua on main axis, seeds per siliqua, oil content and 1000-seed weight except for early vigour and length of siliqua in reciprocal crosses. He suggested that 3 parental lines i.e, Zem 1, Zem 2 and EC 32 and crosses involving either both high or one high GCA parents could be utilized to achieve better results regarding seed yield and related attributes.

Combining ability analysis was conducted by Swanker *et al*. (2002) using 36 F_1 diallel hybrids and their parents for eleven traits. Both general GCA and SCA variances were highly significant for days to flowering, yield per plant, number of primary and secondary branches, days to maturity, 1000-seed weight, plant height, siliqua on main raceme, oil content and protein content. Only eight crosses from both generations showed desirable SCA for grain yield. Ghosh *et al*. (2002) investigated 10 quantitative traits of 29 promising

female and seven male Indian mustard parents used in a line x tester analysis. Seven parents showed significantly superior GCA for seed yield and its components. Both additive and non-additive gene actions were prominent in governing most the major traits including seed yield. Significant GCA and SCA for all the studied characters were determined by Prasad *et al*. (2002) in 21 F_1 hybrids derived from the diallel cross of seven Indian mustard varieties. Predominance of non-additive gene effects along with over dominance was detected for days to flowering and maturity, length of main raceme, number of secondary branches, yield and oil content. Additive gene action was prominent in governing yield per plant. High GCA was detected for Varuna for majority of the traits and parse performance. At least seven crosses showed good SCA for early maturity, length of main raceme, number of secondary branches, yield per plant and oil content.

Singh and Sachan (2003) performed 8x8 diallel cross of Indian mustard and evaluated parents and F_1 excluding reciprocals, for combining ability estimates for different yield attributes and oil contents. Significant general and specific combining ability mean squares for all the characters indicated that both additive and non additive gene effects were important in inheritance of studied traits. They determined the significance of the interactions of GCA and SCA with the environment for all the characters except for number of siliquae on main shoot. Singh *et al*. (2003) estimated combining ability of ten Indian mustard cultivars and their 45 F_1 and 45 F_2 progenies for yield, its components and oil content. General and specific combining ability variances for days to maturity, 1000-seed weight, primary branches, siliqua length, seed yield per plant and harvest index were recorded. Both additive and non-additive gene effects were prevalent in controlling these traits. For plant height, seeds per siliqua and oil content, prominence of additive gene action were detected. The results indicated suitability of further selection from segregating generations.

In an experiment on 45 Indian mustard genotypes and their progenies, Mahto and Haider (2004) detected highly significant general combining ability for all the characters except for seeds per siliqua and high SCA except for primary branches. Significant interactions

i.e, environment x GCA and environment x SCA were detected for most of the characters, except number of primary and secondary branches. Singh *et al*. (2008) determined the combining ability of 11 Indian mustard cultivars along with their F_1s and reciprocals. High additive variance was observed for plant height and biological yield, whereas predominance of non-additive effects was detected for days to 50% flowering, number of primary branches and secondary branches, number of siliqua on the main axis, 100-seed weight, seed yield, harvest index and oil content. Another study was carried out by Yadav *et al*. (2004) to explore the combining ability for oil content, seed yield and its attributes of 3 cytoplasmic male sterile lines and 25 testers of Indian mustard. Presence of heterosis in the crosses was detected. For all the studied characters, relatively higher values of SCA than general combining ability reflected the predominance of non-additive effects.

Sachan *et al*. (2004a) studied the genetics of seed yield, glucosinolate content and cake content by estimating the combining ability in F_1 and F_2 of yellow-seeded Indian mustard lines. Prominence of over dominance along with non-additive gene effects was detected in governing the inheritance of all studied characters. Combining ability and heterotic estimates of yield and yield attributes were conducted by Kumar and Rathore (2004) on Indian mustard under an 8x8 diallel analysis on normal and saline soils. On normal soil, significant differences in GCA and SCA components for days to flowering and maturity, siliqua per plant, 1000-seed weight and seed yield were observed. On saline soil, general combining ability differences for days to flowering and SCA differences for pods per plant were significant. In another study on Indian mustard, Sachan *et al*. (2004b) performed combining ability analysis in *B. juncea* to detect genetic governance mechanism of yield components and oil content. The results indicated predominance of additive gene effects in F_1 and non-additive gene action in F_2 for days to flowering and 1000-seed weight. Only plant height was influenced by additive gene effects in both the generations while all other traits including days to maturity, number of primary and secondary branches, siliquae on main raceme, seed yield and oil contents were non-additively controlled.

Singh and Lallu (2004) crossed nine Indian mustard genotypes in a diallel fashion excluding reciprocal crosses to estimate GCA and SCA for number of branches, siliquae

on main raceme, plant height, 1000-seed weight, seed yield, oil content and protein content. For all the traits, analysis of variance for all the traits for GCA and SCA was significant except for 1000-seed weight in F_2. For various parents and crosses, significant general and specific combining ability effects were observed for seed yield and contributing traits. The crosses with significant SCA showed highly significant heterosis estimates. It was suggested that SCA could be utilized as a suitable parameter to detect the performance of the crosses while exploiting the heterosis. Six parents and their 15 crosses of Indian mustard were investigated by Sharma *et al*. (2004) to study the genetic make-up of seed yield and contributing characters. The results from variance analysis showed significant mean squres for general and specific combining ability for days to maturity, primary branches, plant height, seed yield and harvest index under moisture-stressed (E_1) and irrigated (E_2) environments E_1 and E_2, except SCA for days taken to maturity in E_1 and GCA for plant height in E_2. Singh *et al.* (2005) crossed six indigenous and four exotic genotypes of Indian mustard in a diallel fashion. Forty-five F_1 hybrids (direct crosses) and parents were analyzed for days 50% flowering, days to maturity, seed yield per plant, 1000-seed weight, plant height, siliquae on main shoot, siliqua length, primary and secondary branches, seeds per siliqua, oil content and harvest index. Both type of variances, i.e, additive and non-additive, were found to be important for most of the traits. However, additive genetic variances were prevalent in controlling seeds per siliqua in both years and plant height and oil content in the second year. Significant general and specific combining ability values were noted for different characters indicating the possibility of desirable transgressive segregation.

Evaluation of a set of 10x10 diallel crosses (excluding reciprocal) of Indian mustard by Parmar *et al*. (2005) indicated prevalence of non-additive effects for days to 50% flowering, days to maturity, number of primary and secondary branches, plant height, 1000-seed weight, siliquae per plant, seed yield and oil content. Patel *et al*. (2005) examined eleven lines of Indian mustard for general GCA and discovered predominance of non-additive gene action for number of siliquae per plant, number of seeds per siliqua and seed yield, while for 1000-seed weight, additive gene action was prominent. Combining

ability for seed yield and attributes was estimated in ten cultivars of Indian mustard and their 45 F_1 and F_2 hybrids by Singh *et al*. (2005). Except for GCA estimate for primary branches, higher estimates for GCA and SCA variances were found for all characters. General combining ability variances were generally higher than specific combining ability variances for 7 of the 10 characters. 13 parents and 30 crosses of Indian mustard were evaluated to estimate the combining ability for yield and its co attributes by Goswami and Behl (2005). Highly significant variances for GCA and SCA were found for yield and its traits. Non-additive gene effects were prominent in controlling all the characters. Seven hybrids showed significant SCA effects. For primary branches, siliquae on main shoot and 100-seed weight, duplicate epistasis was detected. Nair *et al*. (2005) also identified the better parents in Indian mustard by investigating their combining ability and detected superior crosses for their potential usage for the improvement of yield ant its contributing traits.

Noshin *et al*. (2007) performed combining ability analysis on a 6x6 diallel experiment of Indian mustard for yield and its components. Variances due to reciprocal effect for the primary branches and length of inflorescence and SCA effects for seed yield per plant were found statistically non-significant. Highly significant variance for GCA and SCA were estimated for rest of the traits. GCA mean squares were higher than SCA indicating the prominence of additive effects. A diallel cross including eight aphid resistant lines of Indian mustard and their 28 F_1s were investigated by Roy and Sinhamahapatra (2009) for combining ability and the nature of gene controlling aphid resistant parameters and seed yield. Both GCA and SCA variances were found to be significant for seed yield. Dominance components of variance was prominent in controlling all the studied traits indicating that heterosis breeding could be favored for the improvement of the traits analyzed in the experiment . Singh and Dixit (2007) worked out combining ability of a 9x9 diallel cross of Indian mustard for yield, yield attributes and oil contents for two generations. SCA was higher in F_1 than in F_2 for majority of the traits in most of the crosses. Significant general and specific combining ability were observed from different parents and crosses for various traits, respectively. Both additive and non-additive type of

gene action was prominent in governing the studied traits. Non-additive component were higher than additive component for majority of the characters showing the importance of the exploitation of heterosis.

After carrying out combining ability analysis for yield and attributes in fifty nine progenies of Indian mustard, Singh (2007) reported presence of significant differences for general and specific combining ability effects. It was evident from analysis that yield and its attributes were governed by the both type of gene action i.e, additive and non-additive. It was also noticed that low and average combining parents were involved in crosses showing high SCA inferring the importance of non additive gene effects. Singh *et al*. (2007a) performed an experiment involving twenty-one Indian mustard lines for days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, siliquae on main raceme, length of main raceme, length of siliqua, seeds per siliqua, seed yield per plant, 1000-seed weight and oil content. Presence of both additive and non-additive gene effects was detected in the expression of different traits. A diallel cross in Indian mustard was conducted by Lohia (2008). He analyzed even parents and their 21 direct F_1 hybrid for combining ability. Analysis revealed that all the nine traits viz., days to flowering, days to maturity, number of secondary branches, plant height, length of main raceme, siliquae per plant, 1000 seed weight, seed yield per plant and oil content were controlled by both additive and non-additive type of gene action. Only ten crosses showed desirable specific combining ability and might be used for the improvement of certain traits of Indian mustard.

Singh *et al*. (2008) studied combining ability of a half diallel cross set of Indian mustard (*Brassica juncea*) for seed yield and its attributes. High estimates for GCA and SCA variances were found for days to flowering, number of primary branches, plant height, number of siliquae per plant, 1000-seed weight and oil contents showing the significance of both the additive and non-additive gene actions in controlling these traits. However, GCA variance was greater than SCA variance for almost all the traits. A 5 x 5 diallel cross of *Brassica napus* was conducted by Akbar *et al*. (2008) and combining ability was

estimated for F_1 generation for plant height, primary branches per plant, siliqua length, siliqua per plant, seeds per siliquae, 1000-seed-weight and seed yield per plant. Highly significant mean squares for all the traits except 1000-seed weight were detected for all the traits.

Nigam and Alka (2009) conducted combining ability analysis of ten Indian mustard parents and their 45 F_1 and 45 F_2 hybrids obtained from a diallel cross. Significant differences were noticed for GCA and SCA. Both additive and non additive gene effects were prominent in governing all the characters. A total of 16 crosses showed considerable SCA for seed yield and predominance of non-additive gene action was apparent for those crosses. To detect combining ability estimates, Aher *et al*. (2009) investigated ten lines and four testers from *Brassica juncea*. The higher values of variance due to specific combining ability indicated the predominance of non-additive gene action in governing days to 50% flowering, number of secondary branches, number of seeds per siliqua, 1000-seed weight, siliquae per plant, seed yield per plant and oil content. However, predominance of additive gene action was detected for plant height, length of main branch and number of primary branches. The results showed that parents with all ranges of GCA were involved in crosses with high SCA. Oghan *et al*. (2009) investigated 21 F_2 progenies obtained from a 7x7 diallel crosses along with parents for combining ability and genetic components. Both additive and non-additive genetic effects were prevalent in controlling these traits. GCA/SCA ratios for days to flowering (0.91), days to maturity (0.95) and grain yield (0.83) showed greater role of additive gene effects. High estimates for narrow-sense heritability for days to flowering (73.12%) and days to maturity (81.99%) and low estimates for grain yield (30.15%) were observed. it was suggested that recurrent selection could be followed for the improvement of the genotypes for studied traits.

Yadav *et al*. (2005) found significant differences due to parents vs. crosses indicating the presence of heterosis in the crosses through conducted an experiment during the rabi seasons of 1998-2000 to study the nature of combining ability for seed yield and other yield-attributing characters through line × tester analysis in rape (*Brassica napus*) [*B.*

napus var. oleifera]). They derived forty-five F_1 from the crosses of two cytoplsmic male sterile lines (Ogura, ISN-706a) and one normal fertile line (NDBN-1) used as females and 15 testers (Westar, FM-27,GSL-6267,GSL-8814, EC129120, PBN 9501, NRCG-7, GSL-6067, HNS-4, GSL-1, GSL-406, NRCG-2, GSL-6303, NRCG-13 and NRCG-14) as males. Among lines, they observed significant differences for plant height and number of secondary branches per plant. Higher magnitude of variances due to testers compared to lines were observed for seed yield per plant, plant height, primary branches per plant, days to flower initiation, days to maturity and oil content. They also found that the estimates of SCA variances were higher than GCA (average) for all the characters studied, indicating the preponderance of non-additive type of gene action in the inheritance of these traits and the cross Ogura × NRCG-13 showed high SCA effects for yield per plant which involved both good combining parents.

Nair *et al*. (2005) worked on combining ability in mustard (*Brassica juncea*) to identify the better parents (Pusa Bold, Rohini, TM-17, ACN-9 and PCR-7) on the basis of their combining ability and to isolate superior crosses for studying them in further generations. The analysis of variances indicated that variances due to lines were significant for plant height and variances due to the testers were highly significant for all traits except days to maturity indicating significant genetic variation. Rohini was identified as the superior parent for the improvement of siliquae number per plant and hence, may be used in breeding programmers for the improvement of this trait. The cross Seeta × Rohini was identified as the promising cross for yield and contributing characters.

Chowdhury *et al*. (2004) studied the nature and magnitude of combining ability of parents and crosses (F_1s) were estimated in a 7×7 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 × low, average × average and average × low GCA parents.

Pietka *et al.* (2003) proposed that the general combining ability (GCA) values in terms of individual glucosinolates are important in breeding. Eleven inbred lines of winter oilseed rape (*B. napus* [var. oleifers]) characterized by very low glucosinolate contents were studied by them. These lines were crossed with five cultivars used as testers. Hybrids were grown in the field and statistical analyses of GCA values were performed separately for particular glucosinolates, as well as F_1 and F_2 generations. Heritability's of regressions were estimated by determining the coefficients between both generations. Most of the coefficients were significant at alpha =0.01 or 0.05, providing that the GCA estimation used in the experiments was satisfactorily reproducible.

Prasad *et al*. (2002) evaluated combining ability of 21 F_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 × low GCA parents. Liu *et al*. (2001) combining ability and heritability of eight main agronomic characters of the crosses obtained by crossing four double-low male sterile lines of rapeseed with glucosinolate lower than 30 micro mol/g and erucic acid lower than 1% with four good restorer lines based on North Carolina II design. They observed sterile ling 121A, known as the sterile ling of Shan you 6, was shown to be most outstanding, with high general combining ability of many yield-contributing characters, thus having relatively high yield potential.

Pietka *et al.* (2001) conducted an experiment to establish the relationship of general (GCA) and specific combining ability (SCA) with glucosinolate content in seeds collected from F_1 and F_2 hybrids generations of winter double row rapeseed. They examined that hybrids produced by crossing cultivars Mar, Polo, Silvia, Lirajet, and Wotan with inbred lines extremely low in glucosinolate content. They also found the calculated GCA values which showed that both inbred lines and cultivars were highly and significantly differentiated in terms of glucosinolate content and composition. They also suggested that an effective

selection for low glucosinolate content is possible for segregating hybrid populations and the possibility of using SCA in improving glucosinolate content was smaller than that of GCA.

Tak and Khan (2000) conducted an experiment to estimate the combining ability, magnitude of variability and gene effect of the available germplasm resources of 15 Indian mustard (*B. juncea*) lines crossed to three genetically different testers. Estimates of genetic variance revealed that the days to flowering was predominantly governed by a non-additive gene action. However both additive and non-additive gene actions were important in the inheritance of most of the characters studied. The line KS-216 showed significant general combining ability effect for earliness, whereas KS-240 and KS-181 were superior general combiners for seed yield.

Goffman and Becker (2001) stated that because of the nutritional and antioxidative properties, tocopherol production is an interesting trait for the lipid quality of oil crops. Total tocopherol content in rapeseed (*Brassica napus* L.) is medium to low, and therefore, higher levels of tocopherol are desirable in this species. The objective of the present study was to determine the inheritance of alpha-, gamma-, and total tocopherol content and the alpha -/ gamma -tocopherol ratio in seed of rapeseed. Two diallel mating designs with six parents each were used. In Diallel I, the parents selected were high or low for total tocopherol content and in Diallel II, the parents were high or low for the alpha -/ gamma -tocopherol ratio. Parents and F_1 hybrids were tested in a screen house in 1998 and under field conditions in 1999 by means of a completely randomized design with two replications. In addition, 10 selected F_2 populations were grown along with their respective parents. Compared with the parents, the F_1 hybrids showed a significantly higher gamma -tocopherol content of about 6 mg kg-1 seed for Diallel I and 24 mg kg-1 seed for Diallel II. General combining ability effects in both diallels were highly significant ($P<0.01$) and much larger than specific combining ability effects for all traits studied. Reciprocal effects were not statistically significant. Gamma-Tocopherol was not correlated with alpha -tocopherol. The results indicate that tocopherol content and composition inheritances are strongly associated with additive gene action in rapeseed. Wos *et al*. (1999) presented

general combining ability (GCA) and specific combining ability (SCA) for 23 cytoplasmic male sterility (CMS) ogura lines. Field trials were executed in four localities (Malyszyn, Marwice, Borowo and Bakow) in Poland. The seed yield of hybrids, GCA and SCA of CMS lines and GCA of pollinators were significant. 23 CMS ogura lines were crossed using three pollinator cultivars Kana, Marita and MAH 1592. Obtained results were used to find the best combinations for hybrid production.

Krzymanski *et al.* (1999) examined combining ability and heterosis for selected eleven winter double low rape inbred lines (PN 3181/95, PN 3451/95 PN 3455/95, PN 3462/95, PN 3707/95, PN 3710/95, PN 3734/95, PN 3999/95, PN 4043/95, PN 4272/95 AND PN 4297/95) with extremely low glucosinolate content. Three foreign cultivars, Lirajet, Silvia, and Wotan, and two Polish cultivars, Mar and Polo, were used as testers. Crosses were made in both directions. The results of calculations made for the F_1 generation concern general and specific combining abilities with regard to parental form and 55 hybrid combinations and reciprocal effects. The results enabled the determination of the best combination of crosses. It was also proved that combining effects depend in some combinations on the direction of crossing.

Krzymanski *et al*. (1999) made diallel (13x13) crossings of double low oilseed rape cultivars and strains. Parental forms and F_1 combinations of diallel were compared in field trials in Poland. Two cultivars and four strains were the parental forms that most frequently occurred in F_1 combinations yielding considerably above the standard cultivar (Bor), two strains gave combinations of the highest fat contents, considerably differing from the standard. The yields oscillated between 126.5 and 209.1% of the standard (38.2 q/ha) and the fat content between 103 and 108% of the standard (47%). Calculations were made to estimate the expected values of seed yield of synthetic varieties, which could be obtained from tested cultivars and strains. Two or three component synthetics composed from the best combining cultivars and strains were taken into account by them.

Wos *et al*. (2000) presented the results of the breeding studies on the development of winter and spring oilseed cytoplasmically male sterile (CMS) lines, restorers and

composite hybrids performed at the Plant Breeding Station in Malyszyn (Poland) in collaboration with the Oil Crop Department of Plant Breeding and Acclimatization Institute in Poznan. Some breeding aspects of the CMS lines, restorers and composite hybrids, including general combining ability and specific combining ability, contents of glucosinolates and erucic acid, winter hardiness and yield, are analysed. The results obtained so far have allowed the introduction of eight winter and four spring composite hybrids of oilseed rape to the State Official Trials. In 1999, the first Polish-French composite hybrid of spring rape named Margo was listed on the Polish Variety List.

Katiyar *et al*. (2000b) studied on heterosis for seed yield in Indian mustard (*Brassica juncea* (L) Czren. and Coss.). Six varieties and 16 lines of *B.juncea* in a tester mating design, and the resulting 96 crosses were evaluated for yield components. Seven combinations exhibited > 30% heterosis and eleven crosses showed 31.2-71.3% heterosis. It is concluded that there is adequate genetic divergence among Indian mustard lines to support a successful hybrid programme. Huang *et al*. (2000) studied three rapeseed (*Brassica napus*) genotypes tolerant of resistant to *Sclerotinia sclerotiorum* and three susceptible genotypes differing in origin were used in reciprocal or complete diallel crosses and found that resistant genotype from China, 018, had the highest general combining ability (4.46) while the French variety Cobra had the lowest general combining ability (-10.54). They also found optimum cross combination in this study was Cobra 018, with high specific combining ability (10.41) and desirable agronomic characters.

Singh *et al.* (2000) worked with genetic analysis in yellow sarson, *Brassica compestris* L. 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 siliqua 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 × low GCA effects showed significant SCA for seed yield.

Wos *et al*. (1998) presented the results of investigated general combining ability of 64 inbred lines and heterosis effects of winter oilseed rape F_1 hybrids. General combining ability was estimated by test top crosses. Field experiments were designed in lattice design, in two replications (four rows per plot, three superscript two plot and sowing rate of 100 seeds per 1 superscript 2). The experiment was carried out in 1996-97. General combining ability (GCA) was significant for seed yield, 1000 seed weight, winter hardiness, beginning and end of flowering, oil and protein content. However, it has been proved that GCA was not significant for plant height. Results of these studies revealed: nine hybrids with significant higher yielding than tester (check) cv. Lirajet, 19 hybrids with significant better winter hardiness than tester, 35 hybrids with significant earlier beginning of flowering in comparison with Lirajet, 22 hybrids with significant earlier ending of flowering, three hybrids with significant higher 1000-seed weight, two hybrids with significant shorter plants than tester, 13 hybrids with significant higher oil content than tester Lirajet. The best hybrids out yielded about 40% higher than tester Lirajet. Nevertheless the average effect of heterosis with respect to the seed yield was 16% in comparison with the tester Lirajet. Moreover, Spearman coefficients of correlation between estimated traits were calculated. Positive significant correlations at P <less or => 0.01 Spearman coefficient of correlation rs = 0.48** was calculated between winter hardiness and yielding. Moreover, negative Spearman coefficients of correlation between winter hardiness as well as beginning and ending of flowering was noted.

Satwinder *et al*. (1997) evaluated diallel crosses involving eight varieties of *Brassica napus* for seed oil yield and seven related components and they found high variation for SCA and GCA for all traits, suggesting both additive and non-additive gene effects. They also found combinations of varieties with high × low or high × average oil contents had high SCA effects.

Pietka *et al*. (1998) reported that winter hardiness of winter oilseed rape cultivars became very important trait after two strong winters which destroyed many plantations of this crop in Poland. These two winters gave rape breeders an opportunity to estimate winter

hardiness of breeding materials and to make effective selections. A field trial with an F_2 generation of a diallel cross (7 x 7) and with an F_1 generation of diallel cross (10 x 10) were sown in autumn 1996. Winter losses of plants on the plots differentiated the hybrids significantly, allowing more sophisticated analysis. Seeds used for sowing the first trial were harvested from F_1 plants which survived the severe 1995-96 winter. The second trial was sown with seeds obtained by hand pollination after removing the anthers. The trials were made in a complete randomized block design with standard plots distributed systematically. Inter block variability was reduced with covariance analysis. The hybrids of both generations were examined in trials without parents. The number of plants which survived the winter were estimated in spring. Diallel analysis on transformed values was done according to Griffing method III. Effects of general (GCA) and specific combining abilities (SCA) and effects of reciprocal (RE) crosses were calculated. All effects except of reciprocal effects in F_1 generation are highly significant. Winter hardiness was shown to be a complicated character whose genetic control depends on additive effects of parent, interaction of parental genotypes and maternal cytoplasm.

Pu (1998) stated that a cytoplasmically male sterile line Ning A3 (MICMS), a *Brassica napus* line with a high level of sinaptic acid, was used as the basic breeding stock. The maintainer line Ning B3 was crossed with an elite cultivar with double low and fertile cytoplasm. Ning A6 and the maintainer line Ning B6 were bred after six generations of breeding. The combining ability of Ning A6 is high and the hybrids showed obvious heterotic vigour. Some hybrid combinations gave good performance in both yield and low content of sinaptic acid. The content of sinaptic acid in Ning A6 is 0.38% mu mol per g DW. Wos *et al*. (1997) studied in the combining ability of 55 inbred lines of rape (*Brassica napus*) and heterosis effects of their 62 F_1 hybrids. GCA was significant for seed yield, 1000-seed weight, time to flowering and fat content. They found that some 24 hybrids had higher yields, 14 earlier onset of flowering, three shorter plants, 14 higher fat content and three had higher protein content than control Global. Average yield increase over Global was 10%. There was a significant positive correlation of seed protein content with 1000-seed weight, and a negative correlation with seed fat content.

Kudla (1997) stated that inbred lines T1170, T1162, T1148 and T1166 were crossed in a factorial design with cultivars Maxol, Mandarin and Silex. Parental forms and 12 F_1 hybrids were evaluated in 1994-95 in a field trial. GCA of inbred lines and cultivars was significant for height to first branch, number of primary branches, siliqua length, seeds/siliqua and 1000-seed weight. T1170 and T1166 transferred some high-yield traits to their progeny. Significant differentiation of SCA was found for height to first branch. Dominance effects appeared high and positive for seed yield/plant and plant height. Additive gene action played a predominant role in the inheritance of height to first branch and seeds/siliqua. Relation of additive and non-additive gene action was generally similar in the inheritance of number of primary branches, siliqua length and 1000-seed weight. F_1 hybrids showed positive heterosis, averaging 14% for seed yield/plant. Thakur and Segwal. (1997) found that GSL8809, HPNI, GSL1501 and HNS8803 were good combiners for seed yield and some of its components and for oil content. They evaluated nine diverse inbreeds and their 36 F_1 hybrids from a diallel cross for yield and its components and for oil content. Mean squares due to general and specific combining ability were significant for all the traits studied, suggesting the importance of both additive and dominance components of variation.

Yadav *et al*. (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) in a study of 8 × 8 diallel analysis (excluding reciprocals). 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.

Kudla (1996) investigated the combining ability of winter oilseed rape (*Brassica napus*) inbred lines, and heterosis effects of F_1 and F_2 hybrids in the growing season of 1994-95. Analysis of variance showed that non-additive gene action had an advantage over additive gene action in the inheritance of plant height and number of primary branches. The significant effects of dominance genes in the F_1 for siliqua length, seeds/siliqua, seed yield/plant and 1000-seed weight did not occur in the F_2. The differentiation of GCA of

inbred lines, based on F_1 hybrids, was significant for siliqua length, seeds/siliqua, seed yield/plant and 1000-seed weight. GCA based on the F_2 was significant for pod length and seeds/siliqua. Inbred lines T1056 and T1150 were good components for crossing to increase seed yield in the F_1. Both lines can be used for breeding high yielding oilseed rape hybrids varieties. In most of the F_1 and F_2 hybrids, significant positive effects of heterosis were found for plant height. F_1 of T1056 x Wotan showed the highest and significant heterotic effect (24.5%) for seed yield/plant. The mean heterotic effect in F_1 hybrids was 10% for seed yield, decreasing to 2% in the F_2 generation.

Patel *et al.* (1996) provided information that combining ability was derived from data on nine yield components in four parental genotypes (*Brassica juncea* cultivars Pusa Bold and TM17*, B. carinata* and *B. napus*) and their 12 F_1 hybrids grown during 1994-95. Variance due to GCA and SCA were significant for all the characters, except number of seeds/silique for GCA variance and 1000-seed weight for SCA variance. Non-additive gene action appeared to predominate for all characters except days to maturity, which was governed by additive gene action. *B. carinata* was the best general combiner for plant height, number of branches/plant, number of siliquae/plant and oil percentage. Among the hybrids, *B. napus* x Pusa Bold was the best specific combination, followed by the reciprocal.

Krzymanski *et al*. (1995) evaluated seed glucosinolate content in hybrids from a diallel set of crosses involving ten *Brassica napus* strains. Only three of the strains showed significant GCA effects for total content of aliphatic glucosinolates but their values were low. SCA effects for the trait were significant only for three of the 45 crosses and heterosis only for two, but their values were high. Most strains appeared to have the same alleles that controlled low glucosinolate content. Heterosis for content of glucosinolates was not correlated with heterosis for seed yield.

Barua and Hazarika (1993) conducted a study during 1993 with five varieties representing two *Brassica napus* types and *Brassica compestris* var toria along with their hybrids from a half diallel set of crosses. Accroding to them, heterosis mainly due to non-additive gene

effect was important for dry matter and seed yield/plant. The important heterotic crosses were BSH1 × M27, B9 × PT303 and PK × M27. Habetinek (1993) worked on *Brassica napus* and found higher GCA effects than SCA effects for all characters except seed weight/ plant. Darmor had the highest GCA for number of seeds/siliqua, siliqua length and 1000 seed weight, while Sonata had the highest GCA for oil content. SCA for seed weight/plant was highest in Sonata × SL2502. Krzymanski (1993) studied yield and oil quality in ten parental and their 45 hybrids. Significant GCA and SCA effects were found for all 19 traits.

Kudla (1993) studied nine maternal lines (5S3 and 4S4), their pollinator (tester) Toplider and 9 F_1 hybrids derived by top crossing. Additive gene effects were most important in control of 1000-seed weight and the number of seed/siliqua, but non-additive effects predominated in control of number of primary branches, seed yield/plant, plant height and siliqua length. Differences in GCA between parents were significant for all characters except siliqua length. The inbred lines T1057 and T6237 transmitted to the progeny high yield potential and T1057 had a good effect also on 1000 seed weight in the hybrids, but reduced seed/siliqua (which was increased by T6237). Favorable GCA effects were shown by T1080, T1097 and T1039 for seed/siliqua, T1097 for number of primary branches and T996 and T1039 for plant height. Pszczola (1993) inter crossed the varieties Bolko, Tor, Diadem, Arabeke, Panter and Libravo in one set of diallel crosses and the varieties BOH 1491 (Bor), Falcon, Tapidor, Ofello and Lircus in another set. The characters evaluated were seed yield, 1000 seed weight, and others of importance. There was significant SCA effect in some crosses for all traits. Maternal (cytoplasmic) effect was apparent for all characters.

Rawat (1992) studied the reciprocal differences in the inheritance of eight yield traits in progeny from a diallel set of cross involving 12 lines of *Brassica juncea*. GCA effects predominated in the control of all the traits. Reciprocal effects were more pronounced than SCA effects, though the later were significant for all traits. The most promising parent lines of the basis of *per se* performance and of combining ability and F_1 performance were BICI624, BICI3S2, BICI439, BICI114 and BICI702. There was only one cross (BICI382 ×

BICI702) in which reciprocal effects acted in a favorable direction for all traits. This allowed the selection of a maternal parent, which was capable of enhancing beneficial non-additive effects in a specific cross. The parents of this cross also showed high GCA for most of the traits, allowing the exploitation also of beneficial additive effects.

Singh *et al.* (1992) determined combining ability from data on 12 quantitative characters in the parents and F_1 hybrids from a 10 line × 4 tester cross of Ethiopian mustard. Several of the lines were identified as being good general combiners. These are HC1, BC2 and BCIDI for maturity traits. FC5 for seed attributes and CAJR4-3, BCIDI, CAR3 and CARS for seed yield and several other desirable traits. The best specific combinations for yield improvement were CAR3 × BC2 and BCIDI × BC2 for using a pedigree selection programme. Yadav *et al*. (1992) evaluated 45 F_1 hybrids of Indian mustard together with ten parents for combining ability with respect to seed yield and its component characters. Veruna, Kranti, RIC1359 and RLCI357 were identified as good combiners for seed yield, earliness, siliqua length, number of seeds/siliqua and 1000 seed weight. The following varieties or parents ECI26743, ECI26745 and ECI26746-1 have emerged as good combiners for plant height, primary branch and secondary branch.

Tamber *et al*. (1991) crossed 23 morphologically diverse *Brassica juncea* lines with four broad-based testers in 1987-88. The resulting 92 F_1 and parents and F_2 and parents were sown in 1988-89 and 1989-90, respectively. Data were recorded on number of days to first flowering and maturity. Analysis of variance of combining ability in both generations revealed that GCA variance due to lines and testers were significant for all characters except for maturity in the F_1 and additive effects in the F_2 were greater than in the F_1. Among the lines, RSK11 was the best general combining parent and was seen to be a suitable parent for evolving lines having short period of maturity. Among the testers, Varuna was a good general combiner in the F_2 generation and an average general combiner in the F_1 generation.

Chauhan *et al.* (1990) reported that there was wide variation in yield and its component in tests of up to 210 *Brassica juncea* geramplasm lines. When 36 *Brassica juncea* crosses and

their 15 parents were tested, there was significant difference in seed yield between genotype. NDRS602, Krishna, Pusa Bold and TM9 showed good general combining ability. Siddique *et al.* (1990) studied a complete diallel cross involving four genotypes of *Brassica compestris* and their F_1's for nine characters including seed yield/plant. Both additive and non additive gene action was found in the inheritance of characters except days to flower, plant height and primary breaches. Preponderance of additive gene action for days to maturity, number of secondary branches/plant, number of siliqua/plant, number seeds/siliqua and non additive gene action for days to flowering, plant height, number of primary branches, siliqua length were found. Among the parents M-27 was the best general combiner for siliqua/plant and seed yield/plant. The hybrids YS-52 × M-27 exhibited highest significant SCA effect for seed yield/plant.

Arya *et al*. (1989) worked on combining ability from data of 12 yield related component characters in parents and F_1 of a 13 line × 3 tester mating design of *Brassica napus*. The varieties Midas, Regent 3-1 and DB054 were identified as good general combiners and DNA 38 × DISNI and N20-1 × Regent as good specific cross combinations. Singh *et al.* (1989) worked with six *Brassica juncea* parents and their resultant 15 F_1 and 15 F_2 populations. They evaluated 11 quantitative and qualitative characters. GCA and SCA variance were significant for all characters. RLM198 showed good general combining ability for plant height, number of siliqua/plant, and yield. The parents, I RNS12 showed good general combining ability for no. of seeds/siliqua and seed weight. The cross RLM198 × R75-1 showed significant SCA for seed yield in both F_1 and F_2.

Thakur and Zarger. (1989) studied yield components in 15 *Brassica juncea* and three testers and their F_1 hybrids. The lines Gonda-3 and R71-2 have had high GCA for yield. Chaudhury *et al*. (1987) investigated thirteen selected *Brassica juncea* genotypes and their 78 hybrids from a half diallel cross. Data were tabulated on genetic variance and combining ability. RH30, RH785 and Varuna showed good performance and GCA for yield/plant, and its component. KC781 × RH30 and RH7513 × Varuna were the hybrids with best SCA effects and mean performance for yield and its components. Badwal and Labana (1987) analysed data on seed yield/plant and eight related traits from a 10 × 10 half

diallel cross in *Brassica juncea*. They reported that both additive and non-additive components of variance controlled the inheritance of seed yield, number of seeds/siliqua, plant height, primary branches, siliqua length; only non-additive variance was significant for secondary branches.

Chaudhury *et al*. (1987) found significant differences for GCA and SCA variances indicating that both additive and non-additive components of gene effects influenced the expression of each characters in a trial of *Brassica chinensis* and four genotypes of *Brassica campestris* with their ten possible combinations (excluding reciprocals). The dominance component was greater than the additive component for all characters except seed size and siliqua length. The best general combiners for yield and its component were BSHI and Pusa Kalyani. The hybrids with the highest *per se* performance and SCA effects were *Brassica chinensis* × Pusa Kalyani and *Brassica chinensis* × Span. The best overall cross for the characters studied was Bell × Pusakalyani. Chauhan (1987) tabulated genetic variance parameters for yield/plant and eight related traits from a 20 partial diallel cross in *Brassica juncea*. Variance due to GCA and SCA effects were highly significant for all traits. Additive genetic effects appeared predominant for three characters and non-additive effects for the remainder, Varuna, RS3 and Cult47 were good general combiners for yield as was RB85 for days to flowering and maturity. Gupta *et al.* (1987a) worked with 8 × 8 diallel cross without reciprocals of *Brassica* genotype. 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 seed/siliqua and seed yield, while additive-gene effects were apparently predominant for plant height. The best general combiner for seed yield was RLM198. The best crosses for further selection were RLM822 × Varuna and RLM19S×RH30.

Gupta *et al*. (1987b) performed an analysis in a 13 × 4 line × tester cross in *Brassica juncea.* Additive gene effects were relatively more important than non-additive for seed yield/plant and most of the five yield component investigated. Among females, the best general combiners were RLM29 for seed yield, P Rai-1 for plant height, RLM240 for no. of primary and secondary branches. Among males, RLM198 was the best general

combiners for seed yield, number of primary branches. Varuna was best for plant height and RL18 for number of secondary branches. The cross PI 1/17 × RH-30 exhibited high performance for seed yield along with significant SCA for number of primary and secondary branches, RLM24 × RH30 and RLM82 × Varuna showed desirable significant SCA effect for seed yield and plant height. Prakash *et al.* (1987) 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/siliqua, 1000 seed weight, and seed yield indicating that dominance was possibly the predominant gene action for these traits. The parents DIR146 and RCL1017 were good general combiners for most of the characters studied.

Rawat (1987) observed a line × tester analysis involving 12 females and five males of *Brassica juncea* of diverse origin. Variance components of GCA and SCA were significant for days of 50% flowering, number of primary branch, plant height, seed weight and seed yield/plant. For secondary branches GCA was important. Pusa Rai 34 and Pusa Rai 45 among the female parents and Pusa Rai 30 among the male parents performed well and were good general combiners. The cross RLM514 × RLM198, RW336×Pusa Rai 30, Pusa Rai 45 × BR40 and RH7710 × Pusa Rai30 showed significant SCA for increased seed yield. Singh and Chauhan (1987) worked with 60 triple test cross families produced by the crossing of 20F_2 parents as males to the parents and F_1s. In Varuna × TM9 additive genetic variance appeared to be predominant for days to maturity, number of primary branch while dominance seemed to be mainly involved in the control of seed yield/plant. In Varuna × RW75-80-1, additive genetic variance was estimated to be predominant for plant height and dominant for days to maturity, number of seeds/siliqua, 1000 seed weight, yeild/plant.

Singh *et al*. (1987) reported data on yield and eight other agronomic characters from an eight parent diallel cross in yellow sarson to indicate the presence of both additive and non-additive gene action, in the inheritance of all traits, with non-additive gene action being predominant for all traits, except plant height. YSK4 and YSK5 were good general combiners for seed yield/plant while the best combinations were YSK5 × YST151 and

K88 × YSK5. Griffing (1956) 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.

2.2 Heterosis

Heterosis was first reported in brown sarson by Sing and Mehta (1954). Subsequently many studies have estimated the extent of heterosis for seed yield. The results indicate significant level of heterosis 13 to 91% In *Brassica juncea* (Banga and Labana 1984; Kumar *et al.*,1990; Thakur and Bhateria, 1993; Rai 1995;), 25 to 110% in *B. campestris* (Dhillon *et al*., 1990 and Yadav *et al*., 1998) and 10 to 72% in *B. napus* (Rai,1995; Thakur and Sagwal, 1997). In oilseed Rape breeding for hybrid and open pollinated varieties, general and specific combining ability effects (GCA and SCA) is important indicators of the potential of inbred lines in hybrid combinations. The line × tester analysis is one of the efficient methods of evaluating large number of inbred as well as providing information on the relative importance of GCA effects of lines and testers and also SCA effects of pairs of parental genotypes for interpreting the genetic basis of important plant traits (Mather and Jinks, 1982). Estimation of genetic parameters for yield components can be important for indirect selection for seed yield. Although combining ability studies in oilseed *Brassica* spp. Are scanty, most of these studies emphasized the preponderance effect of GCA on yield and most of the yield components indicating the importance of additive gene action (McGee and Brown, 1995; Wos *et al*.,1999).

Verma *et al.* (1989) studied the nature and magnitude of combining ability and heterosis in a set of 7×7 diallel crosses (excluding reciprocals) of yellow sarson for yield, yield components and secondary branches per plant, siliquae on main shoot, 1000-seed weight and oil content while it was non-additive for siliquae per plant. Trivedi and Mukharjee (1986) reported that non-additive component in Indian mustard *B. juncea* is important for all the traits 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 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, whereas recessive alleles were preponderant for other traits.

Ramsay *et al.* (1994) reported that variation for both GCA and SCA were responsible for seed yield and other quantitative traits in *B. napus.* Significant GCA and SCA effects were reported for pods per main axis, pods per plant, length of pod, number of seeds per pods, 1000-seed weight and seed yield in *B. napus* (Leon, 1991; Thakur and Sagwal, 1997; Rameeh, 2010), but in other study (Singh *et al*., 1995) the importance of additive genetic effects for pods per plant and 1000-seed weight was emphasized. Thakur and Sagwal (1997) while examining the genetic control of seed yield in oilseed rape found both additive and non additive gene effects to be involved. Oilseed rape (*Brassica napus*) is usually classified as a largely self-pollinated species, significant levels of heterosis related yield and yield components have been obtained in F_1 hybrids of both the spring and winter forms (Downey and Rimer, 1993; Teklewold and Beeker, 2005; Nissimi *et al*., 2006).

Varshney and Rao (1997) estimated combining ability, heterosis and inbreeding depression in yellow sarson for 11 quantitative characters including seed yield. Non-additive genetic variance was preponderant for all the characters in both F_1 and F_2 generation 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 effect and the other wih poor or average sca effects. The

hybrids which exhibited highest heterosis also showed higher inbreeding depression. A nine-parent diallel study was conducted by Thakur and Sagwal (1997) on the yield components and oil content in rapeseed (*B. napus* L.). They reported the importance of both additive and dominance components. Estimates of heterosis over better parent (BP) for various traits indicated significant magnitude including seed yield (-14.8 to 82.8%). Unidirectional dominance was observed for most of the traits studied.

Sheikh and Singh (1998) studied combining ability analysis, 10×10 diallel including reciprocals in Indian mustard for ten characters and found preponderance of non-additive gene action for most of the characters including seed yield and oil content. Additive genetic variance was more important for plant height and length of siliqua for which high estimates of heritability was also observed. Majority of the crosses showed high sca effects for seed yield involved high × low gca parents. Heterosis for yield and yield contributing characters have been studied for identifying the crosses showing significant heterosis and also the parent which conferred heterosis. Information on heterosis of the crosses in *Brassica* varieties are reviewed. Katiyar *et al*. (2004) studied heterosis for seed yield in yellow sarson (*Brassica campestris*). They studied heterosis for seed yield in ninety intervarietal crosses of *B. campestris*. Twenty one crosses (23.3%) showed significant and positive heterosis over better parent while only four crosses (4.4%) were so over the best commercial variety. The crosses YST-151× Pusa Bold (Dwarf) and MYSL 203× EC-333596 showed highest heterosis upto 150.33 and 43.38% over best parent and commercial variety, respectively.

Goswami *et al*. (2004) estimated heterosis for yield and yield components in 30 crosses of Indian mustard in an experiment conducted in 1999-2000 (E_1) and 2000-01(E_2). Result showed that the cross RH 9404 × RH 30 had the maximum heterosis for seed yield per plant (92.88 and 106.23%) during E_1 and E_2 respectively. This cross also showed high heterosis for 1000 seed weight. The crosses RH 9617 × RWH 1 and RH 9621 × RWH 1 were selected because of high heterosis for all the parameters were tested. Satyendra *et al*. (2004) evaluated heterosis for seed yield and its components in Indian mustard (*B. juncea*

L. Czern and Coss). They evaluated 21 Indian mustard hybrids and their parents for 8 quantitative traits. High heterosis (15.99, 15.51 and 12.37%) was obtained for seed yield in the crosses Basanti × NDR 8501. Basanti × Kanti, Basanti× RH 30, respectively. These hybrids showed high heterosis over the best cultivar. Among three crosses, Basanti × kanti may be used for selecting for seed yield and quality traits.

Singh *et al*. (2003) observed heterobeltoisis in Indian mustard for seed yield per plant in eight crosses, namely, KR- 5610 × PR-15(58.38%), YRT-3 × PR-15 (54.33%), RK 1467 × T-6342 (52.60%). Varuna × YRT-3 (35.83%) KRV – Tall × T- 6342 (33.81%), RLM- 198 × RT-3 (34.10%), Varuna × RLM-198 (31.50%) and KR-5610 × KRV-Tall (36.70%). In general the hybrids showed a wide range of heterotic effects for each character. Qi *et al.* (2003) studied heterosis of seed and its components in 66 crosses of 12 parental varieties of *B. napus*. Twenty one crosses showed a significant heterosis in seed yield/plant. The average heterosis for yield over their parent was 70.24% (30.70-218.10%). Eight crosses showed better parent heterosis (3.57-20.48%) in 1000 seed weight, while the parent of 7 crosses showed low 1000 seed weights 47 crosses gave an average 28.02% (0.93-97.87%) more pods/plant in parents while 13 crosses showed 11.6% more seeds/pod in parents. It is concluded that there is large potential heterosis in seed yield with heterosis in pods number/plant making the biggest contribution.

Heterosis in hybrids of 6 cultivars of *Brassica campestris* was estimated by Qi *et al*. (2000). They found that yield of the hybrids ranged from 46 to 125 kg/mu. Significant heterosis for seed yield /plant was found in some hybrids with the highest being 96.4%. Most hybrids showed lower levels of heterosis, with the lowest being 1.4% (1 mu=0.067 ha). Mahak *et al*. (2003) studied heterosis for days to flowering, plant height, no. of primary and secondary branches, days to maturity, 1000 seed weight and seed yield in 10 Indian mustard cultivars and 45 F_1 and F_2's. High heterosis for seed yield was observed in Varuna × Rohini (56.74%), Vardan × Rohini (53.43%), Vaedan × RK9501 (52.86%), Vardan × NDR 8501 (36.73%), Pusa Bold × Rohini (37.68%) and Varuna × NDA 8501 (32.54%).

Ghosh *et al*. (2002) studied heterosis in Indian mustard (*Brassica juncea* L. Czern and Coss). They used 29 promising female and seven male parents and studied 10 quantitative traits. The cross YSRL-10 × Pusa Bold, DBS-10 × Pusa Bold showed high heterosis for seed yield and some of the yield contributing traits. Pathak *et al*. (2002) estimated residual heterosis in F_2 in Indian mustard revealed that heterotic responses have noticed at the F_2 level for yield. 1000 grain weight, no. of siliqua on main raceme, no. of branches (primary and secondary) considerably, while low in magnitude but significant heterosis over between parent have been observed for days to 50 flowering, plant height, days to maturity, length of main raceme, seeds per siliqua and oil content. Kumar *et al.* (2002) studied heterosis in Indian mustard (*B, juncea* .L). They used 36 F1s and 15 parents and studied 9 characters. Highest heterosis for seed yield was achived in the cross 505 × RN490, RN505 × PCR-43, RN- 393 × RN-481. RN393 × RN 453 and RN 505 × RN 481, and these crosses offer the best possibilities of further exploitation for the development of high yielding varieties.

Zheng *et al*. (2002) tested by genetic methods in 15 hybrids of *B. napus* for 8 yield components. In general, the CMS F_1 had significant heterosis, particular F_2 was lower. Result also indicated that of the major yield components, total pod number/ plant had the highest heterosis and would be of more value in a breeding programme than trying to increase seed number per pod or 1000 seed weight. Tyagi (2001) studied 45 hybrids of Indian mustard obtained from crossing 10 cultivars to estimate heterosis. The highest standard heterosis (206.14%) and heterobeltiosis (240.56%) for seed yield per plant was recorded in the cross BIO 772 × Rohini. The heterosis for seed yield had significant positive correlation with the number of secondary branches and biological yield and these two components were also significantly correlated with each other. The number of secondary branches was also positively correlated with the number of primary branches.
Swarnkar (2001) studied heterosis in relation to seed yield and its components in Indian mustard (*Brassica juncea* L. Coss and Czern). They used 36 F_1 htbrids, 36 F_2 generation and parents and studied 11 quantitative traits. High economic heterosis was achieved in

four crosses , KR-5610 × PR-15 (58.60%); YRT-3 × PR-15 (54.33%); RK-1467 × T-6342 × (52.60%) and KR-6510 × KRV-Tall (36.70%.). Dharmendra *et al.* (2001) estimated heterosis among 70 interspecific hybrids generated from 20 parents in yellow sarson. Maximum economic heterosis was observed from siliquae/plant followed by seeds/siliqua and seed yield/plant. The crosses viz. AJL 20 × IB 1997 and AJL 18 × IB 1997, showed high heterosis over economic parent foe siliquae/plant and seed yield/plant. In general, hybrid showing high heterosis for most of the characters suggested importance of non-additive gene action.

Sheikh and Singh (2001) evaluated thirty F_1 hybrids to study the nature and extent of heterosis for eight agronomically important characters. The results indicated the manifestation of high degree of heterosis for seed yield and other component characters. Highest positive heterosis was observed in the cross turn CMS × Glossy mutant (84.4%) followed by oxy-CMS × Glossy mmutant (66.9%),oxy-CMS × Poorbijaya (38.2%). Katiyar *et al*. (2000) estimated heterosis for yield and yield components in six varieties and 16 lines of *Brassica juncea* and their resulting 96 crosses . Seven combinations exhibited 7.30% and 11 combinations 31.2-71.3% heterosis for seed yield/plant. It was concluded that there were adequate genetic divergence among the Indian mustard lines used to support a successful hybrid programme.

Mahto and Haider (2004) have also been recorded from data on 11 yield components in nine *Brassica juncea* varieties and their 36 progenies at Ranchi in 1997 about heterosis. The cross PR 18 × BR 40 showed desirable heterosis in seed yield per plant and siliquae/plant. Kumar *et al.* (1990) studied heterosis in Indian mustard (*Brassica juncea* L.Czern and Coss.). He used 16 parents and 39 F_1s and studied six characters. He observed positive heterosis for seed yield, primary and secondary branches/plant, siliqua length and seeds per siliqua. Highest positive heterosis for seed yield was observed in the cross RLM198 × RH30 followed by the crosses RLM514 × Varuna, RLM18 × Varuna and RS64 × Varuna. The cross RLM198 × RH30 showed highest heterobeltoisis for secondary branches. Larik and Hussain (1990) studied heterosis in Indian mustard (*Brassica juncea*

L. Coss) from data on 6 characters in 3 cultivers and their F_1 hybrids grown during 1987-1988. The cross P43× S9 exceeded the parental lines in yield.

Zheng and Fu (1991) worked with eight F_1 hybrids of *Brassica nigra* L. They evaluated 17 agronomic traits with 4 heterosis standards. Of all traits investigated, seed yield /plant and effective siliqua/plant showed significant heterosis,their mean heterosis(over mean value of the parents) rates being 80.21 and 51.47 per cent, respectively. A male sterile line, European-Xinping A, a maintainer line European-Xinping B and a restorer line 74243-6, were developed from a male sterile plant of *Brassica juncea* by Shi *et al*. (1991). The seedling stage of F_1 hybrids showed fairly strong heterosis, there was also heterosis in seed yield. The F_1 hybrids yielded 19.2-34.8% more than CV Kunming-Goake.

Ahmadi (1993) worked with parents and F_1 hybrids from crosses between resynthesized lines and improved 00 varieties. F_1 were earlier maturing than resynthesized lines and heterosis was observed for spring regret and plant height In trils, the best resynthesized line H128 could only produce 87% of the mean yield of the improved varieties. Krzymanski (1993) found significant heterosis for seed yield, oil content and some flowering traits in 10 parental strains and their 45 hybrids. The mean heterosis for seed yield over the mid parent was 24.71%. The highest heterosis for this traits was seen in the cross of PN2595/91×PN2870/91 (71.81% relative to the mid parental value).

Gupta *et al*. (1993) studied 56 hybrids from a half diallel set of crosses involving 8 genetic stocks with 28 hybrids being derived from crosses of the initial So population and the rest from crosses of S1 families from each of the parents. The use of S1 families generally gave hybrids with a higher degree of commercial heterosis than hybrids using So materials, though the So×So crosses gave high commercial heterosis for yield in many cases. Srivastava and Rai (1993) tested heterosis for seed yield and 3 of its components in hybrids from a half diallel set of 15 crosses involving 3 Indian and 3 foreign varieties. The highly heterotic hybrids YST151× Tobin, YST151× Torch and PT303× Torch, each had one Indian and foreign parent and in general the Indian× foreign hybrids showed a higher

degree of heterosis than the Indian× Indian and Foreign × Foreign. Krishnapal and Ghose (1992) investigated the relationship between heterosis and genetic diversity in the F_1 from crosses involving five genotypes of *B. campestris* and six of *B. juncea*. The results exhibited positive and significant heterosis for the characters seed yield/plant, 1000-seed weight etc.

Pradhan *et al*. (1993) found from the component character analysis concluded that characters such as no. of primary and secondary branches, number of siliqua/plant and siliqua density contributed significantly to positive heterosis for yield. Liu (1994) studied cross compatibility in interspecific hybrids involving *B. juncea* and *B. napus* genotypes. Cross compatibility was highest in combinations with *B. juncea* as the maternal parent. *B. napus* × *B. juncea* crosses made in the summer at Kunming showed a markedly higher compatibility than those made in the spring at Changsha. In the *B. juncea* × *B. napus* hybrids most of the morphological and developmental characters showed intermediate between the parents. The hybrids showed heterosis for some characters like plant height, branches/plant, flowering period etc.

Baisakh (1994) reported heterosis for yield in Indian mustard. He used 10 *Brassica juncea* coltivers and their F_1 hybrids grown during 1990. For yield, relative heterosis was positive and highest in the cross Varuna × Pusabold followed by Kranti× B85 and kranti × Appressed mutant. Information on heterosis have also been recorded by Rai and Singh (1994) from data on 6 yield component in 8 *B. campestris* varieties and their 28 F_1 hybrids. A number of hybrids expressed heterosis for seed yield and its component. The average heterosis over better parent for seed yield was 21.3%. The crosses showed significantly high positive heterosis for seed yield in all cases except had high negative heterosis for yield in DTS × YS151. Singh *et al*. (1996) studied heterosis for yield and oil content in *B. juncea* (L.) Czern and Coss. Heterosis over better parent was recorde in the crosses PR-1108× BJ-679 by 77.6% and BJ-1257 × Glossy mutant by 13.1% for seed yield and oil content, respectively. Oil content was positively associated with 1000- seed weight and seed yield indicating the possibility of simultaneous improvement for these characters.

Thakur and sagwal (1997) estimated heterosis in rapeseed (*B. napus* L.) and showed that heterosis over better parent for the various traits were significant for seed yield (-14.8 to 82.8%), primary branches (+26.0 to 193.6%) and siliqua/plant (21.9 to 162.6%). The cross GSB7027 × HNS8803 gave highest positive heterosis for seed yield per plant. Yadav *et al.* (1997) studied heterosis in toria (*B. campestris* var. toria). He used 6 lines and their 15 F_1 hybrids and studied on 8 yield components, The cross white flower × TC113 had the highest negative heterosis (being desirable) for plant height. The crosses white flower × TS61,TH68 × TC113, white flower × Sangam and white flower × TS61 were best for seed yield.

Agrawal and Badwal (1998) studied the extent of heterosis for yield and other characters in 19 F_1 hybrids of *B. juncea* and compared to 5 commercial cultivars. Eighteen hybrids out yielded the best control variety RLM514. Three of them (MS × Plant Rai 1002, MS × RH848 and MS × RLC1047) were superior over the best control in seed yield by 81.19, 50.65 and 64.94%, respectively. Overall heterosis (taking all hybrids and check into account) for seed yield was very high (59.69%). The agronomic superiority of the 3 hybrids were reflected by 1.5 to 2.0 fold increase in oil yield and one week earliness in flowering as compared to RLM514. Heterosis has been explored and investigated for improvement of various traits in *Brassica* and other crops (Fonseca and Patterson,1968 ; Hassan *et al*. 2006). Hirve and Tiwari (1991) carried out a diallel cross of eight elite *Brassica juncea* genotypes. 28 F_1 and F_2 progenies along with parents were evaluated for days to maturity, secondary branches, siliquae per plant and siliqua length. Some of the crosses showed good heterosis for seed yield and its contributing traits. Four single crosses between five *Brassica* varieties and advanced lines were examined by Khan *et al*. (1992) to detect the inheritance patterns, broad-sense heritability and expected genetic advance of yield and its components. Quantitative inheritance pattern was identified for all the traits. Heritability and genetic advances estimates were generally high to moderate for different characters in all the crosses. Pradhan *et al*. (1993) crossed ten *Brassica juncea* genotypes in a diallel mating design excluding reciprocals to study combining ability and heterosis. Significant better parent heterosis was estimated from USSR x Indian and

Synthetic x USSR crosses. It was observed that number of primary and secondary branches, number of siliquae per plant and siliqua density showed significant contribution towards heterosis for yield.

Heterosis studies were carried out by Agrawal and Badwal (1998) for yield and other characters in 19 F_1 hybrids of *Brassica juncea* and compared with five commercial cultivars. Three hybrids showed better performance than best control variety for seed yield. Some of the hybrids showed 1.5-2.0 fold increase in oil yield and one week earliness in flowering as compared to best control variety. Heterosis for seed yield, related traits and oil content in single and 3-way crosses of Indian mustard was estimated by Chauhan, *et al*. (2000). Significant heterosis was calculated as percentage increase or decrease in single and 3 way crosses over the better parent (heterobeltiosis) and standard variety (economic heterosis). Desirable heterosis for plant height, number of siliquae on main shoots, biological and seed yields and oil contents of Indian mustard genotypes was detected by Tyagi *et al*. (2001). Desirable heterobeltiosis (better performance of F_1 hybrid than batter parent value) was calculated for primary and secondary branches per plant, siliqua length, seeds per siliqua, number of siliquae on main shoots, biological and seed yields, and oil contents.

Heterosis was exploited by Ranjeet and Shweta (2007) in 45 hybrids generated from a 10x10 diallel cross of Indian mustard *Brassica juncea* (L.). For seed yield, heterobeltiosis ranged from - 21.4 to 19.6 % and heterosis from - 23.6 to 29.6 %. For all the traits, significant heterobeltiosis was recorded. Maximum values calculated for heterosis were for main shoot length (56.6%), secondary branches (35.8%), seed yield (29.6%), siliquae on main shoot (28.6%), seeds per siliqua (23.4%) and primary branches (22.4%). Maximum calculated heterobeltiosis were for main shoot length (68.7%), secondary branches (49.8%), siliquae on main shoot (41.6%), seeds per siliqua (39.1%), primary branches (33.4%) and seed yield (19.6%).

Turi *et al*. (2006) used 8 x 8 diallel crossing design to discover mid-parent and better-parent heterosis in *Brassica juncea* L. genotypes.

Many of the 56 hybrids showed negative mid-parent and better-parent heterosis for days to 50% emergence, days to 50% flowering, days to physiological maturity and plant height. Positive heterosis was recorded in many crosses for number of primary branches per plant. Significant negative mid-parent and better-parent heterosis were recorded in few hybrids for days to 50% emergence, days to 50% flowering and in many hybrids for days to physiological maturity and plant height. Better-parent heterosis estimates were 44% for branches per plant, 27% for emergence, 22.63% for plant height, 4.08% for maturity and 3.85% for flowering. Eight lines together with two varieties of *Brassica juncea* L. were investigated by Akbar *et al*. (2007) for plant height, number of primary branches per plant, number of siliquae per plant, 1000 seed weight and seed yield per plant. High estimates of broad sense heritability and genetic advance were observed for siliquae per plant.

Heterosis and combining ability for seed yield and its contributing traits and oil content in seven Indian mustard cultivars/strains and their 21 F_1 hybrids excluding reciprocals, obtained from diallel mating design was studied by Singh *et al*. (2007c). Data analysis through Griffing's method II and model I showed predominance of non additive gene effects for most of the traits, indicating the possibility of exploitation of heterosis. Various crosses exhibited high heterosis and specific combining ability effects. The magnitude to heterosis provides a basis for genetic diversity and guidelines for the choice of desirable parents for developing superior F_1 hybrids to exploit hybrid vigor and or building gene pools to be employed in breeding programme. Study of heterosis has a direct bearing on the breeding methodology to be used for varietal improvement. The promising F_1's can directly be included in evaluation traits, while others exhibiting heterosis for one or other desirable traits may be advanced further to obtain transgressive segregants (Saurabh *et al*., 2005).

Aderfis and Heiko (2005) revealed that heterosis is commercially exploited in rapeseed (*Brassica napus* L.) and its potential use has been demonstrated in turnip rape (*B. rapa* L.) and Indian mustard (*B. juncea* L.). In Ethiopian mustard (*B. carinata* A. Braun), however, information regarding heterosis has not been previously reported. This study, therefore,

was conducted to generate information on heterosis and combining ability in *B. carinata*. Nine inbred parents and their 36 F_1s, obtained by half-diallel cross, were evaluated for 12 traits at three locations in Ethiopia. Analysis of variance showed the presence of significant heterosis for all the traits. Seed yield showed the highest relative mid-parent heterosis that varied from 25 to 145% with a mean of 67%. Relative high-parent heterosis for seed yield varied from 16 to 124% with a mean of 53%. General combining ability (GCA) effects were predominant in all traits except secondary branches and pods per plant. Specific combining ability (SCA) was significant for days to flowering, secondary branches, pods per plant, pod length, seeds per pod, 1000-seed weight and oil content. Interaction effects of GCA x location were significant for all traits except days to flowering, days to maturity, and oil content. All traits had significant SCA × location interaction effects. GCA effect for seed yield was positively correlated with F_1 performance (r = 0.77) and absolute mid-parent heterosis (r = 0.67). The presence of high levels of mid- and high-parent heterosis indicates a considerable potential to embark on breeding of hybrid or synthetic cultivars in Ethiopian mustard.

Huq (2007) conducted an experiment on *Brassica rapa* involving 7×7 half diallel cross. Heterosis and combining ability were estimated for seed yield and other related characters such as days to flowering, days to maturity, plant height, number of primary and secondary branches, length of siliquae, seeds per siliqua, seed yield per plant, thousand seed weight. Out of twenty one crosses Agroni × BARIsar-6, Agroni × Tori-7, Shafal × BARI sar-6 and Agroni × Tori-7 showed significant heterosis over mid and berrer parent. Agroni × Tori-7 best for number of primary branches/plant and siliquae/plant. Iftikhar *et al.* (2000) studied rape variety Tower and three stable M9 mutants for heterosis of yield components of inter-mutant crosses during 1997-99. F_1 generations expressed significant heterosis for number of primary branches, number and length of primary roots and siliquae, seeds/siliqua, yield/plant and oil content. It is concluded that these mutants are a good source of variation for future breeding programmes.

Qian *et al.* (2005) reported the observation on the inter subgenomic heterosis for seed yield among hybrids between natural *Brassica napus* (AnAnCnCn) and a new type of *B. napus*

with introgressions of genomic components of *Brassica rapa* (ArAr). This *B. napus* was selected from the progeny of *B. napus* x *B. rapa* and (*B. napus x B. rapa*) x *B. rapa* based on extensive phenotypic and cytological observation. Among the 129 studied partial intersubgenomic hybrids, which were obtained by randomly crossing 13 lines of the new type of *B. napus* to 27 cultivars of *B. napus* from different regions as tester lines, about 90% of combinations exceeded the yield of their respective tester lines, whereas about 75% and 25% of combinations surpassed two elite Chinese cultivars, respectively. This strong heterosis was further confirmed by reevaluating two out of the 129 combinations in a successive year and by surveying hybrids between 20 lines of the new type of *B. napus* and its parental *B. napus* in two locations. Some DNA segments from *B. rapa* were identified with significant effects on seed yield and yield components of the new type of B. napus and intersubgenomic hybrids in positive or negative direction. It seems that the genomic components introgressed from *B. rapa* contributed to improvement of seed yield of rapeseed.

Heterosis over the mid parent, better parent and commercial, check variety pusa bold was estimated for plant height, days to maturity, number of branches per plant, number of siliquae per plant, seed yield per plant (gm) and 1000 seed weight (g) in 17 crosses of *B. juncea* by Patel *et al.* (2005). The crosses ACN-9 × MCN-126 and ACN-9 × MCN-128 were the best performers for seed yield and number of siliquae/ plant. The maximum magnitude of significant positive heterosis for all the three types were also exhibited by these crosses and hence can be exploited for further utilization in a breeding programme.

Shen *et al.* (2005) observed significant differences in seed yield per plant and seed oil content among the F_1 hybrids and between F_1 progenies and their parents of *Brassica campestris*. However, the heterosis for seed yield per plant was much greater than that for seed oil content. Mid parent heterosis and high parent heterosis of seed yield per plant ranged from 5.50 to 64.11% and from -2.81 to 46.02%, while those of seed oil content ranged from -1.55 to 7.44% and -3.61 to 6.55%, respectively. Wang *et al*. (1999) analysed heterosis and combining abilities of 20 reciprocal cross combinations of five double low

rape (*Brassica napus*) cultivars (lines) showing high seed yield. Positive mean heterosis varied among crosses. The positive mean heterosis of siliqua number/plant was 17.6% was highest, followed by seed number/siliqua and 1000-seed weight. Heterosis of F_1 generations were greatest when Zhihu 1 and Zhongyou 220 were used as parents. Liersch *et al*. (1999) conducted a breeding approach known as CMS ogura system of oilseed rape hybrid cultivars in Poland to evaluate yield and yield component variability of F_1 hybrids and their parental lines also heterosis effect, and qualitative traits such as oil and glucosinolate content in seeds. They found that composite hybrid cultivars yielded higher than restored hybrids.They stated that the yield of hybrids and qualitative traits such as oil and glucosinolate content in seeds are significantly dependent on genotypes and environmental conditions.

Satyndra *et al.* (2004) evaluated twenty one Indian mustard hybrids and their parents for eight quantitative traits: days to flowering, days to maturity, plant height, number of primary branches, length of the main raceme, seed yield, thousand seed weight and oil content percentage, in an experiment. High heterosis (15.99, 15.51 and 12.37%) was obtained for seed yield in the crosses Basanti × NDR 8501, Basanti × Kanti and Basnati × RH 30, respectively. These hybrids showed high heterosis over the best cultivar. Among the crosses, Basanti × Kranti may be used for selecting for seed yield and quality traits.

Yadav *et al.* (2004) had undertaken an investigation to estimate heterosis for seed yield and its components in Indian mustard. Hybrids Siifolia × NDRE-4 (-18.5%) and Trachystoma × NRCM-40 (-6.1%) exhibited the highest heterosis for days to flower initiation and days to maturity over better parent, respectively. The magnitude of heterosis was highest for plant height in Trachystoma × SK 93-1 (27.7%) over BP and (25.8%) over SV both. For the number of primary branches per plant Trachystoma × PR 905 showed 106.5 and 100.0% heterosis over BP and SV, respectively. Trachystoma × PHR -1 (125.1%) showed maximum heterosis over BP and Moricandia × NRCM -79 (9.6%) over SV for the number of secondary branches per plant. Siifolia × SM -1 showed 54.1% hrterosis over BP and netative heterosis (-9.2%) over SV for seeds per siliqua. The highest heterosis for thousand

seed weight was observed in Moricandia x PHR -1 (48.80%), followed by Trachystoma × NRCM 69 (20.6%) over BP and SV, respectively. Significant and positive magnitude of heterosis for oil content was observed in Trachystoma×NDYR -8 (10.1%) over BP and Siifolia × NRCM 79 (8.5%) over SV, respectively . The cross, Moricandia × NRCM 86 exhibited significant and positive heterosis over BP(82.8%) for seed yield per plant, followed by Siifolia × NRCM 86 (76.0%) and Moricandia × NRCM 98 (52.5%).

Mahak and lallu (2004) performed an experiment on Indian mustard strains/cultivars Varuna, Shekhar, Vardan, Laha 101, Pusa Bold, RH -30, Pusa Basant, NDR -8501 and Kranti were crossed in a diallel mating design excluding reciprocals. The parents along with 36 F_1s and 36 F_2s were grown data recorded for plant height, branches per plant, siliquae on main raceme, seed yield per plant, thousand seed weight, seed oil content, de-fatted seed content and protein content. The crosses exhibited highly significant heterosis for most of the characters studied. Mahak *et al.* (2003a) studied heterosis for days to flowering, plant height, number of primary and secondary branches, length of main raceme, days to maturity, thousand seed weight, harvest index, oil content, protein content, and seed yield in 10 Indian mustard cultivars and 45 F_1 and F_2 hybrids. High heterosis for seed yield was observed in Varuna× Rohini (56.74%), Vardan × Rohini (53.43%) Varuna × RK 9501 (52.86%), Vardan × NDR 8501 (36.73%), pusa Bold × Rohini (37.68%), and Varuna × NDA8501 (32.54%).

Pankaj *et al.* (2002) studied heterosis of parents for seed yield, oil content and protein content in an 8 × 8 diallel cross in toria (*Brassica campestri*s var. toria). Trait data were recorded on five plants of each of the 28 F_1's and 28 reciprocal F_1's (RF_1s). 24 F_1's and 21 RF_1s showed significant positive heterosis for seed yield over mid parent (MP) and 16 F_1's and 21 RF_1s over the better parent (BP). Zhang *et al.* (2000) crossed three double low cytoplasmically male sterile (CMS) and five double low restorer lines of *Brassica napus* and they analyzed resulting 15 hybrids for eight yield components. In this experiment they found that the CMS F_1 had significant heterosis, particularly for yield, but that predicted for the F_2 was lower. They also suggested that the major yield components, total siliquae

number/plant had the highest heterosis and would be of more value in a breeding programme than trying to increase seed number per siliqua or 1000-seed weight.

Lu *et al*. (2001) proposed that heterosis is proportional to genetic divergence between respective parents in many crops. They evaluated heterosis in interspecific hybrids between *Brassica napus* (AACC, 2n=38) and *Brassica rapa* (*B. campestris*) (AA, 2n=20) for ten agronomic characteristics and compared to heterosis in hybrids of *B. napus*. They characterized fifteen inter-specific crosses for their cross ability, germination rate, morphology, pollen fertility, and seed production. They found cross ability ranged from 0.8 to 16.7 seeds per flower pollinated, with 7.5 seeds on average; germination of the F_1 seeds varied with combinations from 20.7 to 89.8%; highly significant high-parent heterosis in the number of secondary branches and siliquae number per plant and significant mid-parent heterosis in plant height, length of main inflorescence, and the number of primary branches. They also found that seed number per siliqua in inter-specific hybrid was significantly lower than both parents' and varied with different combinations and inter-specific hybrids showed higher vegetative heterosis than intra-specific hybrids.

Swarnkar *et al*. (2001) carried out heterosis analysis using 36 F_1 hybrids, 36 F_2 generations and parents obtained from 9 × 9 diallel mating design for 11 quantitative traits, viz. days to flowering, plants height (cm), number of primary branches, number of secondary branches, length of main raceme (cm), number of siliquae on main raceme, days to maturity, yield per plant (g), thousand seed weight (g), oil content (%) and protein content (%). High economic heterosis for seed yield was observed to be present in four crosses, KR-5610 × PR-15 (58.38%), YRT-3 × PR-15 (54.33%), RK-1467 × T-6342 (52.60%) and KR-5610 × KRV –Tall (36.70%). The hybrids showing high heterosis over best cultivar can be successfully grown up to 2 or 3 early generations, which may prove beneficial for the Indian mustard growers. Wu *et al.* (2001) evaluated the heterosis of 80 hybrid combinations from TGMS line 402S and its original parent Xianyou 91S, and the combining ability of 40 test cross lines. The results of identification test showed that among 47 combinations yielding over the control Xianyou 15, seventeen ones with 402S

and three ones with Xianyou 91S over yielded more than 20%, reaching the significant level of 1%; and among 51 combinations yielding over their corresponding higher yield parents, 18 ones with 402S and nine ones with Xianyou 91S over yielded at 5 or 1% significant level.

Tyagi *et al.* (2000) reported data on heterosis in intervarietal crosses in mustard (*Brassica juncea* (L.) Czern & cross.). Desirable significant and negative heterosis for plant height was observed in seven crosses, with Varuna × SKNM-90-14 exhibiting the most negative value (-14%). Maximum positive heterosis was recorded for seed yield per plant (-48.0 to 93.3%), with crosses PCR-7 × SKNM90-13, RH-30 × TM18-8 and PCR7 × JM90-12 giving values of 93.3, 81.3 and 77.3%, respectively. In general, positive heterosis for seed yield was accompanied by positive heterosis for siliqua length, seeds per siliqua, 1000-seed weight, biological yield and harvest index. Katiyar *et al*. (2000a) information on heterosis and combining ability is derived from data on seed yield and three yield components in six lines, 16 testers and their 96 F_1 hybrids from a line × tester mating design. Of the hybrids, 64 and 38 showed heterosis for seed yield over the better parent and standard cv. varuna, respectively.

Ali *et al*. (1995) investigated the association between distance and mid-parent heterosis and they found that the correlation between genetic distance and heterosis was positive and highly significant for seed yield, siliquae/plant and seeds/siliqua. They estimated genetic distance among canola [rape] cultivars through multivariate analysis. They analysed thirty cultivars from various sources and clustered into three distinct clusters based upon five morphological characteristics and yield components (crown diameter, branches/plant, siliquae/plant, seeds/siliqua and yield/plant). Two cultivars from each cluster were selected as parents and 15 partial-diallel inter-and intracluster crosses were made between the six selected parents and evaluated at two locations in Michigan, USA in 1990-91.

Hari *et al*. (1995) conducted an experiment to derived information on heterosis from data on eight yield component in seven rape (*Brassica napus*) genotypes and there 21 F_1

hybrids grown during winter 1992 in Hariyana. They found that hybrid HNS9002 × N20-7 had high positive heterosis for primary and secondary branches, siliquae on main shoot and seeds per siliqua. They also found another hybrid, HNS9005 × N20-7, exhibited appreciable heterosis over the better parent (HNS9005) for seed yield and oil content. They also proposed that these hybrids were promising for exploitation of heterosis. They informed that parent N20-7 developed from Japanese material Norin 20 was a promising parent for exploitation in the hybrid breeding programme. Ahmad (1993) worked with parents and F_1 hybrids from crosses between resynthesized lines and improved 00 varieties. F_1 were earlier maturing than resynthesized lines and heterosis was observed for spring regrowth and plant height. In trails, the best resyn. line H128 could only produce 87% of the mean yield of the improved varieties.

Yu and Tang (1995) studied on seven inbred rape lines and their 21 F_1 hybrids which were compared at the seedling stage for acid phosphatase (APS) isoenzyme patterns by polyacrylamide gel electrophoresis (PAGE) analysis. All hybrids with hybrid band(s) in their zymograms showed heterosis in yield, and those without hybrid bands showed no heterosis. Hybrids with two or three hybrid bands and high APS activity showed great heterosis. Hybrids with 2-3 medium or weak hybrid bands had only moderate heterosis. Hybrids derived from parents with very different zymograms showed high heterosis even though they had only one strong hybrid band. When the parents had similar zymograms and the hybrid showed relatively low APS activity, heterosis was low. Since the isoenzymes of APS in *Brassica napus* appeared to be quite stable, they were recommended to serve as a biochemical indicator of heterosis at the seedling stage (the 2-3 leaf stage).

Grant (1985) found heterosis for seed yield up to 72% over better parents. Lefort *et al*. (1987a) while studying *Brassica napus* of Asian and European parental lines and their hybrids, reported that plant height and seed yield showed positive heterosis in the hybrids. Lefort (1982) studied 140 F_1 hybrids of winter oil seed rape (*B. napus* L.) and found that for seed yield average hybrids vigour was 23.5% on the basis of the mid parent. In a few cross combinations the value reached up to 50% in relation to the best parent value. This

emphasizes the interest of hybrids varieties for improving yield. Schuster *et al.* (1978) reported heterosis of 203% for seed yield, 211% for seed no./ siliqua and 187% of no. of siliqua/plant in crosses between diverse lines in each generation of black mustard (*B. nigra* L.). There was lawer heterosis for 1000 seed weight. Zuberi and Ahmed (1973) studies six crosses of four strains of *B. campestris* var Toria for yeild and its component characters. They estimated heterosis for different charaters. According to them heterosis for different characters varied widely due to cross combination.

2.3 Generation mean analysis

The generation mean analysis is commonly used to study the inheritance pattern of quantitative traits by the plant breeders. Components of generation mean were estimated by Sachan and Singh (1987) for days to flower initiation and maturity in three crosses of Indian mustard. All three types of digenic interactions additive x additive, additive x dominance and dominance x dominance was significantly involved in the inheritance of these traits. Genes with higher effects were completely related to higher mean parents for maturity in cross I and flowering in cross II. For maturity in crosses I and III and flowering in crosses I and II, duplicate epistasis was detected. In duplicate epistasis, two pairs of non-alleles affect the same trait and dominant or recessive allele of each pair acts as epistatic. Presence of higher order interactions was observed for days to flowering in cross III and maturity in cross II by the inadequacy of all the fitted models. Viana (2000) reported that epistatic effects involving genic combinations of fixed and non fixed genes, contributed to the genotypic mean of any population. These effects included additive x additive and additive x dominant epistatic components. The additive and dominance components could be biased due to those epistatic effects. The value of bias would dependent on the relative values of the epistatic effects, type of operating epistasis and dominance direction.

Varsha *et al*. (1999) studied six generations namely, P_1, P_2, F_1, F_2, BC_1 and BC_2 of *B. napus* and determined additive, dominance, additive x dominance and dominance x dominance gene effects in two crosses viz. ABU x GS63 and ABU x IRMA. In crosses,

additive and dominance gene effects were prominent in controlling days to flowering, siliqua number, plant height, seed weight and seed yield. All the three types of epistasiss were detected for seed yield in cross ABU x GS63 and for plant height in cross ABU x IRMA. Six generations (P_1, P_2, F_1, F_2, BC_1 & BC_2) of six *B. juncea* crosses were evaluated by Kant and Gulati (2001) for days to 50% flowering, days to 75% maturity, seed yield per plant, 1000-seed weight and oil content. Estimation of genetic parameters m, d, h, i, j & l revealed that additive effects were more important in the inheritance of days to 50% flowering, seed yield per plant, 1000-seed weight and oil content. Presence of additive x additive interaction for days to 50% flowering, days to 75% maturity, seed yield per plant and oil content, additive x dominance for days to 75% maturity, seed yield per plant, and oil content and dominance x dominance for days to 50% flowering, days to 75% maturity and 1000-seed weight was also detected.

Bhat *et al*. (2002) also carried out genetic studies to work out heredity pattern of erucic acid in *Brassica juncea*. Segregation analysis of two zero x high erucic acid crosses from F_2 and BC_1 generations revealed that two dominant genes with additive effects governed higher erucic acid content in *B. juncea*. It was indicated by the experimental data that in *Brassica juncea,* the gene (E_2) linked with A genome had a greater impact to the total erucic acid content than the gene (E_1) located on the B genome. In another experiment, Chauhan and Tyagi (2002) investigated six Indian mustard generations, viz., P_1, P_2, F_1, F_2, BC_1 and BC_2 of two crosses to study the genetics of erucic acid content. Partial dominance of high erucic acid content was detected over low erucic acid content in both the crosses. In the cross TERI (OE) M 21 x PCR 7, the additive-dominance model was adequate indicating absence of epistasiss. However, predominance of epistasiss were observed in the cross TERI (OE) M 21 x Varuna. Estimates for narrow-sense heritability ranged from 0.48 and 0.65, respectively, in the cross TERI (OE) M 21 x PCR 7 and TERI (OE) M 21 x Varuna. For both the crosses, high values for genetic advance (45.0-62.5%) were reported. Additive and dominance effects were important in the inheritance of erucic acid in these crosses but presence of additive x additive interaction along with additive effects indicated

that desirable selection in early segregating generations for low or high erucic acid content would be effective.

Generation means analysis of P_1, P_2, F_1, F_2, BC_1, and BC_2 was carried out by Cheema and Sadaqat (2004) for three crosses of *Brassica napus* i.e. Range x Shiralee, Range x Ester and Rainbow x Ester under irrigation and drought conditions to identify the type of gene action operating for yield and yield components. Variation in type of gene action and number of components of generation mean was observed with the plant traits, crosses and treatments. Significant presence of genotype x environment interaction was noticed in the expression of all the traits. Involvement of the both additive and non-additive gene action in most of the traits in different crosses under the two treatments was reported. However, predominance of non-additive gene action along with duplicate or complementary type of epistasis was prominent. Higher dominance value for oil contents was observed. Four to five parameter models was suggested for plant height, days to first bud, days to maturity indicating that these traits were under the complex control of more than two genes. Changes in gene effect were observed for different traits with the changes in environment. It was suggested that simple selection should be carried out in early generation for the traits controlled by additive gene action and selection in latter generations would be suitable for the traits governed by non- additive gene action.

Khattak *et al*. (2004) analyzed the nature of gene action in mung bean in two sets of crosses involving four parents through generation mean analysis. Joint scaling test was carried out for the mean data of six populations (both parents, F_1, BC_1, BC_2 and F_2). Six-parameter model was used to detect all types of gene effects, due to the presence of epistasis. The analysis revealed complex expression of gene effects for most of the traits in both the crosses. In both crosses, for all the traits, both additive (d) and dominant (h) gene effects were detected except for days to first flower and first pod maturity in ML-5 x NM-54, where dominant gene effects were non significant. No digenic interactions were indicated in case of days to 90% pods maturity and plant height at first flower in cross 6601 x NM 92, and days to first pod maturity and plant height at first flower in cross ML-5

x NM -54. The digenic interactions i.e., additive x additive (i) additive x dominance (j), and dominance x dominance (l) were significantly important in the expression of the studied traits, showing complex gene effects for their inheritance. Singh *et al*. (2007b) evaluated six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of a three varietal crosses (T-59 x RH-30, T-59 x Pusa Bold and T-59 x RL-1359) of Indian mustard through generation mean analysis to estimate the relative importance and contribution of the additive (d), dominance (h) and epistatic (i, j and l) components of genetic variance for yield and yield contributing traits. Significant epistatic gene effects were revealed by the scaling test for all the characters except one cross, T-59 x Pusa Bold for days to flowering. It was indicated by the six parameter model that due to higher magnitude, dominant gene effect (h) were more important than the additive (d) effect for all the ten characters studied except for plant height in one cross. Dominant x dominant (l) and additive x additive (i) components of epistatic effects were of greater importance than additive x dominant (j) components. For main raceme length, number of primary branches, number of secondary branches, seed yield per plant and oil content, complementary epistasis was detected which was desirable in two crosses and would be helpful for improvement of these traits. Presence of h and l estimates with opposite signs indicated duplicate gene action for plant height, siliquae number on main raceme, siliquae length and 1000-seed weight.

To evaluate the genetics of yield components of Indian mustard, Kemparaju *et al*. (2009) studied the six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of 11 primary cross combinations of Indian mustard for four characters i.e. days to 50% flowering, days to maturity, seed yield per plant and harvest index (%). Scaling test was applied to the mean of six generations to estimate the epistasis and genetic parameters m, d, h, i, j and l. Both additive and non-additive type of gene action was prominent in controlling all the traits. Due to relatively greater role played by duplicate epistasis than complementary epistasis, reciprocal recurrent selection was proposed for development of improved varieties. Upadhyay and Kumar (2009) followed generation mean analysis to study heritability and genetic advance for days to 50% flowering, days to maturity, plant height, number of siliqua on main raceme, length of main raceme, seeds per siliqua, primary branches per plant, secondary

branches per plant, 1000-seed weight, seed yield per plant and oil content, using seven Indian mustard cultivars, eight F_1 and eight F_2 hybrids. High heritability along with high genetic advance was estimated for secondary branches per plant and seed yield per plant in different crosses, indicating the presence of additive gene effects.

2.4 Heritability and genetic advance

Singh (1986) studied 22 genotypes of *B. napus* , *B. campestris* and *B. juncea* and reported high heritability and genetic advance in seed yield/plant and no. of seed/siliqua. Lekh *et al.* (1998) conducted an experiment with 24 genotypes of *B. juncea* and 10 genotypes of each *B. campestris*, *B. carinata* and *B. napus* during the rabi season of 1992-93 and 93-94. He evaluated 10 yield components under 3 sowing dates. The highest genotypic co-efficient of variation were calculated for secondary branches. High heritability estimates were observed for all the characters under all environments except harvest index and biological yield. Highest genetic advance and high genotypic and phenotypic co-efficient of variation were recorded for days to 50% flowering.

Beena *et al*. (1998) studied variability in mustard. Information was tabulated on mean, range, genotypic and phenotypic co-efficient of variation and heritability for 6 yield-related traits in 22 mustard (*Brassica juncea*) genotypes grown at Nagpur during the rabi season of 1997-98. Hussain *et al*. (1998) evaluated 14 Toria (*B. campestris* var. toria) and 7 Indian mustard (*B. juncea*) genotypes for 13 characters related to maturity duration and seed yield. High estimates for heritability and genetic advance was obtained for number of secondary branches, biological yield per plant, number of seeds per plant and number of seeds per siliqua both for Toria and Indian mustard. 1000-seed weight and plant height in Indian mustard and number of siliqua per plant and length of main inflorescence in Toria also showed high estimates. Das *et al*. (1998) observed high heritability coupled with high genetic advance for siliquae per plant, number of secondary branches per plant, 1000-seedweight and plant height, indicating predominance of additive gene action in inheritance of these traits.

Larik and Rajput (2000) studied six productive traits in two varieties of *B. juncea* and four varieties of *B. napus*. High broad sense heritability estimates (ranging from 97.70% to 60.24%) was found for all the traits, indicating the involvement of additive gene action. low genetic advance was estimated for dry matter yield, seeds per siliqua and plant height irrespective of their high heritability, possibly due to non-additive gene (dominance and epitasis) effects.. In another study, Ghosh and Gulati (2001) evaluated 37 genotypes of Indian mustard selected from different geographical regions for heritability for 12 yield components. High heritability along with high genetic advance was detected for oil contents, harvest index, number of primary branches, and number of siliquae on main shoot, main shoot length and number of seeds per siliqua, indicating the prevalence of additive gene action for their expression. Shalini *et al*. (2001) evaluated that the values for heritability and genetic gain were moderate to high for 1000-seed weight, number of siliquae per plant and number of secondary branches per plant suggesting a very high response to selection for these yield components of Indian mustard.

Mahmood *et al*. (2003) evaluated four single crosses of *Brassica juncea* for broad-sense heritability, coefficients of variability and genetics advance. Values were estimated for primary branches, plant height, siliqua per plant and seed yield. High heritability along with high genetic advance was determined for number of siliqua per plant indicating good potential for selection. Two crosses 86-4-3 x Poorbi Raya and 86-16-1 x Poorbi Raya showed high heritability and genetics advance for most characters suggesting that fast genetic improvement could be possible through selection. Kumar *et al*. (2007) evaluated 50 Indian mustard genotypes for genetic variability, heritability and genetic advance. For days to 50% flowering, pod length, 1000-seed weight and number of secondary branches, heritability estimates were high. High to moderate genetic advance was estimated for number of secondary branches, pod length, seeds per pod and 1000-seed weight. Sheetal *et al*. (2007) carried out a genetic study of F_1 generation in mustard for yield, its attributes and oil contents. High heritability values were noted for number of siliquae per plant (0.82-0.98) and seed yield per plant (0.91-0.99). High estimates for genetic advance was noticed for number of siliquae per plant and seed yield per plant indicating good potential for

selection for these traits. Acharya and Pati (2008) measured heritability and genetic advance of fifteen Indian mustard cultivars for 50% flowering, days to maturity, plant height, primary branches, secondary branches, number of siliquae per plant, seeds per siliqua, 1000-seed weight and seed yield per plant. High heritability and genetic advance were estimated for plant height, number of secondary branches and number of siliquae per plant indicating that improvement potential was available regarding to these traits. Another study was conducted by Nigam and Alka (2009) on ten Indian mustard parents and their 45 F_1 hybrids (excluding reciprocals) derived from a diallel cross. Data for days to flowering, number of primary branches, seed yield per plant, dry matter plant, harvest index, test weight, oil content, erucic acid content and protein content was recorded. Heterosis estimates were high for seed yield, days to flowering, number of primary and secondary branches and dry matter per plant in some of the crosses, indicating good potential for improvement in Indian mustard genotypes.

Afrin *et al.* (2011) conducted an experiment in *Brassica napus* and studied heritability. The plant height showed highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliquae, number of siliqua per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability. Patel (2011) experimented with three high yielding varieties and two very low quality varieties and their six generation cross product of *Brassica napus*. The result showed that the heritability in broad sense with high to moderate genetic advance was found in thousand grain weight, seed yield per plant. Moderate to high heritability associated with low genetic advance was recorded in days to maturity and days to flowering.

Tahira *et al.* (2011) conducted an experiment with ten wide genetic ranged variety of *Brassica juncea* to study heritability in broad sense and showed siliquae length, plant height and seed yield had high values. Roy *et al.* (2011) conducted an experiment on rapeseed mustard (*Brassica spp.*) and studied variability and heritability. The result

revealed that significant varietal difference except the number of siliquae on main receme. The PCV and the GCV was high in secondary branches per plant and number of siliqua per plant. High heritability along with high genetic advance as percent of mean was reported in plant height, seed yield, secondary branches per plant, siliqua per plant and seeds per siliquae. Ali *et al.* (2013) conducted an experiment with thirty lines of *Brassica carinata* and reported that PCV and GCV ranged from 4.92-48.24% and 3.2-38.1%, respectively. The highest heritability values were recorded for pod length (0.83) followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield plant-1 and pods on main raceme.

Ahmad *et al.* (2013) studied thirty five advanced mutant lines along with a check variety of *Brassica napus* called Abasin-95 for variability analysis and reported that seed yield and days to flowering showed high genetic variability. High heritability and genetic advance was recorded for seed yield. The mutant lines OA5, G1 and 06 showed their superiority in high seed yield, thousand seed weight and earliness in flowering. Khan *et al*. (2013) evaluated thirty F_7 segregating lines and two parents of *Brassica rapa* to study variability, heritability and genetic advance. The result revealed that except thousand seed weight, significant variation was presented among all the genotypes for all the characters. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliquae followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliquae, and siliquae length showed high heritability along with low genetic advance in percent of mean. Considering important performances, the genotypes G-15, G-19, G-1, G-3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program.

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

that indigenous accessions had great proportion of genetic variability. Muhammad *et al.* (2014) studied with four parental genotype along with twelve F_2 generation of *Brassica napus* and reported that days to 50% flowering were significantly different at 5% level of significance and plant height and pod length at 1% level of significance. Plant height and pod length showed high heritability and days to 50% flowering showed moderate heritability.

Hasan *et al*. (2014) studied on heritability of *Brassica napus* and the result stated that plant height, yield per plant and days to 50% flowering showed high heritability. Khan *et al*. (2013) studied twenty genotypes of *Brassica napus* with a check variety and it revealed higher broad sense heritability in pods in main receme, seed per siliquae, primary branches per plant, seed yield per plant and number of siliquae per plant. Genetic variances were higher than the environmental variances for all traits. Walle *et al.* (2014) carried out a study with thirty six genotypes of Ethiopian mustard (*Brassica carinata*) and result revealed that there were significant difference in days to 50% flowering, plant height and primary branches per plant. GCV was lower than the PCV for all yield related characters studied. High heritability with high genetic advance was observed in plant height, number of secondary branches per plant and days to 80% maturity.

CHAPTER 3
MATERIALS AND METHODS

3.1 Experimental site and duration of experiment

The research work was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during October, 2010 to March, 2013. The location of the experimental site was situated at 23.77° North latitude and 90.37° East longitude with an elevation of 8.6 meter above the sea level. Photograph showing the experimental sites (Plate 1 and Plate 2).

3.2 Soil and Climate

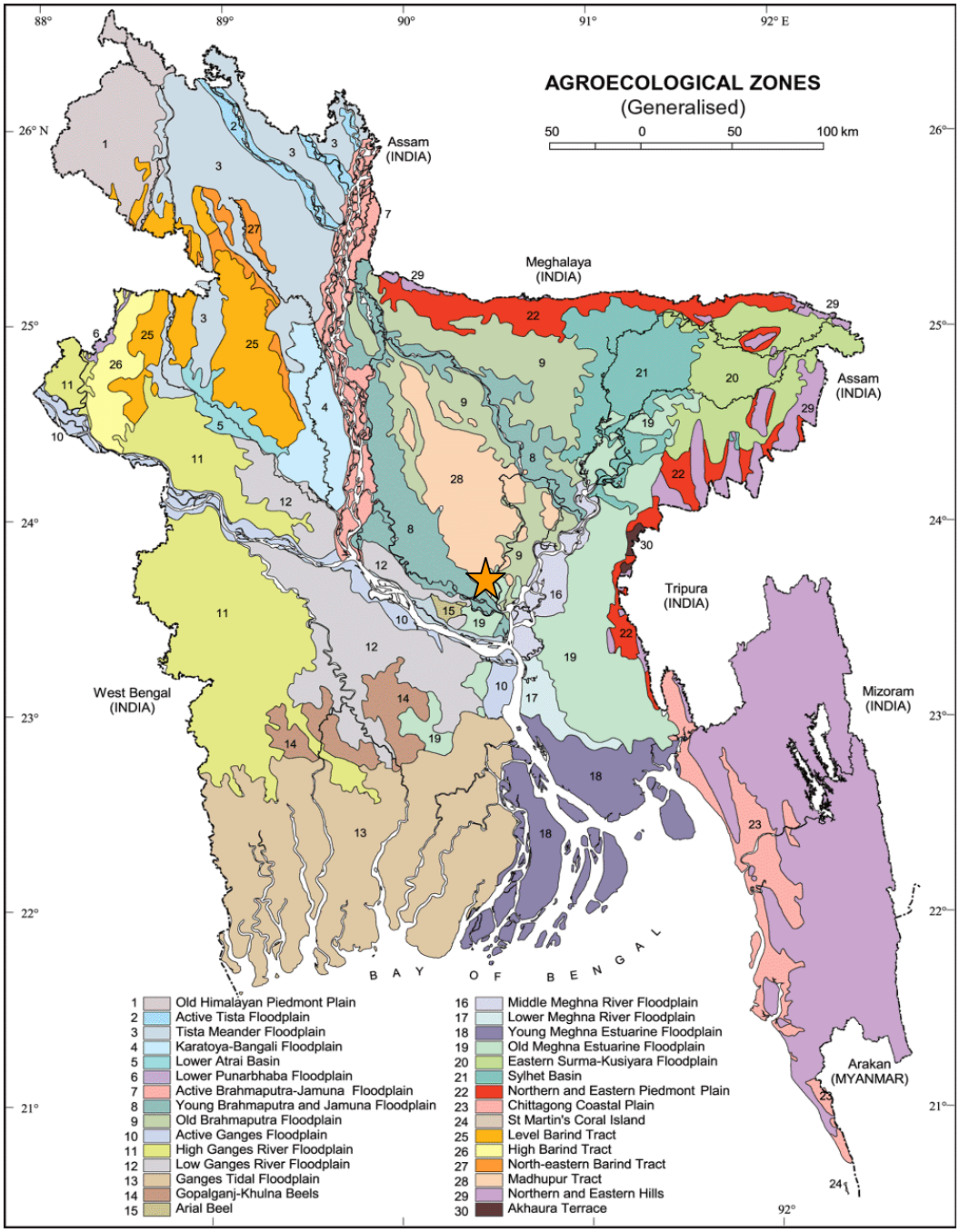
The experimental site was situated in the subtropical zone (Fig. 1). The soil of the experimental site belongs to Agro-ecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content is 0.82% (Appendix I). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II A, II B and II C).

3.3 Plant materials and Methods

The experiment was conducted in three years. In first year a total number of 21 (twenty one) materials were used (Table 1) where six of them were parental varieties of *Brassica rapa* along with the fifteen intervarital hybrids i.e. F_1 (Table 1). In the second year the 15 intervarital crosses and 6 parents were grown in the experimental field and different crosses were made between F_1 and parent 1 (backcross one, BC_1) and F_1 and parent 2 (backcross two, BC_2). In the third year 60 cross materials (Table 4) and 6 parents were grown in the experimental field which consist of fifteen F_1, fifteen F_2, fifteen BC_1, fifteen BC_2 generations derived from the crosses. In first year the materials were collected from the Chairman, Advisory Committee, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh.

Plate 1. A close view at experimental site (siliquae stage) of SAU farm

Plate 2. A field view at experimental site of SAU farm



★ The experimental site under study

Figure 1: Location of the experimental field

Table 1: List of plant materials used in first year and second year

Entry No.	Generation	Materials used
1.	P	TORI 7
2.	P	SAU Sarisha-1
3.	P	SAU Sarisha-2
4.	P	SAU Sarisha-3
5.	P	BARI Sarisha-6
6.	P	BARI Sarisha-15
7.	F_1	SAU-1 X SAU-2
8.	F_1	SAU Sarisha -1 X SAU Sarisha -3
9.	F_1	SAU Sarisha -2 X SAU Sarisha -3
10.	F_1	SAU Sarisha -1 X BARI Sarisha -6
11.	F_1	SAU Sarisha -2 X BARI Sarisha -6
12.	F_1	SAU Sarisha -3 X BARI Sarisha -6
13.	F_1	SAU Sarisha -1 X BARI Sarisha-15
14.	F_1	SAU Sarisha -2 X BARI Sarisha -15
15.	F_1	SAU Sarisha -3 X BARI Sarisha -15
16.	F_1	BARI Sarisha -6 X BARI Sarisha -15
17.	F_1	SAU Sarisha 1 X TORI-7
18.	F_1	SAU Sarisha -2 X TORI-7
19.	F_1	SAU Sarisha -3 X TORI-7
20.	F_1	BARI Sarisha -6 X TORI-7
21.	F_1	BARI Sarisha -15 X TORI-7

Table 2: Cross combinations in half diallel system of six varieties in *Brassica rapa* L.

Parents / Parents	**SAU Sarisha-1**	**SAU Sarisha-2**	**SAU Sarisha-3**	**BARI Sarisha-6**	**BARI Sarisha-15**	**TORI-7**
SAU Sarisha-1	**SAU Sarisha-1**	SAU Sarisha -1 X SAU Sarisha -2	SAU Sarisha -1 X SAU Sarisha -3	SAU Sarisha -1 X BARI-6	SAU Sarisha -1 X BARI-15	SAU Sarisha 1 X TORI-7
SAU Sarisha-2		**SAU Sarisha-2**	SAU Sarisha -2 X SAU Sarisha -3	SAU Sarisha -2 X BARI-6	SAU Sarisha -2 X BARI-15	SAU Sarisha -2 X TORI-7
SAU Sarisha-3			**SAU Sarisha-3**	SAU Sarisha -3 X BARI-6	SAU Sarisha -3 X BARI-15	SAU Sarisha -3 X TORI-7
BARI Sarisha-6				**BARI Sarisha-6**	BARI Sarisha -6 X BARI Sarisha -15	BARI Sarisha -6 X TORI-7
BARI Sarisha-15					**BARI Sarisha-15**	BARI-15 X TORI-7
TORI-7						**TORI-7**

Table 3: Features of the parents used in this research

Sl. no.	Name of parents	Species	Ecotype	Status	Flower colour	No. of chamber in fruit	Plant height	Maturity period (days)	Source	Yield t / ha
1.	TORI 7	*B. rapa*	Brown sarson	Land race	Yellow	2	Medium	80-85	BARI	0.90 - 1.00
2.	SAU Sarisha-1	*B. rapa*	Yellow sarson	Variety	Yellow	2	Medium	75-85	SAU	1.90 - 2.50
3.	SAU Sarisha-2	*B. rapa*	Yellow sarson	Variety	Yellow	2	Medium	75-85	SAU	1.90 - 2.10
4.	SAU Sarisha-3	*B. rapa*	Yellow sarson	Candidate	Yellow	2	Medium	80-85	SAU	2.20 - 2.50
5.	BARI Sarisha-6	*B. rapa*	Yellow sarson	Variety	Yellow	2	Tall	105-110	BARI	1.90 - 2.20
6.	BARI Sarisha-15	*B. rapa*	Yellow sarson	Variety	White	2	Medium	100-105	BARI	1.55 - 1.65

Table 4: List of plant materials used in third year

Entry No.	Generation	Materials used
1.	F_1	TORI 7×SAU Sarisha 1
2.	F_1	TORI 7×SAU Sarisha 2
3.	F_1	TORI 7×SAU Sarisha 3
4.	F_1	TORI 7×BARI Sarisha 6
5.	F_1	TORI 7×BARI Sarisha 15
6.	F_1	SAU Sarisha 1×SAU Sarisha 2
7.	F_1	SAU Sarisha 1×SAU Sarisha 3
8.	F_1	SAU Sarisha 1×BARI Sarisha 6
9.	F_1	SAU Sarisha 1×BARI Sarisha 15
10.	F_1	SAU Sarisha 2×SAU Sarisha 3
11.	F_1	SAU Sarisha 2×BARI Sarisha 6
12.	F_1	SAU Sarisha 2×BARI Sarisha 15
13.	F_1	SAU Sarisha 3×BARI Sarisha 6
14.	F_1	SAU Sarisha 3×BARI Sarisha 15
15.	F_1	BARI Sarisha 6× BARI Sarisha 15
16.	F_2	TORI 7×SAU Sarisha 1
17.	F_2	TORI 7×SAU Sarisha 2
18.	F_2	TORI 7×SAU Sarisha 3
19.	F_2	TORI 7×BARI Sarisha 6
20.	F_2	TORI 7×BARI Sarisha 15
21.	F_2	SAU Sarisha 1×SAU Sarisha 2
22.	F_2	SAU Sarisha 1×SAU Sarisha 3
23.	F_2	SAU Sarisha 1×BARI Sarisha 6

Table 4. (CONT'D)

Entry No.	Generation	Materials used
24.	F_2	SAU Sarisha 1×BARI Sarisha 15
25.	F_2	SAU Sarisha 2×SAU Sarisha 3
26.	F_2	SAU Sarisha 2×BARI Sarisha 6
27.	F_2	SAU Sarisha 2×BARI Sarisha 15
28.	F_2	SAU Sarisha 3×BARI Sarisha 6
29.	F_2	SAU Sarisha 3×BARI Sarisha 15
30.	F_2	BARI Sarisha 6× BARI Sarisha 15
31.	BC_1	(TORI 7×SAU Sarisha 1) × SAU Sarisha 1
32.	BC_1	(TORI 7×SAU Sarisha 2) × SAU Sarisha 2
33.	BC_1	(TORI 7×SAU Sarisha 3) × SAU Sarisha 3
34.	BC_1	(TORI 7×BARI Sarisha 6) × BARI Sarisha 6
35.	BC_1	(TORI 7×BARI Sarisha 15) × BARI Sarisha 15
36.	BC_1	(SAU Sarisha 1×SAU Sarisha 2) × SAU Sarisha 2
37.	BC_1	(SAU Sarisha 1×SAU Sarisha 3) × SAU Sarisha 3
38.	BC_1	(SAU Sarisha 1× BARI Sarisha 6) × BARI Sarisha 6
39.	BC_1	(SAU Sarisha 1× BARI Sarisha 15) × BARI Sarisha 15
40.	BC_1	(SAU Sarisha 2×SAU Sarisha 3) × SAU Sarisha 3
41.	BC_1	(SAU Sarisha 2× BARI Sarisha 6) × BARI Sarisha 6
42.	BC_1	(SAU Sarisha 2× BARI Sarisha 15) × BARI Sarisha 15
43.	BC_1	(SAU Sarisha 3×BARI Sarisha 6) × BARI Sarisha 6
44.	BC_1	(SAU Sarisha 3× BARI Sarisha 15) × BARI Sarisha 15
45.	BC_1	(BARI Sarisha 6×BARI Sarisha 15) × BARI Sarisha 15

Table 4. (CONT'D)

Entry No.	Generation	Materials used
46.	BC_2	(TORI 7×SAU Sarisha 1) × TORI 7
47.	BC_2	(TORI 7×SAU Sarisha 2) × TORI 7
48.	BC_2	(TORI 7×SAU Sarisha 3) × TORI 7
49.	BC_2	(TORI 7×BARI Sarisha 6) × TORI 7
50.	BC_2	(TORI 7×BARI Sarisha 15) × TORI 7
51.	BC_2	(SAU Sarisha 1× SAU Sarisha 2) × SAU Sarisha 1
52.	BC_2	(SAU Sarisha 1×SAU Sarisha 3) × SAU Sarisha 1
53.	BC_2	(SAU Sarisha 1×BARI Sarisha 6) × SAU Sarisha 1
54.	BC_2	(SAU Sarisha 1× BARI Sarisha 15) × SAU Sarisha 1
55.	BC_2	(SAU Sarisha 2× SAU Sarisha 3) × SAU Sarisha 2
56.	BC_2	(SAU Sarisha 2× BARI Sarisha 6) × SAU Sarisha 2
57.	BC_2	(SAU Sarisha 2×BARI Sarisha 15) × SAU Sarisha 2
58.	BC_2	(SAU Sarisha 3× BARI Sarisha 6) × SAU Sarisha 3
59.	BC_2	(SAU Sarisha 3×BARI Sarisha 15) × SAU Sarisha 3
60.	BC_2	(BARI Sarisha 6×BARI Sarisha 15) × BARI Sarisha 6

3.4. Land preparation

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

3.4.1 Application of manure and fertilizer

Urea, Triple Super Phosphate, Muriate of Potash @ 550, 450, 250 kg/ha and Cowdung 10 ton^{-1}ha were used in the experiment. Total TSP and Cowdung were applied in final land preparation. Half of Urea and half muriate of potash (MOP) were applied after three weeks and remaining were applied in the plot after five weeks of transplanting.

3.5 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 70m × 12m = 840 m^2. Each replication size was 70 m × 3.5 m, and the distance between replication to replication was 1 m. The spacing between lines to line was 30 cm. Seeds were sown in lines in the experimental plots on 30 October, 2010. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.6 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. One post sowing irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. Second weeding was done after 35 days of sowing. One top dress of urea was made after 25-30 days of seedling age when the soil was in optimum moisture condition. Aphid infection was found in the crop during the siliqua development stage. To control aphids Malathion-57 EC @ 2ml/liter of water was applied. The insecticide was applied in the afternoon.

3.7 Development of F_1 Hybrids

In first year collected materials (6 parents and crosses materials) were sown in the research area of SAU, maintaining line to line distances 30 cm and replication to replication 1m and each line distances 3 m respectively, during rabi season 2010-11. Normal agronomic practices were applied in the field. At the flowering, these 6 parents were crossed in all possible combinations under half diallel system through hand emasculations and controlled pollinations. Paper bags were used for avoiding the contaminations. Pollinations to emasculated florets were repeated once after two days for maximum seed setting.

In second year the seeds of F_1 crosses and selfed parents were sown under a Randomized Complete Block Design with three replications during rabi season 2011-12 in the field. Three to four seeds were dibbed at sowing. Thinning was done keeping one plant per hole at 3-4 leaf stage. Here also done several crossing in all possible combinations under half diallel system through hand emasculations and controlled pollinations. The crop was managed to avoid insect pests and irrigation was carried out when it was necessary to avoid drought stress. All other standard agronomic practices were followed as recommended for Rapeseeds crop.

3.7.1 Hybridization programme

At the time of flowering, the 6 parents were crossed. The hybridization programme covered one-way crossing among six varieties of *B. rapa* (Inter-variety). The crossing as done have been shown in Table 2. Hybridization of experimental site is presented Plate 3.

3.7.2 Hybridization technique

Both male and female parents were selected on the basis of more desirable morphological characters. Before making crosses, both mature and over mature buds including already opened flowers on the inflorescence of the female parents were removed carefully. The forceps were dipped into alcohol after each touch to check contamination of self pollination.

3.7.3 Emasculation

Few mature unopened flowers buds, which were supposed to open the next day indicated by the yellowish colour at the tip of the buds were selected for emasculation.

Plate 3. Hybridization at experimental site of SAU farm

The emasculation was done by removing the sepals and petals with the help of a pair of the fine pointed forceps. The anthers were then removed very carefully with the forceps, so that the gynoceium was not injured. Emasculation of flowers is presented in Plate 4.

3.7.4 Pollination

After emasculation the anthers that were ready for use in the previously selected male parent were taken and the pollen grains were dusted on the stigmatic surface of the emasculated flowers. The pollinated flowers were then covered with a thin, clean paper bag and clipped and properly labeled for identification. Both emasculation and pollination were done in the same day between 6am- 12pm depending on weather condition. The bags were removed three to four days after pollination and the siliqua were allowed to grow normally. The immature buds, which grew normally at the tip of the inflorescence, were removed from tome to tome. Paper bags to produce pure parental seeds or selfed seeds covered a few of the inflorescences of each parent varieties. The hybrid seed bearing siliqua were collected on proper maturation and seeds of each cross were kept separately on paper bags, both hybrid and selfed seeds were then properly dried and stored in a desecrator till next season. The selfed seeds of parent varieties and their hybrids were sown on last October, each year in the field of SAU farm. Pollination of flowers is presented in Plate 5.

3.8 Development of F_2, BC_1 and BC_2 Generations

In second year to generate F_2 generation, F_1 plant from each cross were selfed at the flowering through hand emasculations and controlled pollinations. BC_1 and BC_2 generations were developed by crossing materials of F_1 generations along with their respective parents. Paper bags were used to avoid contaminations. Pollinations to emasculated florets were repeated once after two days for maximum seed setting.

In third year the seeds of parents involved in F_1crosses, F_1, F_2, BC_1 and BC_2 were sown in the research area of SAU during rabi season 2012-13, following Randomized Complete Block Design with three replications. Three lines for each parental genotype, two for each F_1 hybrids, three for each of the back crosses and eight for F_2 hybrids were planted in each replication. Line to line distance of 30 cm and replication to replication distance of 1m and each line distance of 3m were maintained, respectively.

Plate 4. Emasculation at experimental site of SAU farm

Plate 5. Pollination and bagging at experimental site of SAU farm

Similar standard agronomic practices were carried out as in the development of F_1 hybrids, according to the requirement of the crop.

3.9 Crop harvesting

Harvesting was done from 4th to 20th February (2011, 2012 and 2013) each year depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. In the third year 10 plants were selected at random from the parental line, 10 plants from the F_1, 50 plants from F_2 progenies, 30 plants from BC_1, 30 plants from BC_2 in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.

3.10 Data collection

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

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

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

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

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

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

f) **Number of seeds/siliqua:** Well filled seeds were counted from representative siliquae, which was considered as the number of seeds/siliqua.

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

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

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

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

k) **Oil content (%):** Percent 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 (BARI).

3.11 Statistical analysis

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al*. (1955). The combining ability analysis was also carried out for the Six parents and 15 F_1 genotypes according to procedure outlined by Griffing (1956) method–I, model-II and elaborated by Singh and Chaudhary (2004). Griffing has also considered Eisenhart's model l (fixed effect) and model ll (random effect) situation in the analysis. Heterosis was calculated in terms of percent increase (+) or decrease (-) of a hybrid against its mid and better parents with respect to individual character following the technique adopted by Fonseca and Patterson (1968). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Generation mean analysis was estimated by the formula used by Mather and Jinks (1982).

i) Estimation of genotypic and phenotypic variances:

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

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

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

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

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

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

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

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

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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

iii) Estimation of heterosis and Inbreeding depression:

Heterosis was calculated in terms of percent increase (+) or decrease (-) of a hybrid against its mid and better parents with respect to individual character following the technique adopted by Fonseca and Patterson (1968).

Better parent heterosis (heterobeltiosis) and Mid parent heterosis were calculated as under:

BP heterosis= $\bar{F_1}$-$\bar{BP}$s

MP heterosis= $\bar{F_1}$-$\bar{MP}$

Heterosis Percentage were calculated as

Percent BP heterosis = $\{(\bar{F_1} - \bar{BP}) / \bar{BP}\}$ x100

Percent MP heterosis = $\{(\overline{F_1} - \overline{MP}) / \overline{MP}\}$ x100

Where,

$\overline{MP}$= Mean of mid parents

$\overline{BP}$= Mean of better parent

$\overline{F_1}$= Mean of F_1 generation

Inbreeding depression was calculated as

ID = $\overline{F_1} - \overline{F_2}$

Percent ID = $\{(\overline{F_1} - \overline{F_2}) / \overline{F_1}\}$ x100

The "t" value for heterosis and inbreeding depression was calculated by the following formulae as

Significant test: $t = \frac{\text{Mean Difference}}{\text{Standard Error Difference (SED)}}$

$$\therefore SED = \sqrt{\frac{\delta^2}{n_1} \times \frac{\delta^2}{n_2}}$$

Where,

SE= Standard error

t = tabulated value of 't' at error df at 5% or 1% level of significance

iv) Estimation of heritability:

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

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

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

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

Narrow-sense heritability

$$h^2_n(\%) = \frac{\delta^2_A}{\delta^2_p} \times 100 \quad = \frac{\delta^2_A}{\delta^2_g + \delta^2_e} \times 100$$

Where, h^2_n = Heritability in Narrow- sense

$\delta^2_{A=}$ Additive variance

δ^2_g = Genotypic variance

δ^2_e = Environmental variance

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

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

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

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

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

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

vii) The combining ability analysis

The combining ability analysis was also carried out for the Six parents and 15 F_1 genotypes according to procedure outlined by Griffing (1956) method–I, model-II and elaborated by Singh and Chaudhary (2004). Griffing has also considered Eisenhart's model l (fixed effect) and model ll (random effect) situation in the analysis. In the present research work combining ability analysis were done following method 2 (excluding reciprocals) and model-1.

Total variability was partitioned into component like general combing ability (GCA), specific combing ability (SCA) and error. Information was derived regarding the type

of gene action controlling different traits and pattern of selection for improvement of the rapeseed genotypes.

The mathematical model for the analysis was:

$$Y_{ij} = m+g_i+g_j+S_{ij}+ 1/bc \sum_{kl} \Sigma\Sigma\, e_{ijkl}$$

Where,

i, j =1, 2,....., p

K =1, 2, ..., b

L = 1, 2, ..., c

P = Number of parents

B = Number of blocks or replications

c = Number of observation in each plot

Y_{ij} = The mean of i × jth genotype over K and L

m = The population mean.

g_i = The general combining ability (GCA) effect to ith parent

g_j = The GCA of jth parent

s_{ij} = The SCA effect such that $s_{ij} = s_{ji}$

$1/bc \sum_{kl} \Sigma\Sigma\, e_{ijkl}$ = The mean error effect

The restriction imposed are $\Sigma\, g_i = 0$ and $\Sigma\, S_{ij} + S_{ii} = 0$ (for each i)

The analysis of variance for combining ability was carried out using replication mean of each entry (diallel family) as follows:

Item	**d.f.**	**Sum of squares**	**MSS**	**Expected MSS**
GCA	P-1	S_g	M_g	$\sigma_e^2 + (P+2)\ \frac{1}{(P-1)}\ \Sigma g_i^2$
SCA	P(P-1)/2	S_s	M_s	$\sigma_e^2 + \frac{2}{P(P-1)}\ \Sigma_i\Sigma_j S_{ij}^2$
Error	(b-1)(e-1)	S_e	M_e'	σ_e^2

Where,

GCA = general combining ability

SCA = specific combining ability

p = Number of parents

b = Number of blocks or replications

e = Number of entry (family)

$Y_{i.}$ = Array total of the ith parent

Y_{ii} = Mean value lof the ith parent

Y**.** = Grand total of the ½ p(p-1) crosses and parental lines

Y_{ij} = Progeny mean values in the diallel table

S_e = Sum of square due to error

$$S_g = \frac{1}{(P+2)}\left[\sum_i (Y_{i.} + Y_{ii})^2 - \frac{4}{P} Y..^2\right]$$

$$S_s = \sum_i \sum_j Y_{ij}^2 - \frac{1}{(P+2)} \sum (Y_{i.} + Y_{ii})^2 + \frac{2}{(P+1)(P+2)} Y..^2$$

The GCA and SCA effects of each character were calculated as follows;

$$g_i = \frac{1}{(P+2)}\left[\sum_i (Y_{i.} + Y_{ii})^2 - \frac{2}{p} Y..\right]$$

$$s_{ij} = Y_{ij} - \frac{1}{(P+2)} \sum (y_{i.} + y_{ii} + y_{.j} + y_{ji}) + \frac{2}{(p+1)(p+2)} y..$$

The variance of GCA and SCA were,

$$Var(g_i) = \frac{(p-1)}{p(p+2)} \sigma^2 e$$

$$Var(s_{ij}) = \frac{2(p-1)}{(p+1)(p+2)} \sigma^2 e (i \neq j)$$

Standard error (SE) of an estimate was calculated the square root of the variance of concerned estimate eg.

j Var (g_i) and jVar (s_i)

$\sqrt{Var(g_i)}$ and $\sqrt{Var(s_{ij})}$

3.12 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_{OLI} = 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_{OLOI} = Mean of all the Wr values

Yr' = Standardized mean for each parent

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

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

$(M_{LI} — M_{LO})^2$ = 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.

3.12.1 Test of homogeneity of Wr-Vr variances

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

Where,

Var Vr = Variance of the array variance

Var Wr = Variance of the parent and array covariance

Coy (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

3.12.2 Test of deviation of regression slope from unity

i. Deviation from 0

t_1 = (b-0)/SE, (at n-2 df)

ii. Deviation from unity

t^2 = (l-b)/SE (at n-2 df)

Where,

b = regression co-efficient of Wr on Vr

SE_b = standard error

viii) Generation mean analysis

The concept of generation mean analysis was developed by Haymen (1958) for the estimation of genetic components of variation. This method provided information on the relative importance of average effects of genes (additive effects), dominance deviations and effects due to non-allelic genetic interactions (epistasis). Partitioning of epistatic effects was carried out through this technique. Analysis of this technique is based on different generation of a cross viz., parents, their F_1, F_2 and different backcrosses. The mean values of different generation over replications are used for estimation of gene effects. A computerized program based on the procedures outlined by Singh and Chaudhary (2004) was used to perform the analysis. The analysis was completed in two steps, first scaling tests for epistasis were performed and then on the basis of these tests, genetic components were estimated.

a) Scaling Tests for Epistasis

The testing of epistasis is important before the estimation of genetic components in generation mean analysis because it is helpful in deciding the method of analysis. Four scaling tests for epistasis were described by Mather (1949) as follows:

$A = 2\overline{B}_1 - \overline{P}_1 - \overline{B} = 2\overline{B}_2 - \overline{P}_2 - \overline{F}_1$

$C = 4\overline{F}_2 - \overline{F}_1 - \overline{P}_1 - \overline{P}_2$

$D = 2\overline{F}_2 - \overline{B}_1 - \overline{B}_2$

Variances were calculated for these values as under:

$VA = 4V(\overline{B}_1) + V(\overline{P}_1) + V(\overline{F}_1)$

$VB = 4V(\overline{B}_2) + V(\overline{P}_2) + V(\overline{F}_1)$

$VC = 16V(\overline{F}_2) + 4V(\overline{F}_1) + V(\overline{P}_1) + V(\overline{P}_2)$

$VD = 4V\overline{F}_2 + V\overline{B}_1 + V\overline{B}_2$

The standard error and t value were estimated by taking square root of respective variances and by dividing the effects of A, B, C and D by their respective standard error. Significance of each estimate was tested against “t” value at 5% probability level. Significance of any one or more of these tests was an indication of presence of some sort of epistasis.

b) Estimation of Components of Generation Mean

Various genetic components of generation mean were estimated with the help of six parameter model presented by Hayman (1958).

M = Mean = $\overline{F_2}$

d = Additive effect = $\overline{B_1}$- $\overline{B_2}$

h = Dominance effect = $\overline{F_1}$ - 4$\overline{F_2}$ - 1/2$\overline{P_1}$- 1/2$\overline{P_2}$ + 2$\overline{B_1}$ + 2$\overline{B_2}$

I = Additive x additive gene interaction = 2$\overline{B_1}$ + 2$\overline{B_2}$ - 4$\overline{F_2}$

J = Additive x dominance gene interaction = $\overline{B_1}$ - 1/2$\overline{P_1}$ - $\overline{B_2}$ - 1/2$\overline{P_2}$

I = Dominance x dominance gene interaction = $\overline{P_1}$ + 2$\overline{F_1}$ + 4$\overline{F_2}$ - 4$\overline{B_1}$ - 4$\overline{B_2}$

Where,

P_1 = mean values over replications for the character in $\overline{P_1}$

P_2 = mean values over replications for the character in $\overline{P_2}$

F_1 = mean values over replications for the character in $\overline{F_1}$

F_2 = mean values over replications for the character in $\overline{F_2}$

B_1= mean values over replications for the character in $\overline{B_1}$

B_2 = mean values over replications for the character in $\overline{B_2}$

Variance of each gene effect was calculated as,

Vm = V($\overline{F_2}$)

Vd = V($\overline{B_1}$) + V($\overline{B_2}$)

Vh = V($\overline{F_1}$) + 16V($\overline{F_2}$) + 1/4V($\overline{P_1}$) + ¼ V ($\overline{P_2}$) + 4V($\overline{B_1}$) + 4V($\overline{B_2}$)

Vi = 4V($\overline{B_1}$) + 4V($\overline{B_2}$) + 16V($\overline{F_2}$)

Vj = V($\overline{B_1}$) + ¼ V($\overline{P_1}$) + V($\overline{B_2}$) + 1/4V($\overline{B_2}$) + 1/4V($\overline{B_2}$)

Vl = V($\overline{P_1}$) + V($\overline{P_2}$) + 4V($\overline{F_1}$) + 16V($\overline{F_2}$) + 16V($\overline{B_1}$) + 16V($\overline{B_2}$)

Standard error for each gene effect was estimated as under,

S.E. (m) = (Vm)1/2

S.E. (d) = (Vd)1/2

S.E. (h) = (Vh)1/2

S.E. (i) = (Vi)1/2

S.E. (j) = (Vj)1/2

S.E. (l) = (Vl)1/2

The ‘t’ value was calculated by dividing the estimated values of genetic effect by their standard error. Calculated values were compared with tabulated value at 5% level of significance.

CHAPTER 4
RESULTS AND DISCUSSION

4.1 Mean performance

Mean performance of ten yield related agronomic traits of parents and hybrid combinations are presented in Table 5.

4.1.1 Plant height (cm)

The highest plant height was observed in the parent BARISarisha 6 (116.43 cm) and for hybrid SAUSarisha 2 X TORI 7 (124.16 cm) followed by BARISarisha 6 X SAUSarisha 2 (120.26 cm). Whereas the parent BARISarisha 15 having the lowest (96.86 cm) plant height. The lowest plant height (96.80 cm) was found from the hybrid SAUSarisha 1 X TORI 7.

4.1.2 Number of primary branches per plant

For the character, number of primary branches per plant, parents showed at a range from 3.73 to 8.50. But in the hybrid, the highest value provided by the combination of BARI Sarisha 15 X BARI Sarisha 6 (8.60) which was higher than the parents BARI Sarisha 15 (8.4) and BARI Sarisha -6 (3.73).

4.1.3 Number of secondary branches per plant

For the number of secondary branches per plant, parents showed at a range from 1.5 to 10.13. But in the hybrid, the highest value of number of secondary branches per plant provided by the combination of SAU Sarisha 2 X TORI 7 (13.16) which were higher than the average value of the parents.

4.1.4 Days to 50% flowering

In case of days to 50% flowering for parent, it was ranged from 39 to 46 days. However, the parent SAU Sarisha 2 (39 Days) flowered with the lowest time but the parent TORI 7 (46 Days) taken the longest duration. On the other hand, the hybrid combination of SAU Sarisha 3 X TORI 7 (38 Days) produced the lowest growth duration, which was about 8 days least earlier than its parents TORI 7.

Table 5: Mean performance for 10 different characters in six parents and their fifteen F_1's of *Brassica rapa* L.

Treatments		Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Days to 50% flowering	Days to 80% maturity
Parents	TORI 7	104.50	6.30	10.13	46.33	81.00
	SAU Sarisha 1	112.03	8.50	9.56	41.33	78.33
	SAU Sarisha 2	98.46	6.70	7.90	39.00	78.00
	SAU Sarisha 3	103.70	5.40	4.36	39.66	76.66
	BARI Sarisha 6	116.43	3.73	1.50	46.00	85.66
	BARI Sarisha 15	96.86	8.40	3.63	45.33	84.33
Hybrid	**Mean**	**105.33**	**6.50**	**6.18**	**42.94**	**80.66**
	Range	**96.86-116.43**	**3.73-8.50**	**3.63-10.13**	**39.00-46.33**	**76.66-85.66**
	BARI Sarisha 15 X BARI Sarisha 6	113.10	8.60	2.10	48.00	86.66
	BARI Sarisha 15 X SAU Sarisha 2	98.60	8.53	3.10	44.33	81.33
	BARI Sarisha 15 X SAU Sarisha 3	98.10	6.86	6.13	43.33	84.66
	BARI Sarisha 15 X SAU Sarisha 1	104.76	5.96	0.50	46.00	84.66
	BARI Sarisha 15 X TORI Sarisha 7	107.70	8.33	12.06	44.00	83.66
	BARI Sarisha 6 X SAU Sarisha 2	120.26	8.33	7.36	46.33	84.66
	BARI Sarisha 6 X SAU Sarisha 3	108.96	6.56	9.60	42.00	81.33
	BARI Sarisha 6 X SAU Sarisha 1	111.93	8.33	10.03	46.00	84.33
	BARI Sarisha 6 X TORI 7	123.00	7.40	9.80	44.00	84.00
	SAU Sarisha 2 X SAU Sarisha 3	109.43	5.46	4.33	40.33	80.00
	SAU Sarisha 2X SAU Sarisha 1	97.63	7.83	11.46	42.33	84.00
	SAU Sarisha 2 X TORI 7	124.16	7.76	13.16	39.33	81.00
	SAU Sarisha 3 X SAU Sarisha 1	97.13	5.93	8.70	41.66	81.33
	SAU Sarisha 3 X TORI 7	102.06	5.93	11.80	37.66	79.33
	SAU Sarisha 1 X TORI 7	96.80	6.80	11.50	41.33	82.66
	Mean	**107.57**	**7.24**	**8.10**	**43.10**	**82.90**
	Range	**96.80-123.00**	**5.46-8.60**	**0.50-12.06**	**37.66-48.00**	**79.33-86.66**

Table 5: (CONT'D)

Treatments		No. of siliquae/ plant	siliqua length (cm)	Seeds/ siliqua	Seed yield/ plant (g)	1000 seed weight (g)
Parents	TORI 7	192.43	5.09	15.56	10.89	5.66
	SAU Sarisha 1	225.90	5.39	17.13	10.47	5.83
	SAU Sarisha 2	157.30	5.07	16.26	7.88	5.60
	SAU Sarisha 3	157.53	5.27	13.83	7.76	5.33
	BARI Sarisha 6	77.06	5.66	21.93	5.27	5.66
	BARI Sarisha 15	144.13	4.99	20.46	8.18	5.33
Hybrid	**Mean**	**159.05**	**5.24**	**17.52**	**8.40**	**5.56**
	Range	**77.06-225.90**	**4.99-5.66**	**13.83-21.93**	**5.27-10.89**	**5.33-5.83**
	BARI Sarisha 15 X BARI Sarisha 6	178.60	4.71	15.36	9.64	6.00
	BARI Sarisha 15 X SAU Sarisha 2	148.13	5.77	25.06	8.33	5.00
	BARI Sarisha 15 X SAU Sarisha 3	192.26	3.85	9.90	6.58	5.66
	BARI Sarisha 15 X SAU Sarisha 1	103.53	5.41	19.36	5.79	5.23
	BARI Sarisha 15 X TORI 7	246.86	3.77	7.76	7.99	6.00
	BARI Sarisha 6 X SAU Sarisha 2	200.13	5.31	14.26	14.72	6.00
	BARI Sarisha 6 X SAU Sarisha 3	275.26	4.03	9.96	8.50	5.90
	BARI Sarisha 6 X SAU Sarisha 1	262.06	5.15	13.16	12.94	6.33
	BARI Sarisha 6 X TORI 7	259.43	4.99	15.70	12.77	5.33
	SAU Sarisha 2 X SAU Sarisha 3	179.20	5.14	15.56	4.77	3.60
	SAU Sarisha 2X SAU Sarisha 1	214.30	5.76	19.43	12.11	4.86
	SAU Sarisha 2 X TORI 7	290.66	4.17	7.13	9.73	5.66
	SAU Sarisha 3 X SAU Sarisha 1	226.43	4.61	11.16	7.90	5.23
	SAU Sarisha 3 X TORI 7	201.41	4.87	14.03	9.14	5.23
	SAU Sarisha 1 X TORI 7	267.16	4.27	11.53	10.11	5.76
	Mean	**216.40**	**4.80**	**13.95**	**9.40**	**5.45**
	Range	**103.53-290.66**	**3.77-5.77**	**7.13-25.06**	**4.77-14.72**	**3.60-6.33**

4.1.5 Days to 80% maturity

Considering earliness, the parent SAU Sarisha 3 (77 days) showed the lowest duration for 80% maturation on the other hand, the parent BARI Sarisha 6 (86 days) had taken the longest duration. On the other hand, the hybrid combination SAU Sarisha 3 X TORI 7 (79 Days) matured with lowest growth duration.

4.1.6 Number of siliquae per plant

Number of siliquae per plant were varied from 77.06 to 225.90 where the parent SAU Sarisha 1 produced the highest and BARI Sarisha 6 produced the lowest. Considering hybrid performance, it was ranged from 103.53.00 to 290.66. The hybrid combination SAU Sarisha 2 X TORI Sarisha 7 (290.66) provided the highest number which was much higher than its both parents.

4.1.7 Siliqua length (cm)

Siliqua length of parent was ranged from 4.99 to 5.66 cm. The parent BARI Sarisha 6 produced the longest siliqua while the parent BARI Sarisha 15 had least value. On the other hand, for hybrid the values varied from 3.77 to 5.77 cm. In this regard, the hybrid combination BARI Sarisha 15 X SAU Sarisha 2 exhibited the highest length (5.77 cm) of siliqua and that was a little bit higher than that it's both the parents.

4.1.8 Seeds per siliqua

Seed per siliqua also varied from 13.83 to 21.93 in parents and from 7.13 to 25.06 in hybrids. The hybrid BARI Sarisha 15 X SAU Sarisha 2 produced an excellent number of seeds per siliqua (25.06) which was much higher than the parents (Table 5).

4.1.9 Seed yield per plant (g)

Seed yield per plant was found at diversed in different genotypes including parents and hybrids. Seed yield of parents varied from 5.27 to 10.89 g and 5.79 to 14.72 g in hybrids. The highest seed yield of the parent was found in TORI 7 (10.89 g) where as the lowest in BARI Sarisha 6 (5.27 g). Similarly, the highest seed yield was also observed in the hybrid BARI Sarisha 6 X SAU Sarisha 2 (14.72 g) which was almost higher than it's both parents.

4.1.10 Thousand seed weight (g)

Thousand seed weight in *B. rapa* varied with some extent i.e. from 5.33 to 5.83 gm in parent and that of from 3.60 to 6.33 gm in hybrid. However, the heaviest seeds were produced by the parent SAU Sarisha 1 (5.83 gm) and also by the hybrid combination BARI Sarisha 6 X SAU Sarisha 1 (6.33 gm). The hybrid provided the highest weighted seeds which were higher than it's both parents (Table 5).

4.2 The combining ability

The analysis of variance for combining ability, estimates of genetic component, estimates of general and specific combining ability effects are presented in Tables 6 to Table 10. The ANOVA for ten characters are presented in Table 6 which indicated that the genotypes were differed significantly for all the characters except plant height, number of siliquae per plant and 1000 seed weight. Treatment mean sum of squares (mean of genotypes) were further partitioned into parents, crosses (hybrids) and parent vs crosses. Parents and crosses showed highly significant variances for days to 50% flowering and days to 80% maturity (Table 6). Parents demonstrated highly significant variances for primary branches per plant and significant variances for number of secondary branches per plant and number of seed per siliqua. On the other hand, cross showed significant variances for plant height, yield per plant and highly significant variances for secondary branches per plant, number of seed per siliqua and length of siliqua. Variances due to parent vs cross interaction was also observed highly significant for most of the traits except plant height, days to 50% flowering and yield per plant.

The general and specific combining ability effects are effective genetic parameters in the breeding program. Combining ability analysis of six parents and fifteen F_1's in half diallel cross were performed on ten quantitative traits. 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 mean

Table 6: Analysis of variance (MS values) for ten yield and yield contributing characters in *Brassica rapa* L.

Source of Variation	df	Characters									
		PH	**PB**	**SB**	**NSP**	**NSS**	**LS**	**DF**	**DM**	**YP**	**1000 SW**
Replication	2	298.68*	10.28**	15.88	15279.27	11.62	0.17	0.21	5.92**	20.99*	869.90**
Genotype	20	236.04	5.30**	45.34*	9662.55	63.58**	1.09**	24.85**	26.75**	19.65*	0.00
Parent	5	174.18	9.93**	37.04*	7519.50	28.37*	0.19	33.26**	67.57**	12.58	0.23
Cross	14	270.37*	3.55	48.12**	8101.94	68.99**	1.30**	23.59**	13.02**	22.62*	1.13
Parent vs Cross	1	64.77	6.75**	47.78**	42226.28**	163.97**	2.70**	0.57	14.93**	13.53	-16.98**
Error	40	145.91	1.93	19.93	9293.25	12.84	0.21	1.62	2.10	10.66	0.71

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight. *P<0.05, **P<0.01, respectively.

Table 7: Analysis of variance for combining ability for different traits studied in *Brassica rapa* L.

Source of variation	Characters										
	df	**PH**	**PB**	**SB**	**NSP**	**NSS**	**LS**	**DF**	**DM**	**YP**	**1000SW**
Genotype	20	236.04	5.30	45.34	9662.55	63.58	1.09	24.85	26.75	19.65	0.00
GCA	5	149.15*	2.76**	33.58**	3624.04	23.05**	0.36**	20.36**	22.00**	8.40	0.31
SCA	15	55.19	1.44**	8.95	3086.45	20.58**	0.36**	4.26**	4.56**	5.94	0.29
Error	40	48.64	0.64	6.64	3097.75	4.28	0.07	0.54	0.70	3.55	0.24
GCA/SCA	-	2.70	1.91	3.75	1.17	1.12	1.00	4.77	4.82	1.40	1.06
S^2g/S^2s	-	1.79	0.21	1.33	-5.95	0.02	0.00	0.54	0.57	0.13	0.05

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight. *P<0.05, **P<0.01, respectively.

sum of square due to GCA was significant for all the traits except number of siliqua per plant, yield per plant and 1000 seed weight indicating that the additive gene action was predominant for the expression of these characters (Table 7). The significant mean sum of square due to SCA was also observed for number of primary branches per plant, number of seed per siliqua, length of siliqua, days to 50% flowering and days to 80% maturity indicating that the non-additive gene actions were predominant for the expression of these characters (Table 7). The results showed the agreement with the findings of Malik *et al*. (1995) andzxx Thakur and Sagwal (1997) in rape seed. Similar findings were also reported by Tamber *et al*. (1991) in Indian mustard.

The higher magnitude of GCA variance was observed than that of SCA variance for all the traits under study except length of siliqua (GCA variance=SCA variance=0.36). In earlier study of Verma (2000), reported that SCA variance was higher than GCA variance (non-additive type) for seed yield per plant. Verma *et al.* (1989) reported non-additive type of gene action for siliquae per plant, seed yield per plant in yellow sarson.

4.2.1 Genetic components

The components of genetic variation along with the derived genetic ratios for different yield contributing traits (Table 8) showed that the D and H components which measure additive and dominance variation, respectively were significant for all the traits under study suggesting the importance of both additive and dominance components for the inheritance of all the traits in *B. rapa*. However, the magnitude of dominance was higher than the additive component for all the traits except for primary branches per plant, number of seeds per siliqua, days to 50% flowering and days to 80% maturity which indicated that dominance component had a predominant role in the inheritance of these traits. These results agreed with Chowdhury *et al*. (2004) and Rahman *et al.* (2000) for days to flower and days to maturity in *B. rapa.* Trivedi and Mukharjee (1986) and Yadav and Yadava (1996) found similar result for Indian mustard and yellow sarson, respectively.

Table 8: Estimation of genetic components of variation and their ratios for ten characters in *Brassica rapa* L.

Source of variation	PH	PB	SB	NSP	NSS	LS	DF	DM	YP	1000 SW
D	7.00**	2.54**	5.77**	-686.27**	5.20**	-0.01**	10.57**	21.76**	0.48**	-0.014**
F	-32.02**	3.48**	-8.85**	-1069.94**	-1.15**	-0.04**	5.48**	20.66**	2.99**	-0.028**
E	51.06**	0.78**	6.58**	3192.77**	4.26**	0.07**	0.52**	0.76**	3.72**	0.089**
H_1	-58.71**	0.52**	-9.75**	-5499.22**	-1.65**	0.09**	5.24**	6.39**	0.70**	0.026**
H_2	77.51**	2.65**	17.00**	2888.92**	62.86**	1.07**	12.66**	11.94**	10.50**	0.822**
h^2 (Sharma)	-20.89**	1.98**	2.77**	-1582.73**	-14.27**	-1.57**	-0.99**	3.17**	1.36**	0.747**
h^2 (Singh)	-14.38**	1.03**	6.67**	7349.20**	33.06**	0.54**	-0.16**	2.80**	0.86**	0.109**
$(H_1/D)^{0.5}$	-8.391	0.20	-1.69	8.01	-0.32	-14.59	0.50	0.29	1.46	-1.8465
$H_2/4H_1$	-0.33	1.28	-0.44	-0.13	-9.52	2.94	0.60	0.47	3.76	7.896
h^2/H_2	-0.27	0.75	0.16307	-0.55	-0.23	-1.46	-0.08	0.27	0.13	0.90818
h^2_n	1.75	0.63	1.44	-171.57	1.30	-0.00	2.64	5.44	0.12	-0.0035

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weigh. *P<0.05, **P<0.01, respectively.

The H_2 representing dominance deviation due to relative frequency of positive and negative genes was significant for all the characters (Table 8). These results agree with Chowdhury *et al*. (2004) and Rahman *et al*. (2000) for *B. rapa* L., Trivedi and Mukharjee (1986) for *B. juncea* L. and *B. campestris* L. (Yadav *et al.* 1996).

The net dominance effect, h^2 expressed as the algebraic sum over all loci in the heterozygous condition in all the crosses, was highly significant for all the studied character. This implied that substantial contribution of dominance effects was due to heterogeneity of the loci in all the characters. These results agreed with the findings of Rahman *et al*. (2000) for *B. rapa* L. In an earlier study Chowdhury *et al*. (2004) obtained significant h^2 for days to maturity, plant height, siliquae per plant and seed yield per plant in *B. rapa* while, Trivedi and Mukharjee (1986) observed significant h^2 for days to maturity, 1000-seed weight and seed yield per plant in *B. juncea*. The positive and negative value of h^2 indicated mean direction of dominance and respective genes towards positive and negative sides, respectively.

The results showed that five characters *viz*. primary branches per plant, secondary branches per plant, days to 80% maturity, yield per plant and 1000-seed weight 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, plant height, number of siliquae per plant, number of seeds per siliqua, length of siliqua and days to 50% flowering exhibited the values in negative direction, implying the excess of recessive gene for these traits. These findings agreed with Yadav *et al*. (1996) who worked in *B. campestris* and partial agreement with findings of Rahman *et al*. (2011) for *B. rapa.*

The proportion of positive and negative effects as indicated by F value was highly significant for all the characters. This was agreement in the earlier findings of Rahman *et al*. (2000) for *B. rapa.* Positive F value for primary branches per plant, days to 50% flowering, days to 80% maturity and yield per plant indicated the high frequency of dominant alleles governing these characters. Negative F value for days to flower, plant height, secondary branches per plant, number of siliquae per plant, number of seeds per

siliqua, length of siliqua and 1000-seed weight exhibited a preponderance of recessive alleles (Table 8).

These findings agreed with Chowdhury *et al*. (2004) for days to maturity and plant height in *B. rapa*, Trivedi and Mukharjee (1986) found negative F value for seed yield per plant, seeds per siliqua and siliquae per plant in *B. juncea*. Likewise, Yadav *et al*. (1996) observed negative F value for secondary branches per plant and siliquae per plant in *B. campestris*. Rahman and Chowdhury (2010) found positive F value for days to maturity, primary branches per plant, length of siliqua, siliquae per plant, seeds per siliqua, seed yield and negative F value for days to flower, plant height, secondary branches per plant and 1000-seed weight in *B. rapa*.

The environmental component "E" exhibited highly significant values for all the traits, indicating the influence of environmental factors in the expression of those traits. This finding was agreeing with the earlier findings of Rahman and Chowdhury (2010) for *B. rapa.* Chowdhury *et al*. (2004) obtained significant E value for plant height, primary branches per plant, seeds per siliqua, seed yield per plant and oil content in Turnip rape. However, in this study the magnitude of E for each character was much higher than the respective value of D and H_1 except days to 50% flowering and days to 80% maturity indicating that the characters were influenced much by the environment. These findings disagreed 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 *B. juncea* and Rahman and Chowdhury (2010) for all the studied characters except siliqua length got E value much higher than the respective value of D and H_1 for *B. rapa*.

The average degree of dominance as indicated by the proportion $(H_1/D)^{0.5}$ was more than unity, suggesting that over dominance was operating in the expression for most of the components of yield. These finding also agreed with Chowdhury *et al.* (2004) for turnip rape, Yadav *et al*. (1996) for toria. Rahman and Chowdhury (2010) and Trivedi and Mukharjee (1986) also found over-dominance in graphic analysis of oil yielding attributes in Indian mustard.

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 greater than 0.25 for all the characters except number of siliquae per plant studied suggested asymmetrical distribution of alleles. Most of the characters presently studied indicated equal distribution of positive and negative alleles. These findings disagreed with Chowdhury *et al*. (2004) and Rahman and Chowdhury (2010) for *B. rapa*, while, Trivedi and Mukharjee (1986) found symmetrical distribution for length of siliqua and siliquae plant.

The estimated numbers of effective factors (h^2/H_2) were less than unity for all oil yielding attributes except for length of siliqua. 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. These findings also agreed with Chowdhury *et al.* (2004) for plant height and siliquae per plant in *B. rapa*, Rahman and Chowdhury (2010) for all the characters except length of siliqua, 1000-seed weight and oil content in *B. rapa* Trivedi and Mukharjee (1986) for days to maturity in *B. juncea*.

Heritability in narrow sense was higher for length of siliqua, yield per plant and 1000 seed weight indicating these characters were more or less heritable. For the remaining traits it ranged from moderate to very high. The results were in partial agreement with Rahman *et al*. (2000) for *B. rapa*, Chowdhury *et al.* (2004) in turnip rape, Yadav *et al.* (1996) in toria, Trivedi and Mukharjee (1986) in Indian mustard.

4.2.2 General combining ability (GCA) Effects

The nature and magnitude of additive gene action for a trait could be measured by estimation of GCA effects. Similarly, the magnitude and nature of non-additive ie. dominance and epistasis nature of gene actions could be measured by estimation of SCA effects. A parent with higher significant GCA effects is considered as a good general combiner. A parent showing high GCA and SCA variances is a better parent for creating high yielding specific combination. Parents with significant high GCA effect could be used in conventional breeding programme and crosses with significant high SCA effect could be used in hybrid development. The estimates of GCA effects are presented in Table 9. The

magnitude and direction of the significant GCA effects for six parents provide meaningful comparisons and would given a clue to design the future breeding programme. The results of GCA effects of different characters are presented as follows:

4.2.2.1 Plant height (cm)

Out of six parental GCA there were four parents showed negative GCA effect. The highest negative GCA effects (-4.07) was observed by BARI Sarisha 15. The other parents which represented negative GCA were SAU Sarisha 3 (-3.18), SAU Sarisha 1 (-2.03) and SAU Sarisha 2 (-0.19). The parent BARI Sarisha 6 expressed positive and significant GCA effects (7.70) was considered as good general combiner for the trait aimed to promote desirable plant height in their crosses (Table 9). The parent Tori 7 (1.77) showed positive GCA effects that were desirable general combiners to promote the plant height in *B. rapa*. Chowdhury *et al.* (2004) obtained dwarfness in YSK-8501 in *B. campestris* L. Singh *et al.* (1996) observed dwarfness in glossy mutant in *B. juncea* L. The result showed that BARI 6 and Tori 7 should be good for breeding tall varieties, and SAU Sarisha 1, SAU Sarisha 2, SAU Sarisha 3 and BARI Sarisha 15 were good for short varieties.

4.2.2.2 Number of primary branches per plant

There was only one parent out of six viz. BARI Sarisha 15 (0.74) provided significant and positive GCA effects which indicated that the parent was good general combiners for primary branches (Table 9). The parent SAU Sarisha 3 showed significant and negative GCA effects and indicated that SAU Sarisha 3 and their crosses had less primary branches than others. Other parents showed insignificant positive (SAU Sarisha 1 and SAU Sarisha 2) and negative (Tori 7 and BARI Sarisha 6) effects. Chowdhury *et al.* (2004) obtained more primary branches on sampan in *B. rapa* L. Singh *et al*. (2000) observed maximum the number of primary branches on YSP-842 in *B. campestris* L.

4.2.2.3 Number of secondary branches per plant

For number of secondary branches per plant the significant and positive GCA effects were observed in Tori 7 (3.21) indicated the highest value and considered as the best general combiner for the trait.

Table 9: General combining ability effects of parents in a diallal cross of *Brassica rapa* L.

Parents	Characters									
	PH	**PB**	**SB**	**NSP**	**NSS**	**LS**	**DF**	**DM**	**YP**	**1000 SW**
TORI 7	1.77	-0.07	3.21*	31.31	-2.20*	-0.27*	-0.07	1.06*	0.94	0.02
SAU Sarisha **1**	-2.03	0.34	1.05	15.67	0.51	0.20	-0.65*	-0.57	0.79	0.02
SAU Sarisha **2**	-0.19	0.25	0.29	-6.62	1.14	0.23*	-1.11**	-1.40**	0.18	-0.27
SAU Sarisha **3**	-3.18	-0.95*	-0.45	-1.28	-2.07*	-0.17	-1.90**	-2.28**	-1.45	-0.19
BARI Sarisha **6**	7.70*	-0.31	-1.38	-1.79	0.93	0.14	2.35**	1.76**	0.64	0.22
BARI sarisha 15	-4.07	0.74*	-2.72*	-30.28	1.69	-0.20	1.39**	1.43**	-1.10	0.19
SE (gi)	2.25	0.26	0.83	17.96	0.67	0.09	0.24	0.27	0.61	0.16
SE (sij)	6.18	0.71	2.28	49.34	1.83	0.23	0.65	0.74	1.67	0.43

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight. *P<0.05, **P<0.01, respectively.

The significant and negative GCA effects were expresses in the parent BARI Sarisha 15 (-2.72). Among the rest parents, SAU Sarisha 1 (1.05) and SAU Sarisha 2 (0.29) gave non-significant positive GCA effects while parents, SAU Sarisha 3 (-0.45) and BARI Sarisha 6 (-1.38) gave non-significant negative GCA effects. This indicated that SAU Sarisha 1 and SAU Sarisha 2 and their crosses had more secondary branches per plant than others. Singh *et al.* (1996) obtained the highest secondary branches in BJ-1235 in *B. juncea* L. Chowdhury *et al.* (2004a) observed more secondary branches in Din-2 in *B. rapa* L.

4.2.2.4 Number of siliquae per plant

All the six parents showed non-significant GCA effects for number of siliquae per plant. The parent Tori 7 exhibited the highest positive (31.31) GCA effects for the character, followed by SAU Sarisha 1 (15.67). This parent was selected as the best general combiner and desirable to use in hybridization program to improve the number of siliquae per plant in *B. rapa* L. (Table 9). On the other hand the highest negative and non-significant GCA value were provided by BARI Sarisha 15 (-30.28), followed by SAU Sarisha 2 (-6.62), BARI Sarisha 6 (-1.79) and SAU Sarisha 3 (-1.28). Chowdhury *et al*. (2004) found the highest number of silliquae in Din-2 in *B. rapa.* Singh and Murty (1980) obtained maximum number of siliquae per plant in SS-1 in *B. campestris* L.

4.2.2.5 Number of seeds per siliqua

Out of all the six parents, only Tori 7 (-2.20) and BARI Sarisha 6 (-2.07) were exhibited significant and negative GCA effect. So the parents would be considered as general combiner for the character and could be used for hybrid production with less number of seeds per siliqua development in the breeding programme. Rests of the parents were found to have under insignificant and positive GCA effects. Chowdhury *et al.* (2004) found maximum seeds per siliqua in Dhali in *B. rapa* L. Singh and Murty (1980) obtained more seeds per siliqua in YPS-842 in *B. campestris* L.

4.2.2.6 Length of siliqua (cm)

Out of the six parents, only one parent SAU Sarisha 2 (0.23) showed positive and significant GCA effects. On the other hand, Tori 7 exhibited significant and negative GCA effects (-0.27). The results showed that SAU Sarisha 2 should be good for breeding for

long length of siliqua and Tori 7 was good for short siliqua length. Rest of the four parents, two parents (SAU Sarisha 1 and BARI Sarisha 6) showed non-significant and positive and the remaining two parents (SAU Sarisha 3 and BARI Sarisha 15) showed non-significant and negative GCA effects. Sheikh and Singh (1998) obtained the maximum siliquae length in glossy mutant.

4.2.2.7 Days to 50% flowering

For the trait days to 50% flowering a significant positive GCA effect is useful for shorter growth duration. Out of six parents there were two parents showing highly significant and positive GCA effects. The parent BARI Sarisha 6 (2.35) was the best general combiner followed by BARI Sarisha 15 (1.39) that were desirable general combiners to promote the earliness in *B. rapa* (Table 9). The highest negative and highly significant GCA effects (-1.90) were provided by SAU Sarisha 3 followed by SAU Sarisha 2 (-1.11). The other parent which represented negative and significant GCA was SAU Sarisha 1 (-0.65). The Tori 7 only expressed non-significant and negative (-0.07) GCA effects. Chowdhury *et al*. (2004) found earliness in Din-2 in *B. rapa* L. Singh *et al*. (2000) obtained earliness in YSK-8501 in *B. rapa*. Verma (2000) observed earliness in RC 832 in *B. juncea* L.

4.2.2.8 Days to 80% maturity

BARI Sarisha 6 (1.76), BARI Sarisha 15 (1.43) and Tori 7 (1.06) expressed significant positive GCA effects for days to 80% maturity, while SAU Sarisha 3 (-2.28) and SAU Sarisha 2 (-1.40) gave highly significant negative GCA effects for this character. SAU Sarisha 1 only showed the non-significant and negative (-0.57) GCA effects. The result provided that the parents (SAU Sarisha 3 and SAU Sarisha 2) were desirable general combiners to promote the earliness in *B. rapa* L. On the other hand, significant and positive GCA effects were suitable for breeding for late maturity (Table 8). Chowdhury *et al*. (2004) observed earliness in *B. rapa* L. Singh *et al*. (2000) found earliness in YSC-68 in *B. campestris* L.

4.2.2.9 Yield per plant (g)

All the parents showed non-significant GCA effects in case of yield per plant. The highest positive GCA effects were observed in Tori 7 (0.94), followed by SAU Sarisha 1 (0.79), On the other side, SAU Sarisha 3 (-1.45) and BARI Sarisha 15 (-1.10) produced non-significant and negative GCA effects. Chowdhury *et al.* (2004) found the highest seed yield per plant in Pt-303 in *B. rapa* L.

4.2.2.10 Thousand seed weight (g)

The parents were found under non-significant GCA effects. SAU Sarisha 2 (-0.27) and SAU Sarisha 3 (-0.19) were shown non-significant and negative GCA effect (Table 9). Rests of the parents were found to have under non-significant and positive GCA effects. Chowdhury *et al.* (2004) found the highest seed weight in Dhali in *B. rapa* L.

4.2.3 Specific combining ability (SCA) effects

The specific combining ability effects signify the role of non-additive ie. dominance and or epistatic gene action in the expression of the characters. It denotes the highly specific combining ability leading to the 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 on cross involving high × high combinations, but also in those involving low × high and also from low × low. Thus in practice, some of the low combiners should also be accommodated in hybridization programme. The specific combining ability effects of fifteen crosses for the different morphological characters studied are presented in Table 10. The magnitude and direction of the significant effects for the six parents provide meaningful comparisons and would give a clue to the future breeding programme. The results of SCA effects for different characters are given below:

Table 10: Specific combining ability effects for 10 characters in a diallal crosses of *Brassica rapa* L.

Crosses	Characters									
	PH	**PB**	**SB**	**NSP**	**NSS**	**LS**	**DF**	**DM**	**YP**	**1000SW**
BARI Sarisha **15 × BARI** Sarisha **6**	6.59	0.75	0.41	36.92	1.98	0.21	-1.07	-1.42	2.05	-0.16
BARI Sarisha **15 × SAU** Sarisha **2**	5.87	-0.85	-3.06	-12.90	1.52	0.16	0.55	1.08	-3.11	-1.20*
BARI Sarisha **15 × SAU** Sarisha **3**	-1.59	0.05	1.75	23.90	-4.70*	-0.78**	1.05	2.91**	-0.02	0.40
BARI Sarisha **15 × SAU** Sarisha **1**	-3.46	-0.07	1.48	-28.61	3.32	0.40	-3.15**	-2.05*	0.51	0.15
BARI Sarisha **15 × TORI 7**	-0.67	1.28	2.80	55.20	-3.25	-0.10	1.51*	0.54	2.37	0.34
BARI Sarisha **6 × SAU** Sarisha **2**	-2.49	0.80	3.87	85.35	-3.88	-0.85**	-1.24	-0.76	0.16	0.61
BARI Sarisha **6 × SAU** Sarisha **3**	-4.08	0.52	-2.03	-14.97	7.25	0.73	1.26	-1.30	0.11	-0.18
BARI Sarisha **6 × SAU** Sarisha **1**	3.93	-2.14**	-5.39*	-81.85	2.19	0.42	-3.20**	1.20	-2.54	-0.47
BARI Sarisha **6 × TORI 7**	-9.88	-0.49	-0.32	20.20	-1.76	-0.57*	-0.74	-0.42	-0.76	-0.29
SAU Sarisha **2 × SAU** Sarisha **3**	2.54**	1.14	-1.36*	17.68**	-2.24	-0.23**	1.47	0.87	0.96	0.33
SAU Sarisha **2 × SAU** Sarisha **1**	-7.09	0.23	2.57	5.26	2.80	0.42	1.30	3.37**	2.01	-0.14
SAU Sarisha **2 × TORI 7**	-4.59	-0.48	0.54	12.05	-2.25	-0.33	1.43*	1.58*	-0.58	0.14
SAU Sarisha **3 × SAU** Sarisha **1**	3.06	0.64	4.02	45.85	-6.71**	-0.75**	-0.11	-1.42	-0.99	0.54
SAU Sarisha **3 × TORI 7**	15.65*	0.35	2.11	65.98	-6.79**	0.71**	-2.28**	-1.26	-0.53	0.67
SAU Sarisha **1 × TORI 7**	5.82	1.37	-0.90	15.55	-2.79	0.03	2.30**	1.70*	4.76*	0.29
SED (gi-gj)	3.49	0.40	1.29	27.83	1.03	0.13	0.37	0.42	0.94	0.24
SED (Sij-Sik)	9.23	1.06	3.41	73.63	2.74	0.35	0.97	1.11	2.49	0.64
SED (Sij-Skl)	8.54	0.98	3.16	68.17	2.53	0.32	0.90	1.03	2.31	0.55

Here, PH = Plant height, PB = Number of primary branches per palnt, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days of 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight. *P<0.05, **P<0.01,respectively.

4.2.3.1 Plant height (cm)

The F_1 of cross, SAU Sarisha 2 X SAU Sarisha 3 (2.54) and SAU Sarisha 3 X Tori 7 (15.65) showed positive but highly significant and significant sca effects for plant height, respectively. The rest of the crosses showed non-significant sca effects. The highest non-significant and negative sca effects was observed in the cross combination BARI Sarisha 6 X Tori 7 (-9.88). Chowdhury *et al.* (2004) observed dwarfness in PT-303 x Tori-7 in *B. rapa*. Acharya and Swain (2004) obtained dwarfness in Varuna x Pusa Bahar in *B. juncea*.

4.2.3.2 Number of primary branches per plant

The cross combination BARI Sarisha 6 X SAU Sarisha 1 (-2.14) was found best specific combiner to improve plants with less number of primary branches as they showed highly significant negative sca effects for this trait (Table 10). Chowdhury *et al.* (2004) found more primary branches in Sampad x Tori-7 in *B. rapa*. Singh *et al.* (2000) obtained the maximum number of primary branches per plant in YSK-8501 x SS-1 in *B. rapa*. Sheikh and Singh (1998) observed best positive effect in Pusa x Barani in *B. juncea*.

4.2.3.3 Number of secondary branches per plant

The highest significant negative values of sca effects for the character were revealed by BARI Sarisha 6 X SAU Sarisha 1 (-5.39) and SAU Sarisha 2 X SAU Sarisha 3 (-1.36). The result indicated that crosses with significantly negative effects were good for developing less number of secondary branches per plant. The highest non-significant and positive sca effects was found in the cross combination SAU Sarisha 3 X SAU Sarisha 1 (4.02) (Table 10). Chowdhury *et al.* (2004) found the maximum secondary branches in Sampad x Din-2 in *B. rapa*. Singh *et al.* (2000) observed the highest secondary branches in YSC-68 x SS-2 in *B. rapa*. Acharya and Swain (2004) obtained more secondary branches in BM 20-12-3 x JC 26 in *B.rapa.*

4.2.3.4 Number of siliquae per plant

Among the cross combinations, SAU Sarisha 2 X SAU Sarisha 3 showed highest highly significant and positive sca effects (17.68). The rest of the cross combinations showed the non-significant sca effects. On the other hand, the cross BARI Sarisha 6 X SAU Sarisha 1 (-81.85) and BARI Sarisha 6 X SAU Sarisha 2 (85.35) showed the highest non-significant but negative and positive sca effects, respectively (Table 10). Chowdhury *et al.* (2004) found the maximum siliquae in Sampad x Din-2 in *B. rapa*. Singh and Murty (1980)

observed more siliquae per plant in YSP-842 x SS-3 in *B. rapa*. Acharya and Swain (2004) obtained the highest siliquae per plant in Pusa Bahar x JC 26 in *B. juncea*.

4.2.3.5 Number of seeds per siliqua

Among the cross combinations, SAU Sarisha 3 X Tori Sarisha 7 exhibited highly significant and negative sca effects (-6.79) followed by SAU Sarisha 3 X SAU Sarisha 1 (-6.71) for seeds per siliqua. Significant and negative sca value was observed in BARI Sarisha 15 X SAU Sarisha 3 (-4.70). The other cross combinations showed non-significant either positive or negative sca effects. Hence, SAU Sarisha 3 X Tori 7 was the best specific combiner to decrease the number of seeds in the siliqua (Table 10). Chowdhury *et al.* (2004) found the highest seeds per siliqua in Dhali x Sampad in *B. rapa*. Singh *et al.* (2000) obtained more seeds per siliqua in YSP-842 x YSK-8501 in *B. campestris*. Acharya and Swain (2004) observed the maximum seeds per siliqua in BM 20-12-3 x Pusa Bahar in *B. juncea*.

4.2.3.6 Length of siliqua (cm)

Among the cross combinations, SAU Sarisha 3 X Tori 7 (0.71) showed the highest significant and positive sca effects. The result revealed that this cross combination should be the best hybrid for length of siliqua. On the other hand, BARI Sarisha 6 X SAU Sarish Sarisha 2 (-0.85), BARI Sarisha 15 X SAU Sarisha 3 (-0.78), SAU Sarisha 3 X SAU Sarisha 1 (-0.75) and SAU Sarisha 2 X SAU Sarisha 3 (-0.23) showed highly significant and negative sca effects. The cross combination BARI 6 X Tori 7 (-0.57) expressed significant and negative sca effects. On the other hand, the remaining combinations showed non-significant but negative and positive sca effects for the trait (Table 10). Sheikh and Singh (1998) and Acharya and Swain (2004) observed the maximum siliqua length in Pusa Barani x Glossy mutant and BM 20-12-3 x Pusa Bahar, respectively in *B. juncea*.

4.2.3.7 Days to 50% flowering

Highly significant and negative value from the parameter was obtained in BARI Sarisha 6 X SAU Sarisha 1 (-3.20) followed by BARI Sarisha 15 X SAU Sarisha 1 (-3.15) and SAU Sarisha 3 X Tori 7 (-2.28) and SAU Sarisha 1 X Tori 7 (2.30) showed highly significant and positive sca effects. BARI Sarisha 15 X Tori 7 (1.51) and SAU Sarisha 2 X Tori 7 (1.43) expressed significant and positive sca effects. The results indicated that crosses with significantly positive SCA effects were good for developing late hybrids, while crosses with significantly negative SCA effects were good for developing early hybrids. Singh *et*

al. (2000) obtained earliness on YSK-8501 x SS-2 in *B. campestris*. Singh *et al.* (1996) observed earliness in PR-1108 x BJ-1235 in *B. juncea*.

4.2.3.8 Days to 80% maturity

The cross combination SAU Sarisha 2 X SAU Sarisha 1 (3.37) and BARI Sarisha 15 X SAU Sarisha 3 (2.91) showed highly significant and positive sca effects while significant and positive value form the parameter was obtained from SAU Sarisha 1 X Tori 7 (1.70) and SAU Sarisha 2 X Tori 7 (1.58). Significant and negative sca effects for days to 80% maturity were observed in BARI Sarisha 15 X SAU Sarisha 1 (-2.05). Hence the cross combination BARI Sarisha 15 X SAU Sarisha 1 provided opportunity for early maturity in *B. rapa* hybrid (Table 10). Chowdhury *et al.* (2004) observed earliness in M-27 x Din-2 in *B. rapa*. Singh *et al.* (2000) obtained earliness in SS-3 x SS-1 in *B. campestris*. Acharya and Swain (2004) found early maturity in JC 26 x Jai kisan in *B. juncea*.

4.2.3.9 Yield per plant (g)

The cross combination SAU Sarisha 1 X Tori 7 (4.76) exhibited significant and positive sca effects for yield per plant. The other combinations showed either non-significant positive or non-significant negative sca effects. Thus, SAU Sarisha 1 X Tori 7 was the best specific combinations for the improvement of seed yield per plant in *B. rapa* (Table 10).
Chowdhury *et al.* (2004a) obtained the highest seed yield in M-27 x Din-2 in *B. rapa*. Singh *et al.* (2000) observed more seed yield per plant in YSP-842 x YSK-8501 in *B. campestris*. Acharya and Swain (2004) found the maximum seed yield in Pusa Bold x Pusa Bahar in *B. juncea*.

4.2.3.10 Thousand seed weight (g)

The cross combinations provided non-significant and positive or negative sca values for 1000-seed weight (Table 10) except for the cross combination BARI Sarisha 15 X SAU Sarisha 2 (-1.20) which was significant and negative. The result revealed that BARI Sarisha 15 X SAU Sarisha 2 was a good combiner for decreasing 1000 seed weight of *B. rapa* hybrid.

4.2.4 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. 2 to Fig. 11. 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 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:

4.2.4.1 Plant height (cm)

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 2). The distribution of array points indicated four parents SAU Sarisha 3 (P4), BARI Sarisha 6 (P5), BARI Sarisha 15 (P6) and SAU Sarisha 1 (P2) contained the most dominant alleles as they felt closer to the point of origin. Whereas rest of the parents (Tori 7 and SAU Sarisha 2) felt far from the origin indicated that they possessed the maximum frequency of recessive alleles. Chowdhury *et al.* (2004) obtained nearly complete dominance in *B. rapa*. Sachan *et al*. (2004b) detected predominance of additive gene action.

4.2.4.2 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. 3). The parents SAU Sarisha 3 (P4), Tori 7 (P1), BARI Sarisha 15 (P6), SAU Sarisha 1 (P2) and SAU Sarisha 2 (P3) felt closer to the origin means they contained the maximum frequencies of dominant alleles. The parent BARI Sarisha 6 (P5) felt far from the origin and thus it contained the maximum frequency of recessive alleles. Chowdhury *et al.* (2004) observed nearly complete dominance for the character in *B. rapa*, and Yadav *et al.* (1996) found over dominance in *B. campestris*, respectively. Singh *et al*. (2004) and Parmar *et al*. (2005) as they indicated prevalence of non-additive gene action for number of primary branches. Singh and Dixit (2007) observed that both additive and non-additive gene effects were prominent in controlling the studied trait and non additive component was higher than additive component.

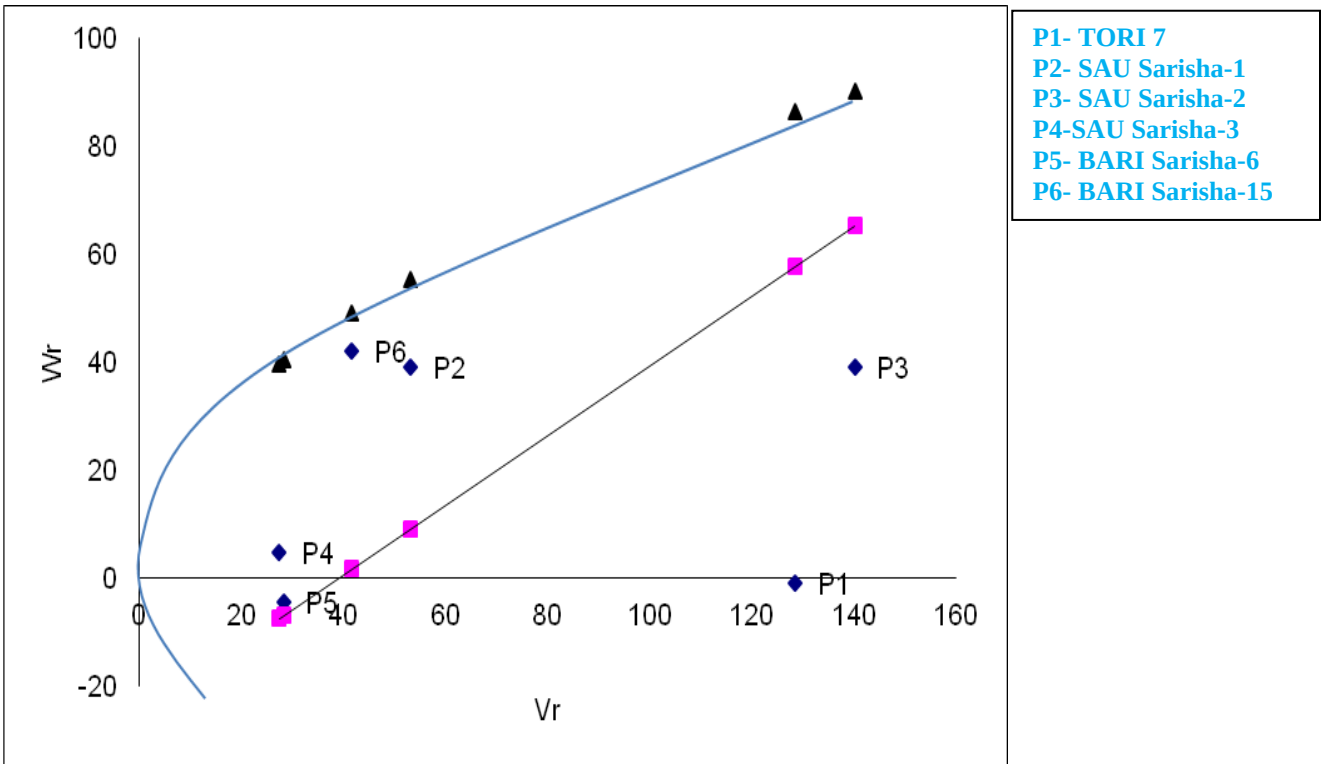


Figure 2. Vr-Wr graph for plant height in *Brassica rapa*

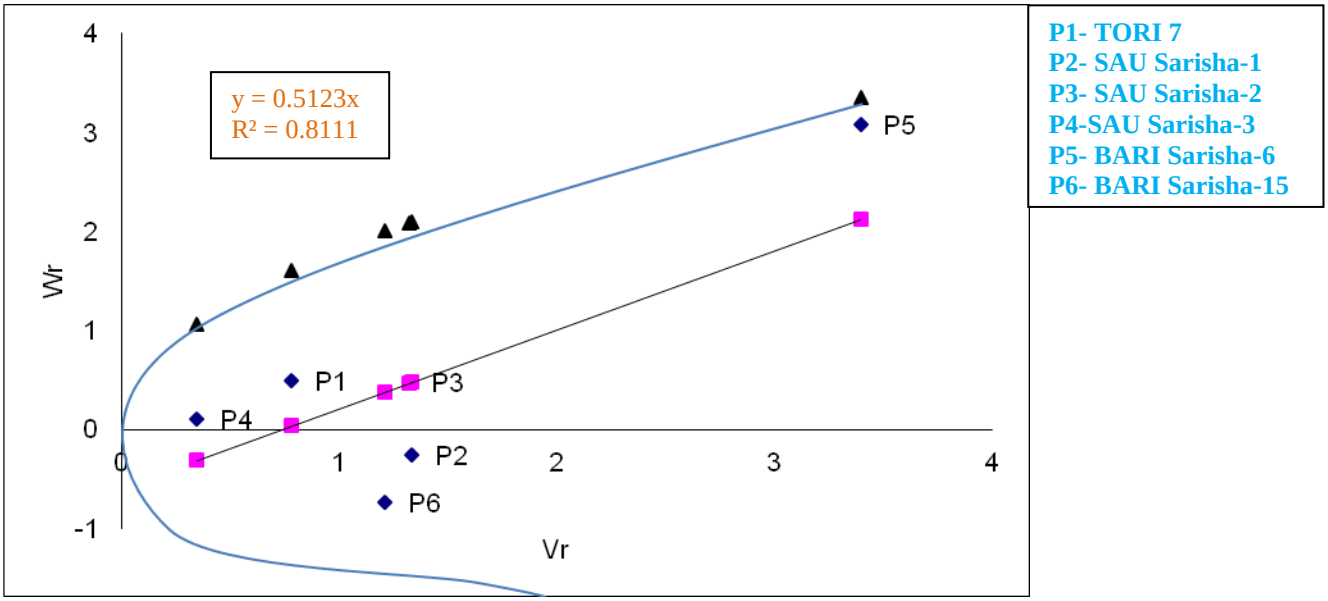


Figure 3. Vr-Wr graph for Primary branches per plant in *Brassica rapa*

4.2.4.3 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. 4). The parent Tori 7 (P1) felt closer to the point of origin suggesting they contained the maximum number of dominant alleles. The parent SAU Sarisha 3 (P4) felt at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parents SAU Sarisha 2 (P3), BARI Sarisha 15 (P6), SAU Sarisha 1 (P2) and BARI Sarisha 6 (P5) felt far from the origin indicating the presence of maximum frequency of recessive alleles in that parents. Chowdhury *et al.* (2004) obtained partial dominance in *B. rapa*, Yadav and Yadava (1996) observed over dominance in *B. campestris*.

4.2.4.4 Number of siliqua 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. 5). The parents Tori 7 (P1), SAU Sarisha 3 (P4) and BARI Sarisha 15 (P6) contained the maximum number of dominant alleles as it felt closer to the point of origin. The parents SAU Sarisha 2 (P3) and SAU Sarisha 1 (P2) felt at the near middle portion, means they contained equal frequencies of dominant and recessive alleles. The parent BARI Sarisha 6 (P5) felt far from the origin indicating the presence of the maximum frequency of recessive alleles in that parent. Chowdhury *et al.* (2004) and Trivedi and Mukharjee (1986) observed over dominance in *B. rapa* and *B. juncea*, respectively.

4.2.4.5 Number of seed per siliqua

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 6). The parents SAU Sarisha 3 (P4), Tori 7 (P1), SAU Sarisha 1 (P2) and BARI Sarisha 6 (P5) contained the maximum dominant alleles as it felt closer to the point of origin. The parents SAU Sarisha 2 (P3) and BARI Sarisha 15 (P6) felt far from the origin indicating the presence of the maximum frequency of recessive alleles in these parents. Chowdhury *et al.* (2004) observed over dominance in *B. rapa*, Trivedi and Mukharjee (1986) found over dominance in *B. juncea*. Patel *et al*. (2005) reported predominance of non-additive type of gene effects.

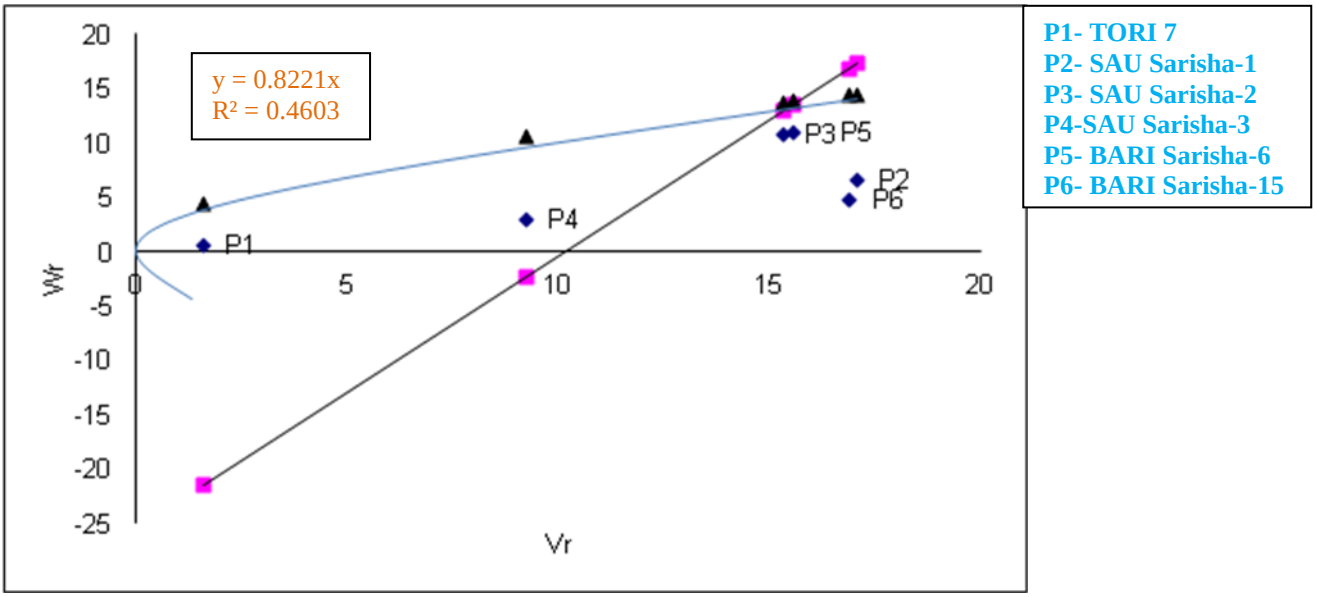


Figure 4. Vr-Wr graph for Secondary branches per plant in *Brassica rapa*

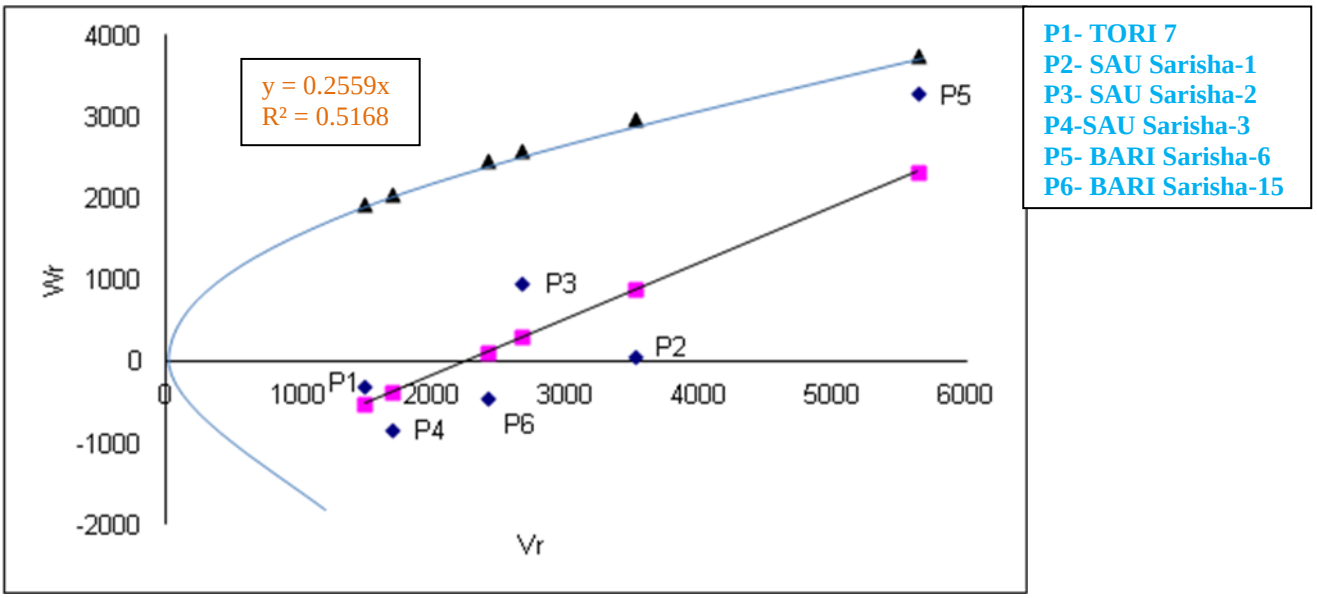


Figure 5. Vr-Wr graph for Number of siliqua per plant in *Brassica rapa*

4.2.4.6 Length of siliqua (cm)

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 7).The parents TORI 7 (P1), SAU Sarisha 1 (P2), BARI Sarisha 6 (P5), SAU Sarisha 3 (P4) and SAU Sarisha 2 (P3) contained the maximum dominant alleles as it felt closer to the point of origin. The parent BARI Sarisha 15 (P6) fell far from the origin and thus it contained the maximum frequency of recessive alleles. Trivedi and Mukharjee (1986) found over dominance in *B. juncea*. Sheikh and Singh (1998) reported additive gene action for siliqua length while Sarkar and Singh (2001) reported significant general combining ability and specific combining ability variances for the respective trait.

4.2.4.7 Days to 50% flowering

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 8). The distribution of array points indicated three parents SAU Sarisha 1 (P2), SAU Sarisha 3 (P4) and BARI Sarisha 6 (P5) contained the most dominant alleles as they felt closer to the point of origin. The parent SAU Sarisha 3 (P4) felt at the nearby middle portion means they contained equal frequencies of dominant and recessive alleles, whereas rest of the parents (SAU Sarisha 2 and Tori 7) felt far from the origin indicated that they possessed the maximum frequency of recessive alleles. Chowdhury *et al.* (2004) observed partial dominance for the character in *B. rapa*.

4.2.4.8 Days to 80% maturity

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 9). The parents BARI Sarisha 15 (P6) and BARI Sarisha 6 (P5) contained maximum dominant alleles as they felt closer to the point of origin. The parent SAU Sarisha 1 (P2) felt at the nearby middle portion means they contained equal frequencies of dominant and recessive alleles. The parents SAU Sarisha 2 (P3), SAU Sarisha 3 (P4) and Tori 7 (P1) felt far from the origin and thus it contained the maximum frequency of recessive alleles. Chowdhury *et al.* (2004) observed partial dominance in *B. rapa*, Trivedi and Mukharjee (1986) found over dominance in *B. juncea*. Sachan *et al*. (2004b) and Parmar *et al*. (2005) found non-additive type of gene action controlling the trait however Singh *et al*. (2008) found that GCA variance was greater than SCA variance indicating prominence of additive effects.

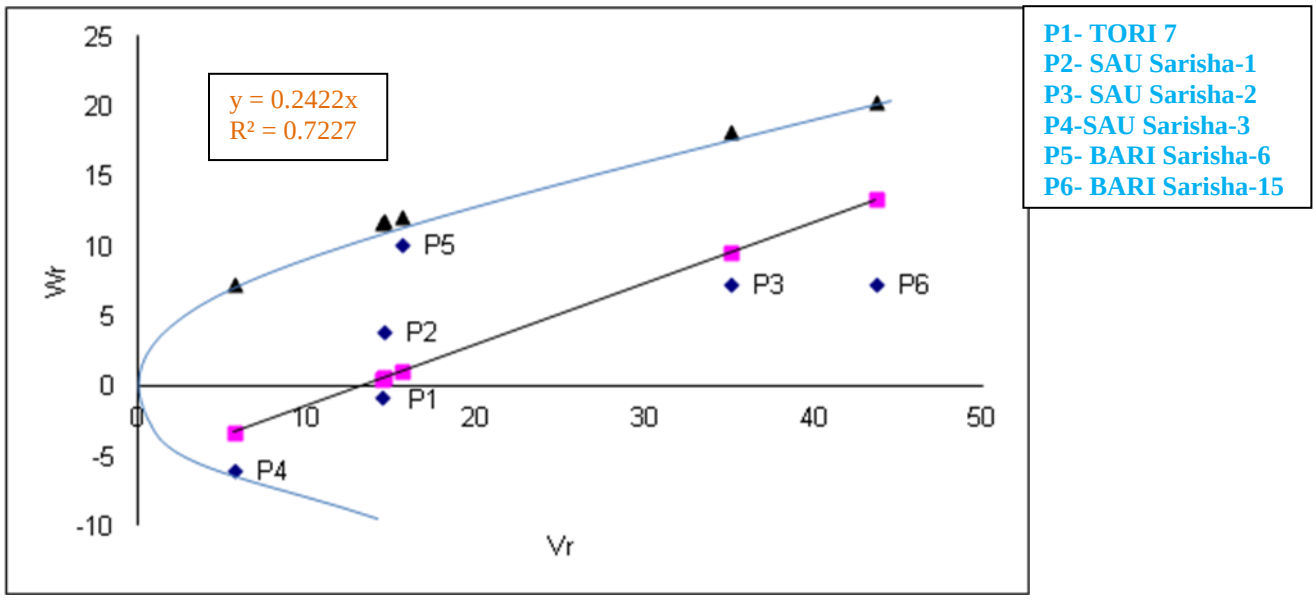


Figure 6. Vr-Wr graph for Number of seed per siliqua in *Brassica rapa*

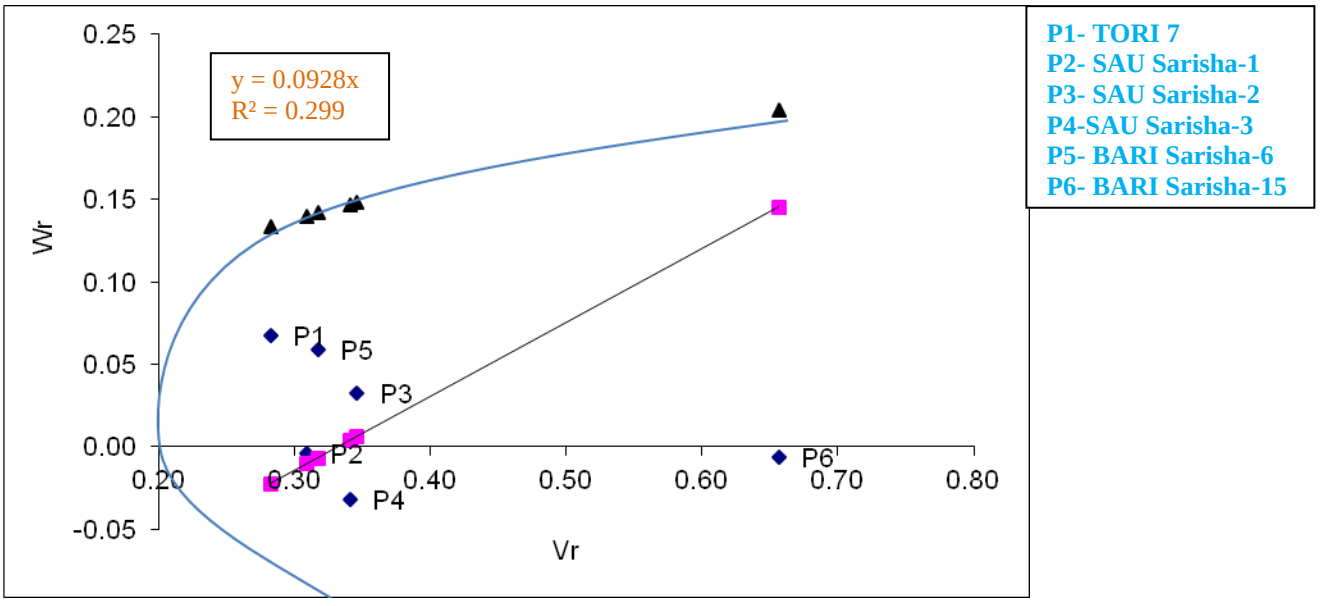


Figure 7. Vr-Wr graph for Length of siliqua in *Brassica rapa*

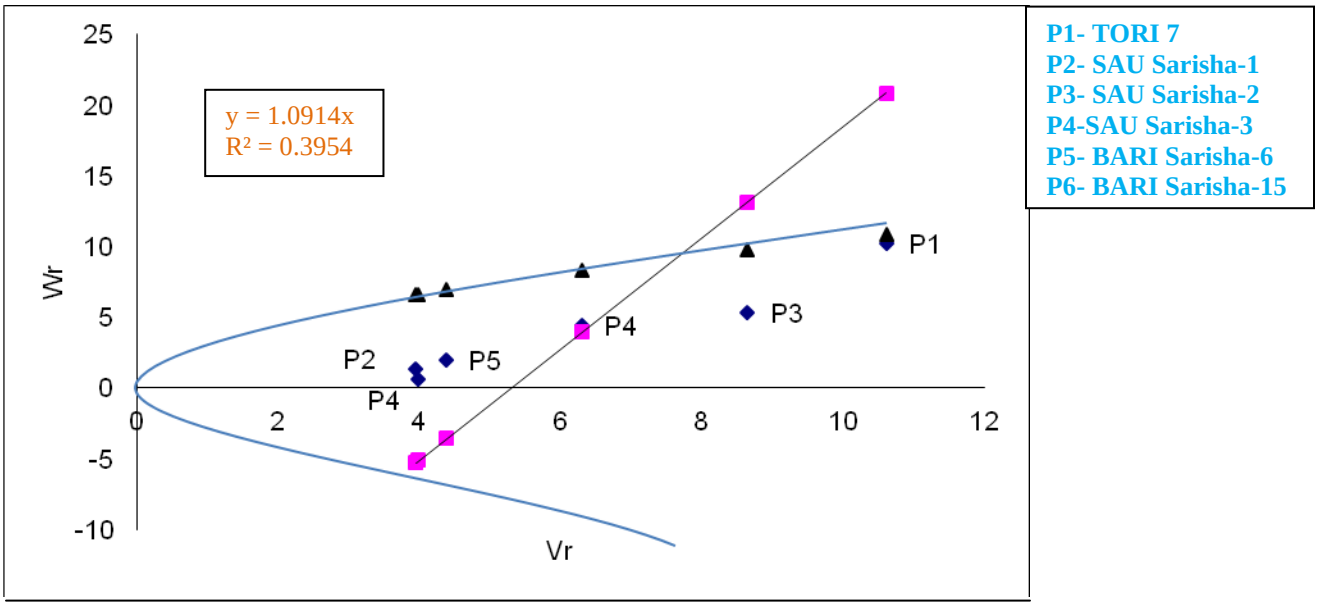


Figure 8. Vr-Wr graph for Days to 50% flowering in *Brassica rapa*

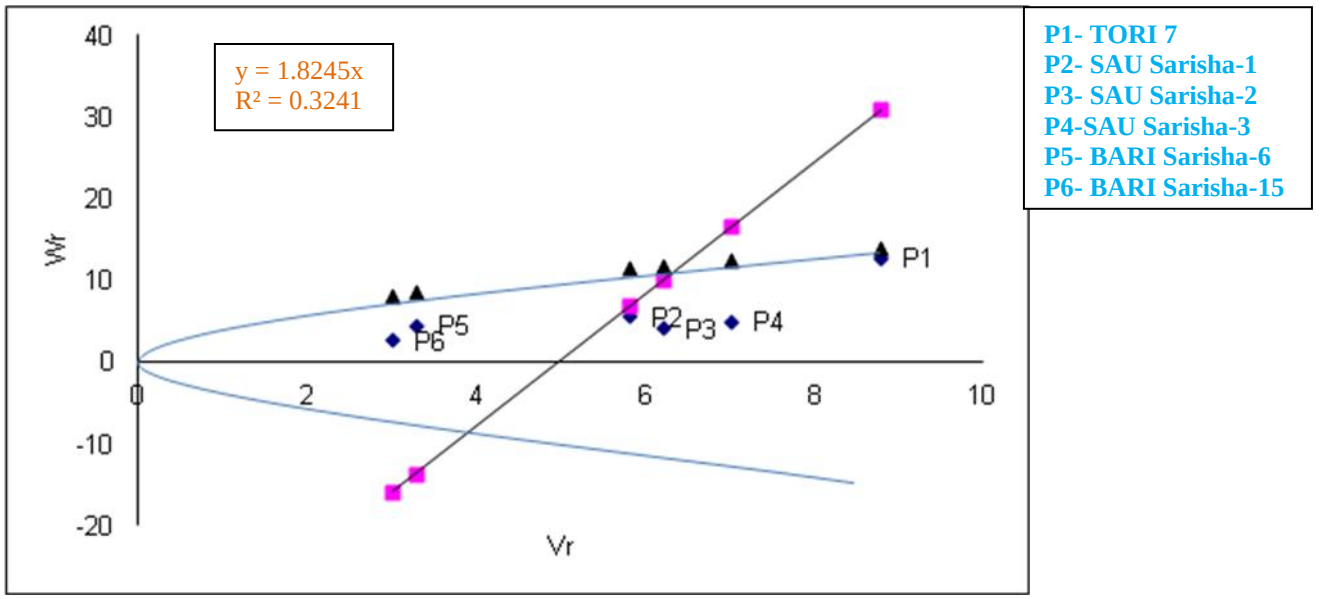


Figure 9. Vr-Wr graph for Days to 80% maturity in *Brassica rapa*

4.2.4.9 Yield per plant (g)

The regression line intersected the Wr axis nearby the point of origin suggesting partial dominance gene action for controlling the trait (Fig. 10). The parents BARI Sarisha 15 (P6), Tori 7 (P1) and SAU Sarisha 3 (P4) felt closer to the point of origin indicating that it contained the maximum dominant alleles. The parent SAU Sarisha 1 (P2) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parents SAU Sarisha 2 (P3) and BARI Sarisha 6 (P5) felt far from the origin indicated that they possessed the maximum frequency of recessive alleles. Chowdhury *et al.* (2004) obtained over dominance in *B. rapa*, Trivedi and Mukharjee (1986) observed over dominance in *B. juncea*, respectively. Rao and Gulati (2001), Swanker *et al*. (2002), Singh *et al*. (2004), Sachan *et al*. (2004b) and Aher *et al*. (2009) observed prominence of non-additive gene action for this trait.

4.2.4.10 Thousand seed weight (g)

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 11). The distribution of array points indicated four parents SAU Sarisha 1 (P2), BARI Sarisha 6 (P5), Tori 7 (P1) and BARI Sarisha 15 (P6) contained the most dominant alleles as they felt closer to the point of origin. The parents SAU Sarisha 2 (P3) and SAU Sarisha 3 (P4) felt far from the origin indicated that they possessed the maximum frequency of recessive alleles. Chowdhury *et al.* (2004) found partial dominance in *B. rapa*, Trivedi and Mukharjee (1986) observed over dominance in *B. juncea*. Lohia (2008) reported that both additive and non-additive types of gene action were involved in controlling seed weight.

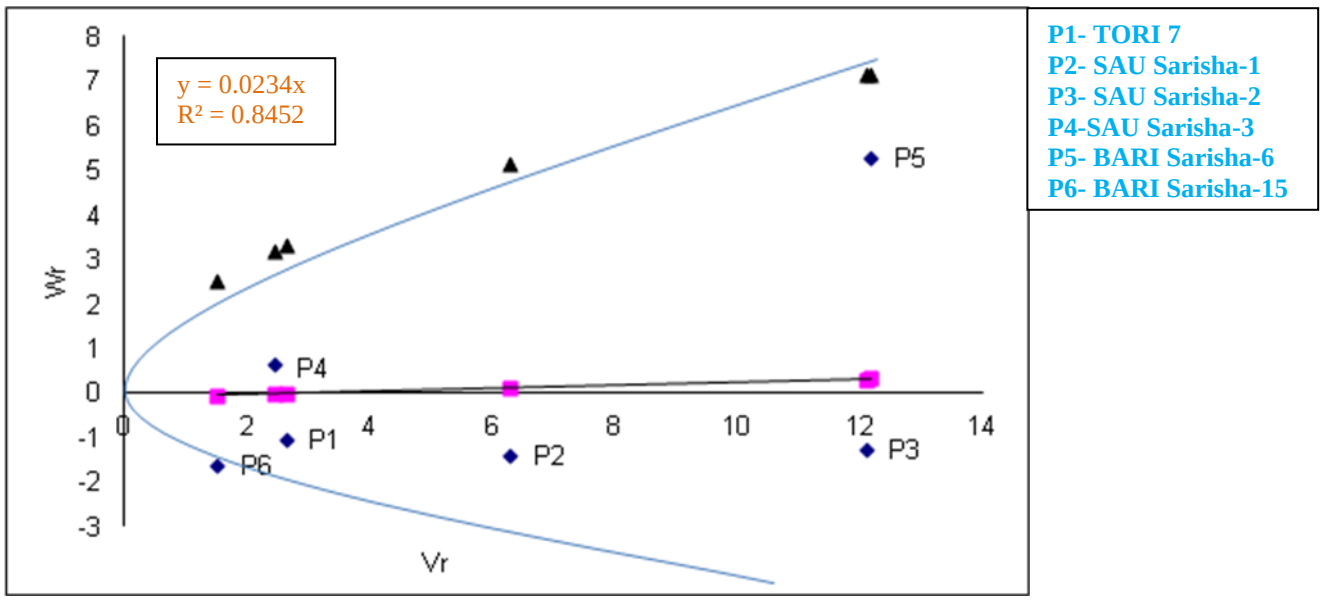


Figure 10. Vr-Wr graph for Yield per plant in *Brassica rapa*

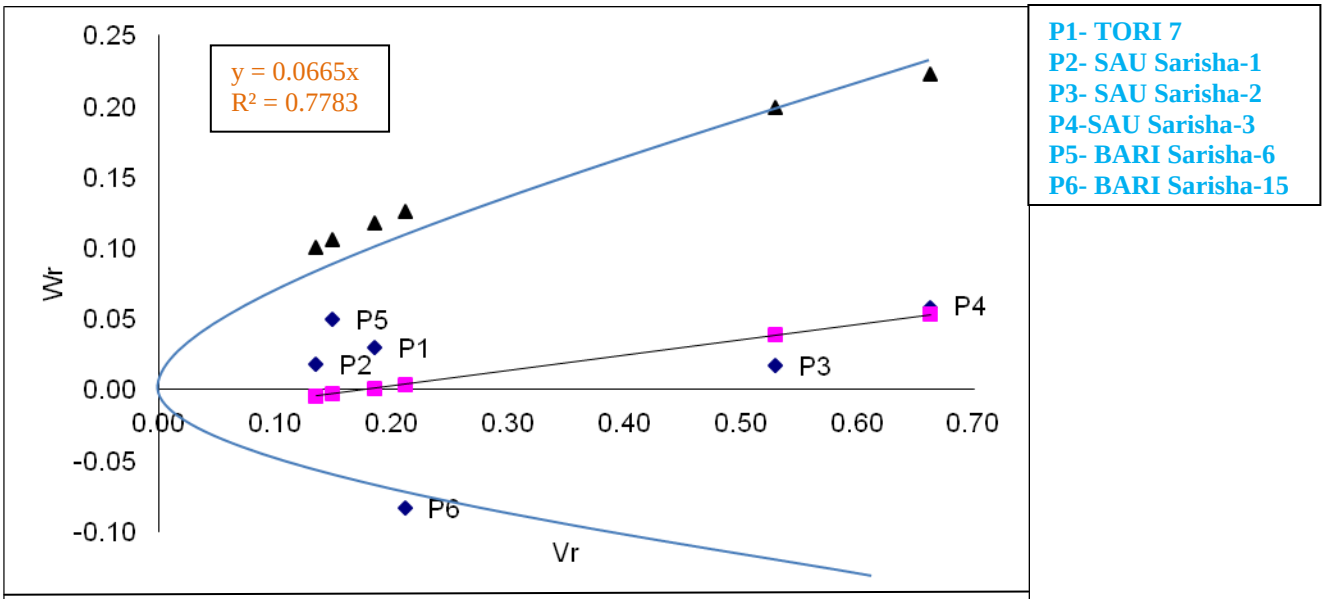


Figure 11. Vr-Wr graph for 1000 seed weight in *Brassica rapa*

4.3 Heterosis

Analysis of variance (Table 11) revealed highly significant (at P=0.01) differences among parents and F_1 crosses for number of primary branches per plant, number of seeds per siliqua, length of siliqua, days to 50% flowering, days to 80% maturity where as significant differences was observed in number of secondary branches per plant and yield per plant indicating existence of considerable genetic variability in the experimental material. On the other hand, plant height, number of siliquae per plant and 1000 seed weight was found non-significant.

All 15 crosses were compared with better parent and mid parent for estimation of better parent heterosis and mid parent heterosis, respectively. Results of heterosis over better parent and mid parent and inbreeding depression are presented in Table 12, 13 and 14, respectively.

4.3.1 Plant height (cm)

Small and medium plant stature in *Brassica* is preferred because it can tolerate heavy winds and can be prevented from lodging; therefore, negative heterosis is useful regarding plant height (Turi *et al*., 2006). Out of the 15 crosses, only one crosses (P2×P5) showed significant heterosis (-16.03) over better parent (Table 12). The rest of the parents expressed non-significant heterosis over better parent and the range of better parent heterosis was -16.97% to 16.27% (Table 12). The highest non-significant negative value of heterosis over better parent was found in P4×P5 (-16.97). Data for heterosis over mid parent expressed that the only one cross (P4×P6) showed significant positive heterosis whereas the rest of the cross combinations showed non-significant heterosis (Table 13). For plant height, mid parent heterosis was varied from -9.18% to 16.38% (Table 13). On the other hand, negative value of mid parent heterosis (Table 13) was observed in P4×P5 (-9.18), P2×P5 (-8.88), P2×P6 (-4.30) and P5×P6 (-0.75). Meena *et al*. (2014), Turi *et al*. (2006), Nissimi *et al*. (2006), Pourdad and Sachan (2003) and Engqvist and Becker (1991) reported significant negative heterosis for the trait. On the other hand, Hu *et al*. (1996) reported significant positive heterosis on plant height.

Table 11: Mean squares for different morphological traits in *Brassica rapa* L. genotypes

Source of Variation	df	Characters								
		PH	**PB**	**NSP**	**NSS**	**LS**	**DF**	**DM**	**YP**	**1000 SW**
Replication	2	298.68	10.27	15279.27	11.61	0.16	0.20	5.92	20.98	869.89
Genotype	20	236.04	5.30**	9662.54	63.58**	1.08**	24.84**	26.75**	19.65*	0.00
Error	40	145.91	1.93	9293.25	12.83	0.21	1.62	2.10	10.65	0.70

^{ns} = Non-significant, * = Significant at 5% probability level, ** = Significant at 1% probability level

Here, PH = Plant height, PB = Number of primary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight

Table 12: Estimation of heterosis over better parent of ten morphological traits in *Brassica rapa* L genotypes

Character	Better parent (BP) heterosis															Range
	P1×P2	P1×P3	P1×P4	P1×P5	P1×P6	P2×P3	P2×P4	P2×P5	P2×P6	P3×P4	P3×P5	P3×P6	P4×P5	P4×P6	P5×P6	
PH	-0.93	-1.63	3.07	2.57	16.27	5.03	2.23	-16.03*	-8.90	1.20	-12.63	4.87	-16.97	9.70	-12.50	-16.97 to 16.27
PB	-0.30	0.47	-0.33	-0.10	0.13	-1.10	-1.07	-1.10	-2.47**	-0.13	-1.03	1.07	1.10**	0.73	-1.23	-2.47 to 1.10
NSP	56.63	-11.07	-3.84	-5.67	-5.94	-59.23**	-9.05	-72.33	-137.30*	10.50	65.27	174.73**	6.37	50.73	8.57	-137.30 to 174.73
NSS	-2.10	-3.27	2.13	-4.37*	-8.87**	-6.37**	-2.13*	-8.63**	-4.30*	-6.43**	-6.47**	-7.30**	-7.57*	-4.20	-5.80**	-8.87 to 2.13
LS	-0.39	-0.30	-2.60	-0.34	-0.54**	-0.48**	-3.33	-0.33*	-0.19**	-2.96	-0.53*	-0.64**	-3.34	-3.34	-0.52*	-3.34 to -0.19
DF	0.67	-0.67	-2.00**	-1.67	0.33	-1.00	-1.07	0.03**	-0.33**	-1.00	-2.33	-0.33	-1.67	0.00	1.41	-2.33 to 1.41
DM	2.67*	-1.33*	1.00	-3.00**	-3.67*	-2.00	1.00	-1.33	-2.33	-2.00	-1.00	-1.67	-1.00	-1.67	1.33	-3.67 to 2.67
YP	1.33	0.71	0.48	1.22	0.12	-1.93	-1.26	-1.51	-3.07	-1.21	-0.46	1.06	0.28	1.14	-1.07	-3.07 to 1.33
1000 SW	-0.13	-0.30	-0.20	-0.07	-0.27	-0.17	0.37	0.30	-0.53	-0.23	-0.17	0.07	-0.10	0.27	-0.03	-0.07 to 0.37
OC (%)	0.21	-0.53	-0.89	0.20	-0.45	0.25	0.78	0.66*	0.53	0.52	0.58	1.10	0.12	0.12	0.20	-0.89 to 1.10

^{ns} = Non-significant, * = Significant at 5% probability level, ** = Significant at 1% probability level

Here, PH = Plant height, PB = Number of primary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight, OC (%) =Oil content percentage

Table 13: Estimation of heterosis over mid parent of ten morphological traits in *Brassica rapa* L genotypes

Character	Heterosis over mid parent (MP)															Range
	P1×P2	P1×P3	P1×P4	P1×P5	P1×P6	P2×P3	P2×P4	P2×P5	P2×P6	P3×P4	P3×P5	P3×P6	P4×P5	P4×P6	P5×P6	
PH	3.55	3.07	6.92	14.20	16.38	5.25	2.88	-8.88	-4.30	2.05	-5.70	9.68	-9.18	13.67*	-0.75	-9.18 to 16.38
PB	0.33	5.72	0.25	0.45	0.40	-0.65	-0.15	-0.22	-1.87**	0.33	-0.60	1.22	1.13**	1.05	-0.95	-1.87 to 5.72
NSP	61.97	43.98	16.60	57.92	63.90	1.85	9.57	-3.42	-55.07	41.25	73.10*	195.88**	44.95	102.63**	21.88	-55.07 to 195.88
NSS	-1.55	-0.25	2.30	-0.87	-5.31*	-3.90**	-1.75	-5.68*	-1.30	-3.58	-5.98**	-6.77**	-4.23	-0.82	-5.75**	-6.77 to 2.30
LS	-0.35	-0.11	-1.23	-0.31	-0.39*	-0.29**	-1.80	-0.27*	-0.08**	-1.62	-0.53*	-0.34*	-1.87	-1.87	-0.35	-1.87 to -0.11
DF	1.67	-0.67	0.17	1.33	2.00	0.00*	-0.85**	4.32**	3.20	1.17	0.67**	1.33*	3.50**	3.83	4.35**	-0.85 to 4.35
DM	3.00**	- 0.33	2.17	0.33*	-0.50	-0.67	1.33	2.33*	1.17	-0.33	1.33*	0.50	3.00**	2.17*	1.50	-0.67 to 3.00
YP	1.42	0.83	0.54	1.44	1.11	-1.60	-1.10	-1.08	-1.87	-1.03	-0.36*	1.92	0.56	2.18*	-0.30	-1.87 to 2.18
1000 SW	-0.02	-0.17	0.00	0.08	0.10	-0.15**	0.45	0.33	-0.28	-0.17	-0.17	0.30	-0.05	0.43**	0.18	-0.28 to 0.45
OC (%)	0.75	0.05	-0.74	0.46	-0.06	0.29	1.17*	0.94**	0.69	0.95**	0.69	1.34	0.24	0.45**	0.4	-0.74 to 1.34

^{ns} = Non-significant, * = Significant at 5% probability level, ** = Significant at 1% probability level

Here, PH = Plant height, PB = Number of primary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight, OC (%) =Oil content percentage

Table 14: Estimation of inbreeding depression of ten morphological traits in *Brassica rapa* L genotypes

Character	Inbreeding depression															Range
	P1×P2	P1×P3	P1×P4	P1×P5	P1×P6	P2×P3	P2×P4	P2×P5	P2×P6	P3×P4	P3×P5	P3×P6	P4×P5	P4×P6	P5×P6	
PH	2.19	4.77	4.93	19.69	6.63	30.59**	23.40**	7.09	-6.79	7.17	8.17	9.49	1.75	11.75	3.15	-6.79 to 30.59
PB	1.23*	1.51*	0.09	0.67	0.40	1.19	0.92	1.05	-1.32	0.36	0.69	3.06*	1.41**	2.19**	-0.07	-1.32 to 3.06
NSP	76.00	91.70	98.89	70.00	59.39	87.25	119.19*	80.43	-49.62	29.35	24.04	202.91**	68.17	121.05**	2.07	-49.62 to 202.91
NSS	-2.77	1.55	-0.15	2.11	-2.22	-0.98	-3.97	-3.07	-0.97	-0.67	0.27	-4.98**	0.51	3.47	-0.07	-4.98 to 3.47
LS	-0.19	0.36	0.36	-0.02	-0.27	0.12	-0.34	-0.22	-0.26**	0.31	0.15	-0.37*	0.41	0.41**	0.04	-0.37 to 0.41
DF	4.41	2.01*	2.53**	4.38**	2.35	3.97**	-1.00	-1.05**	4.42**	2.21	-1.67*	-0.33	0.97	0.15	0.87	-1.67 to 4.42
DM	6.36**	1.39	2.83*	0.87	-1.53	1.17	-0.47	0.41	0.25	-3.99*	-3.96**	-0.04	-0.31	1.25	0.21	-3.99 to 6.36
YP	2.27	2.87**	2.34	2.81	2.14	1.00	1.69	1.08	-2.11	0.44	2.14	2.83	2.38	3.59**	0.15	-2.11 to 3.59
1000 SW	0.32	0.41	0.09	0.05	0.48	0.01	0.79*	0.55	-0.47	-0.03	-0.27	0.06	-0.03	0.35*	-0.21	-0.47 to 0.79
OC (%)	0.51	4.00**	-2.05	-0.27	-0.73	1.37**	0.90	0.75*	0.73	0.15	-0.34	0.58	0.60	-0.08	-0.28	-2.05 to 4.00

^{ns} = Non-significant, * = Significant at 5% probability level, ** = Significant at 1% probability level

Here, PH = Plant height, PB = Number of primary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight, OC (%) =Oil content percentage

Plate 6. Hybrid (SAU Sarisha 3 X BARI Sarisha 6) showing plant height status compare to parent

Plate 7. Hybrid (SAU Sarisha 3 × TORI 7) showing branching status compare to parent

The difference in the results could be due to the differences in the genotypes and weather conditions of the experimental plot. Among the 15 crosses, significant inbreeding depression (Table 14) was observed in P2×P3 (30.59) and P2×P4 (23.40) where the value of inbreeding depression was ranged from -6.79 to 30.59 (Table 14).

4.3.2 Number of primary branches per plant

In *Brassica*, short stature with vigorous structure containing more number of primary branches provides opportunity for more yields. Similarly, shorter plants with greater numbers of branches are desirable due to their ability to withstand winds. So, positive heterosis is desirable for number of primary branches (Turi *et al*., 2006). Heterosis estimates over better parent showed that out of 15 crosses, P2×P6 (-2.47) and P4×P5 (1.10) had highly significant negative and positive values, respectively where the values ranged from -2.47% to 1.10% (Table 12). Of these crosses, highly significant heterosis over mid parent (Table 12) was noted for P2×P6 (-1.87) and P4×P5 (1.13).

Heterosis over mid parent for this trait ranged from -1.87% to 5.72% (Table 13). Similarly, shorter plants with greater numbers of branches are desirable due to their ability to withstand winds. Meena *et al*. (2014), Turi *et al*. (2006), Nasrin *et al*. (2011), Turi *et al*. (2006), Nassimi *et al*. (2006), Satwinder *et al*. (2000), Jorgensen *et al*. (1995), Krzymanski *et al*. (1997), Fray *et al*. (1997) and Liu *et al*. (1996) reported positive heterosis on primary branches per plant. Regarding inbreeding depression, it could be seen that P3×P6 (3.06), P1×P3 (1.51) and P1×P2 (1.23) showed significant, and P4×P6 (2.19) and P4×P5 (1.41) showed highly significant value. The value of inbreeding depression was ranged from -1.32 to 3.06 (Table 14).

4.3.3 Number of siliquae per plant

A greater number of siliqua on the main raceme are desirable for higher yields in rapeseed. Therefore, positive heterosis is preferred for the number of pods on the main raceme. Among the crosses, the range of better parent heterosis for this trait was -137.30% to 174.73% (Table 12). P3×P6 exhibited highly significant positive value (174.73) whereas P2×P3 showed highly significant negative value (-59.23). The only cross combination

P2×P6 showed significant negative value (-137.30). Highly significant positive heterosis over mid parent (Table 13) was observed in P3×P6 (195.88) and P4×P6 (102.63) whereas P3×P5 showed positive and significant value (73.10). The value of mid parent heterosis was ranged from -55.07% to 195.88 % (Table 13). This finding was in agreement with the earlier findings of Fray *et al*. (1997) and Jorgensen *et al*. (1995). Out of the 15 cross combinations, P3×P6 (202.91) and P4×P6 (121.05) showed highly significant and P2×P4 (119.19) demonstrated significant positive inbreeding depression value (Table 14). It was ranged from -49.62 to 202.91 (Table 14).

4.3.4 Number of seeds per siliqua

Heterosis for number of seeds per siliqua over better parent ranged from -8.87% to 2.13% (Table 12). The entire hybrid expressed significant and negative heterosis over better parent (Table 12) except P1×P2 (-2.10), P1×P3 (-3.27), P1×P4 (2.13) and P4×P6 (-4.20). The highest highly significant negative value was observed in the hybrid P1×P6 (-8.87). Of these crosses, negative significant heterosis over mid parent was noted for six cross combinations eg. P3×P6 (-6.77**), P3×P5 (-5.98**), P5×P6 (-5.75**), P2×P3 (-3.90**), P2×P5 (-5.68*) and P1×P6 (-5.31*) (Table 13). The value of mid parent heterosis was ranged from -6.77% to 2.30% (Table 13).

This finding was in disagreement with the earlier findings of Satwinder *et al*. (2000) and Jorgensen *et al*. (1995). P3×P6 showed highly significant and negative inbreeding depression over their F_1's (Table 14). Inbreeding depression was ranged from -4.98 to 3.47 (Table 14).

4.3.5 Length of siliqua (cm)

Length of siliqua is one of the major yield contributing traits for *B. rapa*. So, for this trait positive heterosis has an immense importance. For length of siliqua better parent heterosis was ranged from -3.34% to -0.19 % (Table 12). Heterosis estimated over better parent (Table 12) showed that out of 15 crosses, 7 crosses showed negative significant value P3×P6 (-0.64**), P1×P6 (-0.54**), P2×P3 (-0.48**), P2×P6 (-0.19**), P3×P5 (-0.53*), P5×P6 (-0.52*) and P2×P5 (-0.33*).

Plate 8. Hybrid (SAU Sarisha 1 X BARI Sarisha 6) showing number of siliquae per plant status compare to parent

Plate 9. Hybrid (TORI 7 X SAU Sarisha 3) showing siliqua length status compare to parent

Highly significant and negative heterosis over mid parent (Table 13) was observed in the hybrid P2×P3 (-0.29) and P2×P6 (-0.08); and significant and negative heterosis was found in P3×P5 (-0.53), P1×P6 (-0.39), P3×P6 (-0.34) and P2×P5 (-0.27). It was ranged from -1.87% to -0.11% (Table 13). Meena *et al*. (2014), Satwinder *et al*. (2000) and Jorgensen *et al*. (1995) found similar results in their experiments. Highly significant positive and negative inbreeding depression was observed in the hybrid P4×P6 (0.41) and P2×P6 (-0.26), respectively. On the other hand, P3×P6 showed significant and negative inbreeding depression (-0.37) for the trait (Table 14). Inbreeding depression was ranged from -0.37 to 0.41 (Table 14).

4.3.6 Days to 50% flowering

Early flowering in *Brassica* can provide adequate time for grain formation process and can certainly cause early maturity and higher yields; therefore, negative heterosis is desirable for flowering (Turi *et al*., 2006). Among the crosses, the range of better parent heterosis was -2.33 % to 1.41 % (Table 12). P1×P4 (-2.00) and P2×P6 (-0.33) crosses exhibited the highly significant negative better parent heterosis (Table 12) and P2×P5 showed highly significant positive heterosis (0.03). Highly significant and positive heterosis over mid parent was observed in P5×P6 (4.35), P2×P5 (4.32), P4×P5 (3.50) and P3×P5 (0.67) whereas P2×P4 (-0.85) showed highly significant and negative heterosis (Table 13). On the other hand, the hybrid P3×P6 (1.33) and P2×P3 (0.00) showed significant positive heterosis. The heterosis over mid parent was ranged from -0.85% to 4.35% (Table 13). Turi *et al*. (2006) and Nassimi *et al*. (2006) reported significant negative mid parent heterosis for flowering in *B. napus*. Pourshad and Sachan (2003) and Engqvist and Becker (1991) also found significant negative heterosis with earlier flowering hybrids. Inbreeding depression was the highly significant and positive (Table 14) for the hybrid P2×P6 (4.42), P1×P5 (4.38), P2×P3 (3.97) and P1×P4 (2.53). Negative and highly significant inbreeding depression was found in P2×P5 (-1.05). On the other hand, P1×P3 (2.01) and P3×P5 (-1.67) showed significant inbreeding depression. Inbreeding depression was ranged from -1.67 to 4.42 (Table 14).

Plate 10. Hybrid (SAU Sarisha 3 × TORI 7) showing flowering status compare to parent

4.3.7 Days to 80% maturity

Early maturity is useful in most of the plant species especially *Brassica* where delayed maturity causes losses to yield and quality of oil due to rise in temperature; therefore, negative heterosis is desirable for early maturity (Turi *et al*., 2006). Early maturing genotypes lower losses due to shattering, tolerate or escape heat stress and provide sufficient time for seeding the next crop. For days to 80% maturity, the range of better parent heterosis was -3.67 % to 2.67 % (Table 12). The hybrid P1×P5 (-3.00) showed highly significant negative heterosis over better parent whereas P1×P6 (-3.67) and P1×P3 (-1.33) showed significant negative heterosis. On the other hand, only the hybrid P1×P2 (2.67) showed significant and positive heterosis over better parent for the trait. Highly significant and positive heterosis was noticed for the hybrid P1×P2 and P4×P5. The value was same 3.00. P2×P5 (2.33), P4×P6 (2.17), P3×P5 (1.33) and P1×P5 (0.33) expressed positive and significant heterosis over mid parent (Table 13) for the trait. It was ranged from -0.67% to 3.00%. The result was in agreement with the findings of Das *et al*. (2004), Turi *et al*. (2006), Nasrin *et al*. (2011), Yadav *et al*. (2012), Nassimi *et al*. (2006) and Pourdad and Sachan (2003). Highly significant positive and negative inbreeding depression was observed in P1×P2 (6.36) and P3×P5 (-3.96), respectively whereas P1×P4 (2.83) and P3×P4 (-3.99) showed significant positive and negative value, respectively. It was ranged from -3.99 to 6.36 (Table 14).

4.3.8 Yield per plant (g)

Yield per plant is an important yield contributing parameter for *B. rapa*. Thus positive heterosis is important for improving seed yield of *B. rapa*. None of the cross combinations showed considerably heterosis over better parent (Table 12). P4×P6 (2.18) and P3×P5 (0.36) showed significant positive and negative heterosis over mid parent (Table 13) for the trait, respectively. It was ranged from -3.07% to 1.33% (Table 12) for better parent and mid parent ranged from -1.87% to 2.18% (Table 13). Meena *et al*. (2014), Yadava *et al*. (2012), Vaghela *et al*. (2011), Hirve and Tiwari (1991), Dhillon *et al*. (1990), Duhoon and Basu (1981), Verma *et al*. (2011), Aher *et al*. (2009), Engqvist and Becker (1991), Hu *et al*. (1996), Satwinder *et al*. (2000), Jorgensen *et al*. (1995), Krzymanski *et al*. (1997) and Fray *et al*. (1997) reported positive heterosis on yield per plant. Highly significant and

positive inbreeding depression was observed in P4×P6 (3.59) and P1×P3 (2.87) while it was ranged from -2.11 to 3.59 (Table 14).

4.3.9 Thousand seed weight (g)

Among the cross combinations, no cross combinations showed significant heterosis over better parent (Table 12). P4×P6 (0.43) and P2×P3 (-0.15) showed highly significant positive and negative heterosis over mid parent for this trait (Table 13), respectively. It was ranged from -0.07% to 0.37% for better parent (Table 12) and -0.28% to 0.45% for mid parent (Table 13). Engqvist and Becker (1991), Hu *et al*. (1996), Satwinder *et al*. (2000), Jorgensen *et al*. (1995), Krzymanski *et al*. (1997) and Fray *et al*. (1997) reported positive heterosis on 1000 seed weight. Inbreeding depression for 1000 seed weight expressed positive and significant for P2×P4 (0.79) and P4×P6 (0.35) while it was ranged from -0.47 to 0.79 (Table 14).

4.3.10 Oil content (%)

The oil percent is one of the important traits of rapeseed because it is useful in food and industrial applications. Therefore, positive heterosis is desirable on oil percent. Heterosis effects over better parent only P2×P5 (0.66) showed significant positive heterosis (Table 12). P2×P5 (0.94), P3×P4 (0.95) and P4×P6 (0.45) showed highly significant positive heterosis and P2×P4 (1.17) showed significant positive heterosis over mid parent for this trait (Table 13), respectively. Heterosis over better parent it was ranged from -0.89% to 1.10% (Table 12) and over mid parent it was ranged from -0.74% to 1.34% (Table 13). Krzymanski *et al*. (1997) found significant heterosis on oil content but some other researchers were reported negative or absence heterosis on oil content as a common phenomenon in oil seed *Brassica* (Brandle and Mc Vetty, 1990; Schuler *et al*., 1992; Goffman and Becker, 2001; Ofori and Becker, 2008). Inbreeding depression for oil content expressed highly positive significant for P1×P3 (4.00) and P2×P3 (1.37) and positive significant for P2×P5(0.75). It was ranged from -2.05 to 4.00 (Table 14).

4.4 Generation Mean Analysis

4.4.1 Estimates of scaling test and gene action of plant height

Scaling test

The estimates of scaling tests for plant height are presented in Table 15. Highly significant negative scale A was observed for SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 3 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15. On the other hand, scale B was highly significant and positive B scale was in the SAU Sarisha 1 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. Non significant and positive scale C was in Tori 7 × BARI Sarisha 15. Negative and non significant scale D was observed for the cross SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. In Tori 7 × BARI Sarisha 15 all the scales were insignificant where as in the cross SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6 where all the scales showed significant value. Non significant value of scale indicated the adequacy of additive dominance model for the inheritance of the above crosses on plant height.

The significant scaling tests (one or more scales in A, B, C and D) indicated the presence of digenic epistasis for the trait and non-significance of the scaling tests for the trait indicated the absence of non-allelic interactions. The six-parameter model of Jinks and Jones (1958) was used for further tests of the absence or presence and nature of non-allelic gene interactions through the parameters against the respective standard errors following a conventional ‘t’ test.

Gene action

Gene affects for plant height in *Brassica rapa* hybrids results shown in Table 15. The estimated mean effect parameter (m) was found to be highly significant for plant height in all the crosses. Initially, it was clear that all studied traits were quantitatively inherited.

Estimated d (additive component) was negative and highly significant in SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3 and

Table 15: Estimates of scaling test and gene effects for plant height in different crosses of *Brassica rapa* L.

Cross	Scaling test			
	A	B	C	D
TORI 7 × SAU sarisha 1	0.96±3.64	-10.20±4.57*	16.16±6.89*	12.70±2.71**
TORI 7 × SAU sarisha 2	0.96±3.64	-10.20±4.57*	16.16±6.89*	12.70±2.71**
TORI 7 × SAU sarisha 3	-5.47±3.48	-16.85±3.03**	-12.96±5.63*	4.68±2.38*
TORI 7 × BARI sarisha 6	-6..03±3.61	-24.47±4.21**	-50.34±6.82**	-9.91±2.73**
TORI 7 × BARI sarisha 15	-4.28±3.69	2.43±4.20	6.23±6.24	4.04±2.94
SAU 1 × SAU sarisha 2	-16.79±3.16**	-8.98±3.78*	-111.84±6.26**	-43.02±2.13**
SAU 1 × SAU sarisha 3	-31.21±3.06**	-5.96±3.65	-87.86±4.95**	-25.34±2.44**
SAU 1× BARI sarisha 6	-4.57±4.21	-32.36±4.81**	-46.14±5.24**	-4.59±3.22
SAU 1× BARI sarisha 15	19.70±22.69	22.25±4.85**	18.54±5.52**	-11.70±11.76
SAU 2 × SAU sarisha 3	-32.46±3.00**	-7.61±3.53*	-24.56±5.49**	7.75±2.57**
SAU 2 × BARI sarisha 6	0.22±3.20	1.87±3.33	-25.37±5.55**	-13.73±2.34**
SAU 2 × BARI sarisha 15	1.52±4.48	15.01±5.41**	-19.68±7.94*	-18.10±2.78**
SAU 3 × BARI sarisha 6	-17.81±3.44**	-10.20±4.46*	-14.08±5.78*	6.96±2.82*
SAU 3× BARI sarisha 15	1.47±4.92	15.28±5.73**	-19.03±8.81**	-17.90±2.78**
BARI 6 × BARI sarisha 15	-15.46±2.71**	-0.58±2.80	-18.58±23.60	-1.26±11.76

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
Tori 7 × SAU sarisha 1	109.13±0.91**	1.09±1.99	-21.85±6.16**	-25.40±5.42**	5.58±2.14**	34.63±10.55**	Duplicate	dominant decreasers
Tori 7 × SAU sarisha 2	109.13±0.91**	1.10±1.99	-21.85±6.15**	-25.40±5.42**	5.58±2.14**	34.63±10.55**	Duplicate	dominant decreasers
Tori 7 × SAU sarisha 3	101.82±0.88**	0.98±1.59	-6.30±5.25	-9.37±4.77*	5.68±1.82**	31.70±8.52**	Duplicate	dominant decreasers
Tori 7 × BARI sarisha 6	104.98±1.01**	-2.41±1.84	34.03±6.1**	19.83±5.47**	9.22±2.10**	10.67±10.06	Complementary	dominant increasers
Tori 7 × BARI sarisha 15	108.46±1.00**	-3.24±2.15	8.29±6.35	-8.08±5.88	-3.36±2.29	9.94±10.64	Complementary	dominant increasers
SAU 1 × SAU sarisha 2	82.68±0.79**	-4.12±1.41**	91.30±5.05**	86.05±4.27**	-3.90±1.70*	-60.26±8.45**	Duplicate	dominant increasers
SAU 1 × SAU sarisha 3	86.63±0.79**	-11.98±1.86**	53.55±5.25**	50.68±4.89**	-12.62±2.06**	-13.51±8.96	Duplicate	dominant increasers
SAU 1× BARI sarisha 6	98.97±0.83**	6.74±2.75*	0.31±6.76	9.19±6.45	13.89±2.96**	27.74±12.22*	Complementary	dominant increasers
SAU 1× BARI sarisha 15	105.68±1.32**	3.32±11.53	19.10±23.57	23.40±23.52	-1.27±11.56	-65.36±46.47	Duplicate	dominant increasers
SAU 2 × SAU sarisha 3	102.26±0.95**	-11.57±1.72**	-13.46±5.52*	-15.51±5.15**	-12.42±1.98**	55.58±8.82**	Duplicate	dominant decreasers
SAU 2 × BARI sarisha 6	103.38±0.87**	-8.61±1.55**	18.29±5.15**	27.479±4.683**	-0.82±1.90	-29.57±8.34**	Duplicate	dominant increasers
SAU 2 × BARI sarisha 15	104.48±0.78**	-2.77±2.30	49.87±6.65**	36.21±5.56**	-6.74±2.46**	-52.74±12.16**	Duplicate	dominant increasers
SAU 3 × BARI sarisha 6	106.45±0.89**	7.94±2.18**	-14.67±6.09*	-13.92±5.65*	-3.805±2.441	41.93±10.49**	Duplicate	dominant decreasers
SAU 3× BARI sarisha 15	104.53±0.78**	-2.98±2.31	47.54±6.93**	35.80±5.57**	-6.90±2.49**	-52.56±12.77**	Duplicate	dominant increasers
BARI 6 × BARI sarisha 15	103.61±5.84**	-2.62±1.39	12.20±23.59	2.52±23.53	-7.43±1.69**	13.53±24.25	Complementary	dominant increasers

*P<0.05, **P<0.01,respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

SAU Sarisha 2 × BARI Sarisha 6. These results indicated that these cross materials used in this study had decreasing alleles for plant height and selection could be effective if shorter cultivars were desired. Meanwhile positive and significant values were detected in the cross SAU Sarisha 1 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 6. The obtained results indicated that selection on plant height could be effective for these crosses in early generations.

In crosses, TORI 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15, the estimated h (dominance component) was positive and highly significant. The highly significant effects of h for plant height was indicating the importance of dominance gene effects in the inheritance of the trait. These results were in harmony with those reported by Rashwan (2002), Abd-Elkader (2006) and El-Ameen (2008). They found that dominance effect were importance in the inheritance of yield and its components. On the other hand, highly significant and negative value of h was obtained TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6. These results indicated that the alleles responsible for less value of the trait were dominant over the alleles controlling high value.

For plant height in all crosses (except SAU Sarisha 1 × BARI Sarisha 6 cross) the contribution of dominance effect (h) was greater than additive effect (d). Therefore, dominance genes are the most important factors contributing to the genetic control of plant height. Cheema and Sadaqat (2004) indicated the major role of non-additive type of gene action attributable to dominance and epistatic effects on plant height. Singh and Singh (1994) and Rao and Gulati (2001) concluded similar findings as those in present studies that plant height is under the control of dominance. Larik and Rajput (2000) studied *B. juncea* and *B. napus* together and reported the involvement of additive effects in the phenotypic expression of the plant height, which is corroborated of the present studies. Sheikh (1998) performed the combing ability studies in *B. juncea* and observed predominance of additive effects. The differences in findings of Sheikh (1998) and those in the present studies could be related with the genetic differences in the breeding material

and methodology adopted for genetic analysis. A negative estimate of dominance in some cases might be due to epistasic gene action in the cross-combinations. d and h were positive and the relative values of d and h were more or less equal indicating both dominant and additive gene had almost equal contribute on the expression of the character. It may be concluded that dominance was present with additive type gene action.

The estimated i (additive × additive) was significant to highly significant in all the cross combinations (except TORI 7 × BARI Sarisha 15, SAU Sarisha 1× BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15). The significant effect of additive × additive type epistasis was indicating the importance of this component and also suggesting an enhancing effect in the inheritance of plant height. Additive × additive interaction effect is important for plant breeders for genetic improvement of traits via selection (Dhanda and Sethi, 1998; Yadav and Narsinghani, 1999).

The estimated j (additive × dominance) was positive and highly significant for TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, TORI 7 × SAU Sarisha 3, TORI 7 × BARI Sarisha 6 and SAU Sarisha 1 × BARI Sarisha 6 while, highly significant and negative j was detected in SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. Significance of (j) revealed that selection through selfing (self-fertilization) was not effective for improvement of the trait (Farshadfar *et al*., 2001; Sharifi, 2005) because among the digenic interactions, additive × dominance type was more fixable and more useful for plant breeders (Sunil Kumar, 2005).

The value of l was positively significant and highly significant for TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, TORI 7 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6. Positive and significant results confirm the importance role of dominance x dominance gene interactions in the genetic system which controls the character, plant height. On the contrary, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15 were showed negative and highly significant estimated value of l. These results suggested the scope of heterosis breeding for the development of superior populations of these cross combinations.

In SAU Sarisha 1 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15, the estimates of the interaction (i and l) were either smaller than their standard error or not significantly larger than them. Therefore, there was no evidence of non-allelic interaction for the character plant height which agreed with the conclusion from individual scaling test results. For the remaining crosses at least one of the two (i and l) interaction parameters were significantly different from zero. This was again complete in harmony with scaling tests.

The estimates of components of genetic variance indicate that duplicate epistasis interaction (h and l having opposite sign) was predominant for plant height for all the cross combinations except TORI 7 × BARI Sarisha 6, TORI 7 × BARI Sarisha 15, SAU Sarisha 1 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15 (h and l having same sign) marked the complementary epistasis. Duplicate type of epistasis will reduce the net gain occurring from heterozygosity due to the cancellation of dominance and epistatic effects (Dhall and Hundal, 2006). Complementary gene action, acts in favor of heterosis causes the increase of heterosis, and duplicates gene action, which acts against the heterosis, causes decrease of heterosis.

A number of researchers reported that all the three types of gene action i.e., additive, dominance and interaction components were found to play a role in the inheritance of yield contributing traits. However, their degree differed with crosses. This could be due to differences in magnitude of the gene effects and genetic background of the parents (Murthy and Deshpande, 1997).

Significant additive and dominant gene and additive × additive, additive × dominant and dominant × dominant gene interaction were present in Tori 7 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 2 and SAU Sarisha 2 × SAU Sarisha 3 and these gene interaction were duplicate type. So, for the mention crosses early selection for plant height would not be effective. In that case, delay selection or selection after few generations would be effective.

The generation mean analysis revealed that individual crosses greatly differed for the gene action and on an overall basis, all the types of gene action, additive, dominance and epistasis are important. The latter two types predominating for many crosses thereby indicating that epistasis cannot be ignored. Similar conclusions have been reported by Martin and Lippert (1975), Sharma and Saini (1977) and Jagadeesha (2000) in chilli. Since epistasis was present in many cases, success of selection, which should be undertaken in advanced generations, will depend on the epistasis type. Selection for epistatic interactions warrants inbreeding following by selection. In other words, when epistatic interactions are present, selection between inbred families is the most effective method. However, the rate of inbreeding must be regulated in such a manner that it may ward off natural selection of homozygotes (at slow inbreeding) interfering with allelic fixation. At the same time, it should not be so rapid, which may cause extinction of many lines. Inter-line selection favors either originally more heterozygous lines or those that can manage to preserve over dominant loci or blocks in a heterozygous state by some or other mechanism (Sharma, 1994).

The additive, additive × additive or any other digenic complementary gene interaction are fixable and thus can be exploited effectively for the improvement of the traits through pedigree method of selection (Ram, 1994). Jindal *et al*. (1993) and Amawate and Behl (1995) suggested that duplicate epistasis might restrict the expression, and selection of a trait in early segregating generations. The selection in early generations would not be effective for fixable components of variation. Such gene effects can however be exploited by intermating the selected segregants and delaying the selection to the advanced generations (Jindal *et al*., 1993). Delayed selection (Sharma and Sharma, 1995) or selection after biparental intermating (Misra *et al*., 1994) would be more effective to get a good response in such cases. The biparental hybridization between recombinants in early segregating generation (F_2) would produce better genetic combinations, through which the accumulations of desirable genes could be achieved. The other possibilities could be diallel selective mating system as proposed by Jensen (1970) or the recurrent selection procedures (Singh and Pawar, 1990) for the exploitation of non-additive genetic variability.

Table 16: Estimates of scaling test and gene effects for primary branches per plant in different crosses of *Brassica rapa* L.

Cross	Scaling test			
	A	B	C	D
TORI 7 × SAU sarisha 1	-3.34±0.67**	-5.67±0.92**	-4.84±1.38**	2.09±0.52**
TORI 7 × SAU sarisha 2	-3.34±0.67**	-5.67±0.92**	-4.84±1.38**	2.09±0.52**
TORI 7 × SAU sarisha 3	-3.04±0.65**	-2.96±0.58**	-4.86±1.67**	0.57±0.80
TORI 7 × BARI sarisha 6	-0.98±0.69	0.66±0.57	-1.76±1.14	-0.721±0.62
TORI 7 × BARI sarisha 15	-3.68±0.72**	-1.42±-0.79	-0.80±1.59	2.15±0.79**
SAU 1× SAU sarisha 2	-3.83±0.79**	-2.62±-0.82**	-6.04±1.51**	0.20±0.59
SAU 1 × SAU sarisha 3	2.01±0.82**	-1.02±-0.74	-4.64±1.12**	-0.80±0.58
SAU 1 × BARI sarisha 6	2.01±0.82*	-1.02±-0.74	-4.64±1.12**	-0.80±0.58
SAU 1 × BARI sarisha 15	-0.17±0.76	1.64±-0.62**	1.54±1.16	0.03±0.66
SAU 2 × SAU sarisha 3	-3.77±0.66**	-0.55±-0.71	-0.77±1.27	1.77±0.52**
SAU 2 × BARI sarisha 6	-2.69±0.59**	-2.21±-0.52**	-3.35±0.97**	0.77±0.47
SAU 2 × BARI sarisha 15	1.32±0.68	-2.02±0.92*	-6.67±1.31**	-1.66±0.55**
SAU 3 × BARI sarisha 6	32.84±1.33**	-34.65±1.47**	-68.30±2.63**	-0.40±0.57
SAU 3 × BARI sarisha 15	-1.29±0.70	-1.75±0.92	-6.02±1.33**	-1.48±0.56**
BARI 6 × BARI sarisha 15	3.97±0.66**	-1.86±0.82*	-9.02±1.18**	-1.59±0.42**

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
TORI 7 × SAU sarisha 1	4.97±0.18**	0.83±0.36*	-4.14±1.20**	-4.18±1.05**	1.16±0.43**	13.20±2.02**	Duplicate	dominant decreasers
TORI 7 × SAU sarisha 2	4.97±0.18**	0.83±0.36*	-4.14±1.20**	-4.18±1.05**	1.16±0.43**	13.20±2.02**	Duplicate	dominant decreasers
TORI 7 × SAU sarisha 3	4.79±0.36**	0.07±0.31	-0.56±1.64	-1.15±1.60	-0.03±0.36	7.16±2.08**	Duplicate	dominant decreasers
TORI 7 × BARI sarisha 6	5.06±0.24**	-0.27±0.38	1.89±1.28	1.44±1.25	-0.82±0.42*	-1.12±1.92	Duplicate	dominant increasers
TORI 7 × BARI sarisha 15	5.56±0.33**	-0.86±0.42*	-3.91±1.64*	-4.31±1.64**	-1.13±0.46*	9.42±2.31**	Duplicate	dominant decreasers
SAU 1 × SAU sarisha 2	4.21±0.23**	-0.15±0.35	-1.05±1.32	-0.40±1.18	-0.60±0.42**	6.86±2.07	Duplicate	dominant decreasers
SAU sarisha 1 × SAU 3	4.51±0.21**	-1.78±0.38**	-1.55±1.24	-1.40±1.15	-2.70±0.44**	6.79±1.98**	Duplicate	dominant decreasers
SAU sarisha 1 × BARI sarisha 6	4.34±0.18**	0.38±0.44	1.39±1.24	1.61±1.16	-0.49±0.49	1.42±2.10	Complementary	dominant increasers
SAU sarisha 1 × BARI sarisha 15	5.35±0.25**	-0.31±0.42	-1.94±1.36	-0.07±1.33	-0.91±0.48	-1.38±2.04	Complementary	dominant decreasers
SAU sarisha 2 × SAU sarisha 3	5.10±0.20**	-1.14±0.32**	-3.22±1.16**	-3.55±1.05**	-1.61±0.36**	7.89±1.81**	Duplicate	dominant decreasers
SAU sarisha 2 × BARI sarisha 6	4.42±0.18**	-0.27±0.30	-0.41±1.01	-1.55±0.95	-0.24±0.34	6.46±1.57**	Duplicate	dominant decreasers
SAU sarisha 2 × BARI sarisha 15	3.84±0.18**	0.03±0.40	4.37±1.23**	3.32±1.11**	0.35±0.44	0.01±2.09	Complementary	dominant increasers
SAU sarisha 3 × BARI sarisha 6	4.13±0.19**	0.622±0.422	33.18±1.70**	0.80±1.14	0.90±0.45	66.70±3.12**	Complementary	dominant decreasers
SAU sarisha 3 × BARI sarisha 15	3.92±0.19**	-0.05±0.41	3.98±1.25**	2.96±1.12**	0.22±0.45	0.09±2.12	Complementary	dominant increasers
BARI sarisha 6 × BARI sarisha 15	3.62±0.14**	-1.35±0.31**	3.61±0.99**	3.18±0.84**	-1.05±0.43*	2.65±1.73	Complementary	dominant increasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

According to Comstock *et al*. (1949), use of reciprocal recurrent selection could improve the traits when both additive and non-additive gene effects are involved in the expression of the characters. Heterosis breeding in rapeseed is feasible because presence of complementary gene action and prevalence of the high magnitude of non-additive gene effects for most of the traits studied.

4.4.2 Estimates of scaling test and gene action of primary branches per plant

Scaling test

The estimates of scaling tests for number of primary branches per plant are presented in the Table 16. Negative and non significant scale A was observed for TORI 7 × BARI Sarisha 6, SAU Sarisha 1× BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. On the other hand, SAU Sarisha 2 × BARI Sarisha 15 showed non significant and positive scale A. The rest of the crosses in the scale A was highly significant and negative except SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 6 (positively significant). Tori 7 × SAU Sarisha 1 and Tori 7 × SAU Sarisha 2 had showed highly significant and negative scale among A, B, C and D. On the other hand, Tori 7 × SAU Sarisha 3, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 2 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 6 had showed significant value among the scales except the scale D. TORI 7 × BARI Sarisha 15 and SAU Sarisha 2 × SAU Sarisha 3 were significant for the scale of A and D. Significant results of scaling tests parameters indicate inadequacy of the additive-dominance model to interpret the gene effects involved in the materials. Epistatic contributions are important in the inheritance of these traits in the particular materials investigated (Mather and Jinks, 1982). In TORI 7 × BARI Sarisha 6, the values of the A, B, C and D scaling tests were not significant. This finding indicates the absence of epistasis (non-allelic interaction) and the additive-dominance model was adequate to demonstrate the genetic variation.

Gene action

The estimated mean effect parameter (m) was found to be highly significant for primary branches per plant in all the crosses. These results indicated that the above mentioned studied traits in such crosses were quantitatively inherited.

The estimated d (additive component) was negative and significant in TORI 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3 and BARI Sarisha 6 × BARI Sarisha 15 where as positive and significant value of d was observed in TORI 7 × SAU Sarisha 1 and TORI 7 × SAU Sarisha 2. The additive (d) gene effects were found to be highly significant positive**,** suggesting the potential for obtaining further improvement of the trait by using pedigree selection program. These results were in close agreement with those of Bhor and Dumber (1998), Sangwan *et al*. (1998), Rahman and Saad (2000) and Abd-Elhady (2003). Meanwhile, negative and significant values of d indicated that the crosses used in this study have decreasing alleles for the character. The rest of the crosses showed insignificant relationship on additive component. On the other hand, additive component [d] was non-significant for that crosses revealed low importance of additive gene effects in genetic control of primary branches per plant studied. These results were in close agreement with Sharma *et al*. (1997).

Significant and negative value of h was obtained in TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, TORI 7 × BARI Sarisha 15 and SAU Sarisha 2 × SAU Sarisha 3. On the other hand, estimated h (dominance component) was positive and highly significant in SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 6, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. This result indicated the presence of dominance gene effect in the inheritance of the character. For all the crosses (except SAU Sarisha 1 × SAU Sarisha 3) the contribution of dominance effect (h) was greater than additive effect. Therefore, dominance genes are the most important factors contributing to the genetic control of the primary branches per plant. A negative estimate of dominance in some cases might be due to epistasic gene action in the cross-combinations.

The estimated i (additive× additive) was negatively and highly significant in TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, TORI 7 × BARI Sarisha 15 and SAU Sarisha 2 × SAU Sarisha 3. SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15 was positive and highly significant, indicating early generation selection for the primary branches per plant might be effective.

The estimated j (additive × dominance) was positive and highly significant for TORI 7 × SAU Sarisha 1 and Tori 7 × SAU Sarisha 2 while, negative and significant to highly significant j was detected in TORI 7 × BARI Sarisha 6, TORI 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3 and BARI Sarisha 6 × BARI Sarisha 15. The negative sign of interaction in some cases also suggested dispersion of genes in the parents.

The value of l was positively highly significant for TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, TORI 7 × SAU Sarisha 3, TORI 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6, and SAU Sarisha 3 × BARI Sarisha 6. These results suggest the scope of heterosis breeding for the development of superior populations of these cross combinations.

The results indicated that the dominance × dominance effects were greater in magnitudes that additive × additive and additive × dominance in all cases which recorded non-allelic interaction except in the cross of TORI 7 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. When non-additive portion is larger than additive, the improvement of this trait needs intensive selection through later generations (Khattab *et al*., 2010).

Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect will produce new recombinants capable of improving the character. Therefore, the improving of this character could be achieved through hybrid breeding method.

The magnitude of additive gene effects (d) was small relative to the corresponding dominance effects (h) in most cases, suggesting that pedigree selection method is a useful breeding program for improving these populations. However, the negative value of d

indicated that the alleles responsible for less value of the inferior parent of the trait were dominant over the alleles controlling high value in better parent.

4.4.3 Estimates of scaling test and gene action of number of siliqua per plant

Scaling test

The estimates of scaling tests for number of siliqua per plant are presented in the Table 17. It was revealed that Tori 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2 and SAU Sarisha 2 × SAU 3 was significant for scale A, B and D. Non significant and positive scale B was observed for TORI 7 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15 where as BARI Sarisha 6 × BARI 15 showed non significant and positive value. On the other hand, both the scale A and C was significant negatively in TORI 7 × BARI Sarisha 6 but SAU Sarisha 1 × SAU Sarisha 2 and SAU Sarisha 1 × SAU Sarisha 3 both were positively and negatively significant on scale A and C, respectively. In the cross TORI 7 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 6 were negative and positive but highly significant in the scale A and B, respectively. The cross SAU Sarisha 1 × BARI Sarisha 6 was insignificant both the scale A and B but the reverse situation was in the cross SAU Sarisha 1 × BARI Sarisha 15 where both scale A and B was highly significant. Non significant value of the scale indicated the adequacy of additive dominance model for the inheritance of the character.

Gene action

The highly significant effect of parameter m was found for number of siliqua per plant in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited. The estimated d (additive component) was negative and highly significant in TORI 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15 where as negative and significant value of d was observed in SAU Sarisha 1× SAUSarisha 2, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 15**.** Negative and significant values of d indicated that the crosses used in this study had decreasing alleles for the character. The rest of the crosses showed insignificant

Table 17: Estimates of scaling test and gene effects for number of siliqua per plant in different crosses of *Brassica rapa* L.

Cross	Scaling test			
	A	B	C	D
TORI 7 × SAU sarisha 1	-237.54±57.08**	-276.05±60.04**	-183.93±110.76	164.83±30.71*
TORI 7 × SAU sarisha 2	-237.54±57.08**	-276.05±60.04**	-183.93±110.76	164.83±30.71**
TORI 7 × SAU sarisha 3	-165.87±43.07**	6.57±38.55	-278.83±63.25**	-59.76±21.71**
TORI 7 × BARI sarisha 6	-97.35±45.58*	15.83±27.67	-165.71±54.61**	-42.09±23.29
TORI 7 × BARI sarisha 15	-247.04±40.56**	59.35±40.36	-109.77±58.64	38.95±22.95
SAU 1× SAU sarisha 2	233.83±35.79**	-60.51±36.73	-345.28±61.01**	-25.47±13.94
SAU 1× SAU sarisha 3	78.95±46.60**	-17.49±37.44	-328.53±33.86**	-116.04±27.45
SAU 1× BARI sarisha 6	78.95±46.60	-17.49±37.44	-328.53±33.86**	-116.04±27.45**
SAU 1× BARI sarisha 15	-87.27±33.61**	189.72±29.72**	88.34±48.94	-7.04±26.72
SAU 2 × SAU sarisha 3	-117.35±38.84**	-106.87±40.51**	-34.91±72.47	94.66±23.08**
SAU 2 × BARI sarisha 6	-99.09±26.68**	2.28±20.62	-182.79±38.19**	-42.99±16.04**
SAU 2 × BARI sarisha 15	-170.64±32.54**	2.40±38.21	-278.92±59.31**	-55.33±18.62**
SAU 3 × BARI sarisha 6	-1.76±13.97	98.75±32.35**	35.47±30.46	-30.75±20.60
SAU 3× BARI sarisha 15	-158.44±36.67**	5.55±42.54	-241.38±69.10**	-44.24±19.38*
BARI 6 × BARI sarisha 15	173.97±38.89**	-27.17±58.41	-36±86.69**	-82.79±20.16**

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
TORI 7 × SAU sarisha 1	209.03±12.09**	13.92±18.92	-267.70±79.09**	-329.66±61.43**	19.25±24.31	843.26±134.16**	Duplicate	Dominant decreasers
TORI 7 × SAU sarisha 2	209.03±12.094*	13.92±18.92	-267.70±79.09**	-329.66±61.43**	19.25±24.31	843.2±134.16**	Duplicate	Dominant decreasers
TORI 7 × SAU sarisha 3	115.23±6.05**	-30.47±18.02	163.51±52.33**	119.53±43.42**	-86.22±24.31**	39.76±95.90	Complementary	Dominant increasers
TORI 7 × BARI sarisha 6	142.64±6.74**	6.98±18.98	142.10±52.28**	84.19±46.59	-56.59±22.31*	-2.66±93.54	Duplicate	Dominant increasers
TORI 7 × BARI sarisha 15	146.30±5.88**	-76.30±19.71**	-14.01±53.19	-77.91±45.91	-153.20±22.96**	265.60±98.27**	Duplicate	Dominant decreasers
SAU sarisha 1× SAU sarisha 2	82.88±3.49**	-25.57±12.06*	52.79±40.74	50.94±27.89	-86.66±16.97**	243.40±77.79**	Complementary	Dominant increasers
SAU sarisha 1× SAU sarisha 3	89.41±5.66**	-89.12±14.44**	82.77±48.95	73.21±36.70*	-119.45±19.35**	311.18±89.71**	Complementary	Dominant increasers
SAU sarisha 1× BARI sarisha 6	76.60±3.15**	38.18±26.72	228.66±57.11**	232.08±54.91**	-30.727±28.7	-135.62±112.12	Duplicate	Dominant increasers
SAU sarisha 1× BARI sarisha 15	141.68±9.7**	-56.26±18.33**	-40.96±55.47	14.09±53.44	-138.50±21.19**	-116.54±88.17	Complementary	Dominant decreasers
SAU sarisha 2 × SAU sarisha 3	149.84±8.68**	-35.98±15.20*	-148.06±56.06**	-189.32±46.17**	-5.23±18.23	413.55±94.62**	Duplicate	Dominant decreasers
SAU sarisha 2 × BARI sarisha 6	106.89±5.64**	-12.11±11.41	130.93±35.60**	85.98±32.09**	-50.69±14.17**	10.82±59.53	Complementary	Dominant increasers
SAU sarisha 2 × BARI sarisha 15	98.38±5.66**	-34.62±14.77*	213.30±46.24**	110.67±37.24**	-86.52±17.03**	57.5±83.73	Complementary	dominant increasers
SAU sarisha 3 × BARI sarisha 6	98.02±6.31**	-36.94±16.29*	83.39±42.08*	61.51±41.21	-50.26±16.82**	-158.50±71.93*	Duplicate	Dominant increasers
SAU sarisha 3× BARI sarisha 15	101.98±6.14**	-33.40±14.98*	167.23±50.45**	88.49±38.76*	-82.00±17.61**	64.39±91.49	Complementary	Dominant increasers
BARI sarisha 6 × BARI sarisha 15	79.84±7.60**	-80.53±13.25**	305.79±57.22**	165.59±40.33**	-73.40±25.2**	35.56±101.62	Complementary	Dominant increasers

*P<0.05, **P<0.01 respectively. All the numerical data contain geneS effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

relationship on additive component.On the other hand, additive component [d] was non-significant for that crosses revealed low importance of additive gene effects in genetic control of siliqua per plant studied.

Highly significant and negative value of h was obtained in Tori 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2 and SAU Sarisha 2 × SAU Sarisha 3. On the other hand, estimated h (dominance component) was positive and significant in TORI 7 × SAU Sarisha 3, TORI 7 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 6, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. The significant value of h indicated that the dominance effect was important in the inheritance of the trait, number of siliqua per plant. Also, in this trait the additive × additive (i) and dominance × dominance (l) gene effect were significant in TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2 and SAU Sarisha 2 × SAU Sarisha 3, which may lead to hinder the progress of selection leading to losses of favorable genotypes during the early generation of selection.

The estimated i (additive× additive) was negatively and highly significant in TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2 and SAU Sarisha 2 × SAU Sarisha 3. On the other hand, estimated I (additive× additive) was positive and significant in Tori 7 × SAU Sarisha 3, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15.

The estimated j (additive × dominance) was negative and highly significant for all the crosses except (TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, SAU Sarisha 1 × BARI Sarisha 6 and SAU Sarisha 2 × SAU Sarisha 3). The negative sign of interaction in some cases also suggested dispersion of genes in the parents.

The value of l was positive and highly significant for TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2, TORI 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 2 × SAU Sarisha 3. Only the cross combination SAU Sarisha 3 × BARI Sarisha 6 was negative and significant. In some crosses the additive genetic effects was equally important as non additive. Therefore, reciprocal recurrent breeding method can effectively utilize the fixable and unfixable genetic components of

variation for these particular crosses.Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect acts in favour of heterosis causes the increase of heterosis and duplicates gene action, which acts against the heterosis, causes decrease of heterosis.

All the three types of gene action i.e., additive, dominance and interaction components were found to play a vital role in the inheritance of number of siliqua per plant in some of the crosses. However, their degree differed with crosses. This could be due to differences in magnitude of the gene effects and genetic background of the parents (Murthy and Deshpande, 1997).

4.4.4 Estimates of scaling test and gene action of number of seed per siliqua

Scaling test

Scaling test for number of seed per siliqua for the fifteen crosses is presented in the Table 18. Only the cross TORI 7 × BARI Sarisha 6 was highly significant for all the scale. Insignificant but positive and negative A scale was observed SAU Sarisha 2 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15, respectively. Scale A, B and C was highly significant and negative for both SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. On the other hand, both scale B and C was highly significant and negative but scale A was highly significant and positive for SAU Sarisha 3 × BARI Sarisha 6. Highly significant and positive scale B and C and C and D was prevailed in the cross TORI 7 × SAU Sarisha 2 and TORI 7 × SAU Sarisha 3; and SAU Sarisha 1 × SAU Sarisha 3 respectively. In SAU Sarisha 2 × SAU Sarisha 3, both A and B scale was positive and insignificant. Both (scale A and B) and (scale A and C) was highly significant in TORI 7 × BARI Sarisha 15 and SAU Sarisha 1 × SAU Sarisha 2, subsequently. The cross SAU Sarisha 1 × BARI Sarisha 6 and SAU Sarisha 1 × BARI Sarisha 15 were negative and highly significant in the scale B but positive and highly significant in scale D. Significant values of scaling tests in all the crosses showed the presence of non-allelic genetic interaction.

Table 18: Estimates of scaling test and gene effects for number of seed per siliqua in different crosses of *Brassica rapa* L

Cross	Scaling test			
	A	B	C	D
TORI 7 × SAU Sarisha 1	2.51±1.44	4.32±1.52**	7.96±2.54**	0.56±0.96
TORI 7 × SAU Sarisha 2	2.51±1.44	4.32±1.52**	7.96±2.54**	0.56±0.96
TORI 7 × SAU Sarisha 3	1.61±1.31	-4.66±1.25**	-6.68±2.37**	-0.20±0.86
TORI 7 × BARI Sarisha 6	-4.15±1.31**	-12.62±1.24**	-10.44±2.24**	3.16±0.78**
TORI 7 × BARI Sarisha 15	9.73±1.15**	-8.34±1.06**	-0.80±1.96	-1.09±0.69
SAU Sarisha 1× SAU Sarisha 2	1.74±1.44	-8.25±1.25**	-1.72±2.27	2.39±0.90**
SAU Sarisha 1× SAU Sarisha 3	-1.66±1.52	-16.36±1.21	0.90±2.24**	9.46±0.92**
SAU Sarisha 1× BARI Sarisha 6	-1.66±1.52	-16.36±1.21**	0.90±2.24	9.46±0.92**
SAU Sarisha 1× BARI Sarisha 15	0.50±1.24	-10.54±1.29**	1.26±1.80	5.65±0.83**
SAU Sarisha 2 × SAU Sarisha 3	1.69±1.09	1.42±1.08	-4.49±1.93*	-3.81±0.82**
SAU Sarisha 2 × BARI Sarisha 6	0.98±0.98	-7.83±0.99**	-10.52±1.71**	-1.83±0.83*
SAU Sarisha 2 × BARI Sarisha 15	-3.65±1.25**	-12.93±1.01**	-15.49±1.73**	0.54±0.85
SAU Sarisha 3 × BARI Sarisha 6	4.45±1.12**	-6.48±1.29**	-11.20±2.08**	-0.13±1.12
SAU Sarisha 3× BARI Sarisha 15	-4.27±1.32**	-12.63±1.35**	-14.91±2.05**	0.99±1.15
BARI Sarisha 6 × BARI Sarisha 15	-1.68±1.44	-8.92±1.46**	5.74±2.40*	8.17±0.90**

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
TORI 7 × SAU Sarisha 1	58.12±11.60**	12.48±18.68	-37.15±68.03	-28.85±59.58	17.37±28.41	50.26±109.78	Duplicate	Dominant decreasers
TORI 7 × SAU Sarisha 2	17.73±0.36**	-1.45±0.62*	-2.68±2.18	-1.13±1.92	-0.90±0.85	-5.70±3.55	Complementary	Dominant decreasers
TORI 7 × SAU Sarisha 3	17.18±0.35**	-1.48±0.49**	0.15±1.96	0.40±1.72	1.52±0.70*	5.86±3.07	Complementary	Dominant increasers
TORI 7 × BARI Sarisha 6	16.47±0. 29**	0.73±0.52	-7.10±1.84**	-6.33±1.57**	4.23±0.61**	23.11±3.08**	Duplicate	Dominant decreasers
TORI 7 × BARI Sarisha 15	16.34±0. 27**	5.48±0.42**	-3.75±1.61*	2.19±1.38	9.03±0.62**	-3.58±2.59	Complementary	Dominant decreasers
SAU Sarisha 1× SAU Sarisha 2	16.72±0. 35**	2.53±0.58**	-9.55±2.02**	-4.79±1.81**	5.00±0.83**	11.30±3.25**	Duplicate	Dominant decreasers
SAU Sarisha 1× SAU Sarisha 3	19.04±0. 29**	1.48±0.53**	-17.66±1.76**	-14.91±1.58**	1.10±0.74	14.90±2.88**	Duplicate	Dominant decreasers
SAU Sarisha 1× BARI Sarisha 6	17.40±0. 33**	4.40±0.64**	-24.61±2.06**	-18.93±1.85**	7.35±0.82**	36.96±3.41**	Duplicate	Dominant decreasers
SAU Sarisha 1× BARI Sarisha 15	19.73±0. 27**	2.52±0.63**	-12.61±1.82**	-11.31±1.67**	5.52±0.84**	21.35±3.10**	Duplicate	Dominant decreasers
SAU Sarisha 2 × SAU Sarisha 3	16.23±0. 32**	2.98±0.50**	4.03±1.80*	7.62±1.65**	0.13±0.66	-10.74±2.79**	Duplicate	Dominant increasers
SAU Sarisha 2 × BARI Sarisha 6	14.88±0. 32**	1.07±0.53*	-0.55±1.76	3.67±1.67*	4.41±0.61**	3.16±2.73	Duplicate	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 15	15.40±0. 29**	1.25±0.61*	-1.90±1.82	-1.08±1.70	4.63±0.72**	17.67±3.01**	Duplicate	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 6	17.34±0. 43**	0.96±0.71	-5.48±2.32*	0.26±2.25	1.01±0.80	10.68±3.53**	Duplicate	Dominant decreasers
SAU Sarisha 3× BARI Sarisha 15	15.55±0. 29**	1.24±0.62*	-2.15±1.91	-1.99±1.72	4.17±0.83**	18.90±3.24**	Duplicate	Dominant decreasers
BARI Sarisha 6 × BARI Sarisha 15	20.69±0. 33**	3.36±0.61**	-22.47±2.06**	-16.35±1.80**	3.61±0.85**	26.96±3.44**	Duplicate	Dominant decreasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

Gene action

The highly significant effect of parameter m was found for number of seed per siliqua in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited.

The estimated d (additive component) was positive and non significant for all the crosses except Tori 7 × SAU Sarisha 1, Tori 7 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 6. Additive effect [d] was not significant indicating that selection is not effective in early generation. Tori 7 × SAU Sarisha 2 and Tori 7 × SAU Sarisha 3 was showed negative and significant value of d (additive component).

Significant and negative value of h was obtained in Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15. Only one cross combination eg. SAU Sarisha 2 × SAU Sarisha 3 showed significant and positive value of h.

The estimated i (additive× additive) was negative and highly significant for Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 2 × BARI Sarisha 6 showed positive and significant value of i(additive× additive).

The estimated j (additive × dominance) was positive and significant for all the crosses except Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6.

The value of l was positive and highly significant for Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 6, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. Negative and highly significant value of l was estimated in SAU Sarisha 2 × SAU Sarisha 3.

Significant value with opposite sign of h and l showed the presence of duplicate epistasis. Preponderance of dominant gene action for this trait indicated the usefulness hybrid program of rapeseed. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect will produce new recombinants capable of improving the character. Therefore, the improving of this character could be achieved through hybrid breeding method.

4.4.5 Estimates of scaling test and gene action of length of siliqua

Scaling test

Tori 7 × SAU 1 and Tori 7 × BARI Sarisha 15 were insignificant for all the scales (Table 19). The reverse situation was in the cross of SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 2 × BARI Sarisha 6 where all the scales were highly significant. Only A and D scale was highly significant negative and significant positive in the cross Tori 7 × BARI Sarisha 6 and SAU Sarisha 1 × BARI Sarisha 6, respectively. Insignificant scale D was in SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15 but the cross Tori 7 × SAU Sarisha 2 contained positive and insignificant scales C. Both the cross SAU Sarisha 1 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15, the scale C and D was significant and positive. On the contrary, negative and significant scale B and C was in Tori 7 × SAU Sarisha 3, SAU Sarisha 1 × SAU Sarisha 2 and SAU Sarisha 1 × SAU Sarisha 3.

Gene action

The highly significant effect of parameter m was found for length of siliqua in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited.

The estimated d (additive component) was positive and significant for Tori 7 × BARI 15, SAU Sarisha 1 × SAU Sarisha 3 and BARI Sarisha 6 × BARI Sarisha 15. Highly significant negative value of d was observed in Tori 7 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 6.

Table 19: Estimates of scaling test and gene effects for length of siliqua in different crosses of *Brassica rapa* L

Cross	Scaling test			
	A	B	C	D
Tori 7 × SAU Sarisha 1	0.51±0.21	0.62±0.23	0.06±0.38	-0.53±0.17
Tori 7 × SAU Sarisha 2	0.51±0.21*	0.62±0.23**	0.06±0.38	-0.53±0.17**
Tori 7 × SAU Sarisha 3	0.68±1.11	-0.55±0.19**	-1.84±0.33**	-0.99±0.56
Tori 7 × BARI Sarisha 6	-0.83±0.20**	-0.14±0.23	-0.55±0.35	0.21±0.15
Tori 7 × BARI Sarisha 15	0.05±0.15	-0.03±0.15	0.33±0.26	0.15±0.11
SAU Sarisha 1 × SAU Sarisha 2	-0.47±0.25	-1.00±0.23**	-0.93±0.46*	0.27±0.16
SAU Sarisha 1 × SAU Sarisha 3	-0.33±0.23	-0.11±0.24**	0.33±0.37**	0.38±0.15**
SAU Sarisha 1 × BARI Sarisha 6	-0.30±0.23	-0.11±0.24	0.33±0.37	0.38±0.15*
SAU Sarisha 1 × BARI Sarisha 15	-0.19±0.20	-0.05±0.18	0.87±0.07**	0.56±0.12**
SAU Sarisha 2 × SAU Sarisha 3	0.51±0.17**	-3.17±0.36**	-4.48±0.44**	-0.39±0.14**
SAU Sarisha 2 × BARI Sarisha 6	3.62±0.33**	-0.69±0.19**	-5.39±0.44**	-0.53±0.15**
SAU Sarisha 2 × BARI Sarisha 15	4.07±0.34**	-0.73±0.16**	-5.14±0.39**	-0.16±0.13
SAU Sarisha 3 × BARI Sarisha 6	-0.89±0.18**	-0.39±0.15*	-0.850±0.28**	0.21±0.11
SAU Sarisha 3 × BARI Sarisha 15	-3.68±0.50**	-1.07±0.35**	-4.97±0.62**	-0.10±0.13
BARI Sarisha 6 × BARI Sarisha 15	-0.23±0.24	-0.38±0.20	0.72±0.30*	0.70±0.14**

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
Tori 7 × SAU Sarisha 1	65.53±15.61**	0.54±13.69	-56.91±74.69	-77.65±68.18	5.82±18.64	114.42±103.04	Duplicate	Dominant decreasers
Tori 7 × SAU Sarisha 2	4.91±0.06**	-0.02±0.11	0.72±0.37	1.07±0.34**	-0.05±0.13	-2.21±0.58**	Duplicate	Dominant increasers
Tori 7 × SAU Sarisha 3	4.83±0.04**	0.46±0.55	2.03±1.13	1.98±1.13	0.62±0.56	-2.11±2.25	Duplicate	Dominant increasers
Tori 7 × BARI Sarisha 6	4.84±0.05**	-0.37±0.10**	-0.74±0.33*	-0.43±0.30	-0.34±0.12**	1.42±0.56*	Duplicate	Dominant decreasers
Tori 7 × BARI Sarisha 15	4.84±0.04**	0.19±0.07*	-0.72±0.25**	-0.31±0.23	0.04±0.09	0.28±0.41	Duplicate	Dominant decreasers
SAU Sarisha 1 × SAU Sarisha 2	4.85±0.06**	0.07±0.09	-0.83±0.37*	-0.54±0.32	0.26±0.12*	2.02±0.59**	Duplicate	Dominant decreasers
SAU Sarisha 1 × SAU Sarisha 3	5.12±0.04**	0.22±0.10*	-3.26±0.33**	-1.35±0.28**	1.75±0.19**	4.69±0.59**	Duplicate	Dominant decreasers
SAU Sarisha 1 × BARI Sarisha 6	5.05±0.05**	-0.17±0.11	-1.04±0.34**	-0.77±0.30*	-0.11±0.14	1.21±0.58*	Duplicate	Dominant decreasers
SAU Sarisha 1 × BARI Sarisha 15	5.11±0.03**	0.04±0.09	-1.20±0.27**	-1.12±0.24**	-0.06±0.12	1.37±0.47**	Duplicate	Dominant decreasers
SAU Sarisha 2 × SAU Sarisha 3	4.83±0.05**	-0.00±0.09	-0.82±0.34*	0.79±0.28**	1.33±0.17**	2.89±0.58**	Duplicate	Dominant increasers
SAU Sarisha 2 × BARI Sarisha 6	4.35±0.06**	0.00±0.09	-0.80±0.35*	1.06±0.30**	-1.46±0.18**	3.26±0.57**	Duplicate	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 15	4.38±0.04**	-0.02±0.09	-1.25±0.31**	0.33±0.26	-1.66±0.17**	4.46±0.55**	Duplicate	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 6	4.60±0.04**	-0.08±0.07**	-0.78±0.25	-0.43±0.22	-0.25±0.09*	1.72±0.42**	Duplicate	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 15	4.40±0.04**	0.01±0.09	-1.35±0.39**	0.21±0.26	-1.30±0.29**	4.54±0.73**	Duplicate	Dominant decreasers
BARI Sarisha 6 × BARI Sarisha 15	5.14±0.03**	0.34±0.12**	-1.70±0.31**	-1.4±0.28**	0.04±0.13	2.08±0.57**	Duplicate	Dominant decreasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

Significant and negative value of h was obtained in almost all the crosses except Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, Tori 7 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6.

The estimated i (additive× additive) was positive and highly significant for Tori 7 × SAU Sarisha 2, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 2 × BARI Sarisha 6. On the other hand, highly significant and negative value of i was observed in SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. Only one cross combination (SAU Sarisha 1 × BARI Sarisha 6) showed significant and negative value of i.

The estimated j (additive × dominance) was positive and highly significant for SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 2 × SAU Sarisha 3. Negative and highly significant value of additive × dominance was found in Tori 7 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 15. On the other hand, positive and negative but significant estimation of j was found in SAU Sarisha 1 × SAU Sarisha 2 and SAU Sarisha 3 × BARI Sarisha 6, respectively.

The value of l was positive and highly significant for all most all the crosses except Tori 7 × SAU Sarisha 2(highly significant and negative), Tori 7 × BARI Sarisha 6 (positive and significant), Tori 7 × SAU Sarisha 1(non significant and positive), Tori 7 × SAU Sarisha 3 (non significant and negative) and Tori 7 × BARI Sarisha 15 (non significant and positive).

Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect.

4.4.6 Estimates of scaling test and gene action of days to 50% flowering

Scaling test

Tori 7 × BARI Sarisha 6 was negative and highly significant for both scale B and C but these two scales were negative insignificant for SAU Sarisha 3 × BARI Sarisha 15 (Table

20). Scale A was positive insignificant in SAU Sarisha 1 × SAU Sarisha 3 where as BARI Sarisha 6 × BARI Sarisha 15 was positive significant. Accordingly the table 15 SAU Sarisha 2 × BARI Sarisha 6 was positive insignificant in the scale B. Both scale C and D was highly significant and positive in SAU Sarisha 1 × BARI Sarisha 6. Scale A, B and C was highly significant and negative in the crosses Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 2 and SAU Sarisha 2 × SAU Sarisha 3 but highly significant and positive was both in the SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 6. In all the scales, Tori 7 × SAU Sarisha 1 showed insignificant value. However, both the crosses Tori 7 × SAU Sarisha 2 and SAU Sarisha 1 × BARI Sarisha 15, scale A, B and C were significant and negative where as the scale D was positive and highly significant.

Gene action

The highly significant effect of parameter m was found for days to 50% flowering in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited. The estimated d (additive component) was positive and highly significant for SAU Sarisha 2 × BARI Sarisha 6 and positive and significant for SAU Sarisha 3 × BARI Sarisha 6. The rest of the crosses showed insignificant result.

Highly significant and negative value of h was obtained in Tori 7 × SAU Sarisha 2, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15 and SAU Sarisha 2 × BARI Sarisha 6. Mean while, Tori 7 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 15 showed highly significant and positive value of dominance effect. On the other hand, SAU Sarisha 3 × BARI Sarisha 6 showed only the positive and significant value of h.

The estimated i (additive × additive) was positive and highly significant for SAU Sarisha 1 × SAUSarisha 3 and SAU Sarisha 3 × BARI Sarisha 15. On the other hand, highly significant and negative value of additive × additive type gene interaction was observed in Tori 7 × SAU Sarisha 2, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15 and SAU Sarisha 2 × BARI Sarisha 6.

Table 20: Estimates of scaling test and gene effects for days of 50% flowering in different crosses of *Brassica rapa* L .

Cross	Scaling test			
	A	B	C	D
Tori 7 × SAU Sarisha 1	-11.69±1.52	-7.52±1.05	-12.15±1.36	3.52±1.12
Tori 7 × SAU Sarisha 2	-11.69±1.52**	-7.52±1.05**	-12.15±1.36**	3.52±1.12**
Tori 7 × SAU Sarisha 3	-6.15±0.94**	-5.01±0.90**	-9.63±1.47**	0.76±0.96
Tori 7 × BARI Sarisha 6	1.71±1.32	-7.12±1.73**	-8.51±2.46**	-1.55±1.20
Tori 7 × BARI Sarisha 15	-6.92±1.12**	-10.48±1.08**	-14.82±1.90**	1.29±1.13
SAU Sarisha 1 × SAU Sarisha 2	-5.68±0.98**	-3.94±1.08**	-5.91±1.78**	1.85±0.95
SAU Sarisha 1 × SAU Sarisha 3	1.26±1.73	-2.08±1.16**	5.30±1.91*	3.06±0.75*
SAU Sarisha 1 × BARI Sarisha 6	1.26±1.73	-2.08±1.16	5.30±1.91**	3.06±0.75**
SAU Sarisha 1 × BARI Sarisha 15	-7.21±1.82**	-6.67±1.83**	-6.93±3.17*	3.47±1.21**
SAU Sarisha 2 × SAU Sarisha 3	-4.15±1.59**	-6.19±1.36**	-8.39±2.40**	0.97±0.82
SAU Sarisha 2 × BARI Sarisha 6	13.41±1.35**	2.41±1.35	27.77±2.26**	5.97±1.20**
SAU Sarisha 2 × BARI Sarisha 15	8.05±1.21**	8.98±1.25**	20.14±2.15**	1.55±1.06
SAU Sarisha 3 × BARI Sarisha 6	8.79±1.42**	8.63±1.41**	16.28±2.60**	-0.57±0.50
SAU Sarisha 3 × BARI Sarisha 15	7.88±1.37**	-0.50±1.23	-2.64±2.29	-5.01±0.86**
BARI Sarisha 6 × BARI Sarisha 15	1.94±085*	-1.09±0.93	2.16±1.40	-0.57±0.50

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
Tori 7 × SAU Sarisha 1	52.27±10.39**	2.58±18.82	-4.350±59.997	10.973±56.111	-0.01±23.79	-35.63±95.95	Complementary	Dominant decreasers
Tori 7 × SAU Sarisha 2	37.59±0.33**	-1.18±0.91	-6.057±2.266**	-7.057±2.259**	-2.08±0.92*	26.27±3.91**	Duplicate	Dominant decreasers
Tori 7 × SAU Sarisha 3	38.56±0.36**	-0.52±0.64	-1.94±1.93	-1.53±1.93	-0.57±0.65	12.69±2.96**	Duplicate	Dominant decreasers
Tori 7 × BARI Sarisha 6	41.38±0.47**	0.06±0.75	8.08±2.54**	3.10±2.41	4.41±1.07**	2.30±3.91	Complementary	Dominant increasers
Tori 7 × BARI Sarisha 15	39.92±0.44**	0.10±0.70	0.02±2.29	-2.59±2.27	1.78±0.78*	20.00±3.40**	Complementary	Dominant increasers
SAU Sarisha 1 × SAU Sarisha 2	37.81±0.37**	-0.78±0.59	-2.03±1.97	-3.71±1.90	-0.87±0.69	13.35±2.96**	Duplicate	Dominant decreasers
SAU Sarisha 1 × SAU Sarisha 3	37.26±0.26**	0.03±0.40	0.80±1.43	3.00±1.31**	1.66±0.50**	-2.00±2.23	Duplicate	Dominant increasers
SAU Sarisha 1 × BARI Sarisha 6	46.36±0.19**	0.41±0.64	-5.86±1.74**	-6.12±1.50**	1.67±1.00	6.95±3.20*	Duplicate	Dominant decreasers
SAU Sarisha 1 × BARI Sarisha 15	41.73±0.45**	-0.90±0.80	-9.55±2.75**	-6.95±2.42**	-0.26±0.99	20.84±4.52**	Duplicate	Dominant decreasers
SAU Sarisha 2 × SAU Sarisha 3	38.53±0.30**	0.48±0.56	-2.95±1.95	-1.95±1.65	1.02±0.89	12.31±3.29**	Duplicate	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 6	44.29±0.45**	5.63±0.77**	-12.1±2.49**	-11.95±2.40**	5.50±0.88**	-3.871±3.846	Complementary	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 15	42.52±0.41**	-0.33±0.66	-1.93±2.23	-3.10±2.12	-0.46±0.77	-13.94±3.42**	Complementary	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 6	46.84±0.21**	-0.00±0.26	3.19±1.58*	1.14±1.00	0.08±0.66	-18.57±2.80**	Duplicate	Dominant increasers
SAU Sarisha 3 × BARI Sarisha 15	41.84±0.36**	83.44±0.22*	41.84±0.36**	83.44±0.22**	41.84±0.36**	83.44±0.22**	Complementary	Dominant increasers
BARI Sarisha 6 × BARI Sarisha 15	84.78±0.23**	0.09±0.44	1.81±1.43	0.29±1.30	1.41±0.60*	-2.90±2.34	Duplicate	Dominant increasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

The estimated j (additive × dominance) was positive and highly significant for Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 15. On the other hand, Tori 7 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15 showed positive and significant value of j. Only one cross combination Tori 7 × SAU Sarisha 2 showed significant and negative effect of additive × dominance type of gene interaction.

The value of l was positive and highly significant for all most all the crosses except SAU Sarisha 1 × BARI Sarisha 6 (significant and positive) and the rest of the crosses like Tori 7 × SAU Sarisha 1, Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15 showed insignificant dominance × dominance type of gene interaction.

Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect will produce new recombinants capable of improving the character. Therefore, the improving of this character could be achieved through hybrid breeding method.

4.4.7 Estimates of scaling test and gene action of days to maturity

Scaling test

Scaling test for days to 80% maturity for the fifteen crosses is presented in the Table 21. The scale test results revealed that Tori 7 × SAU Sarisha 1 was insignificant for all the scales where as Tori 7 × SAU Sarisha 2, Tori 7 × BARI Sarisha 15 and SAU Sarisha 2 × SAU Sarisha 3 were showed significant score for these crosses. Tori 7 × SAU Sarisha 3 and Tori 7 × BARI Sarisha 6 was positive insignificant for the scale B where as all the other scales were highly significant. On the other hand, the scale B was negative and insignificant. Only A scale was positive and highly significant in BARI Sarisha 6 × BARI Sarisha 15 but the case was reverse in case of SAU Sarisha 1 × SAU Sarisha 2 where that scale was only insignificant. However, A scale was highly significant and positive and

both the scale B and D were highly significant and negative in SAU Sarisha 2 × BARI Sarisha 15. Both C and D scale was highly significant and positive in SAU Sarisha 3 × BARI Sarisha 6 whereas the other two scales were positive and non significant. In the cross SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 1 × BARI Sarisha 15, the scale C was negative and positive but significant, respectively. Additionally, B scale was highly significant and negative in SAU Sarisha 1 × SAU Sarisha 3 but in SAU Sarisha 1 × BARI Sarisha 15, highly significant and positive scale A was found.

Gene action

The highly significant effect of parameter m was found for days to maturity in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited.

The estimated d (additive component) was negative and highly significant for Tori 7 × SAU Sarisha 2 and SAU Sarisha 1 × SAU Sarisha 2. The positive and significant value of d was observed in Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. The rest of the crosses showed insignificant result.

Highly significant and negative value of h was obtained in SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6. On the other hand, the dominance effect was found positive and highly significant for Tori 7 × SAU Sarisha 2, Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15.

The insignificant value of i (additive × additive type gene interaction) was observed in Tori 7 × SAU Sarisha 1, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. On the other hand, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 2 × BARI Sarisha 6 and SAUSarisha 3 × BARI Sarisha 6 showed highly significant and negative effect of additive × additive type of gene interaction. Meanwhile, the rest of the all studied cross combinations showed highly significant and positive value with regard to the additive × additive type gene interaction.

Table 21: Estimates of scaling test and gene effects for days to maturity in different crosses of *Brassica rapa* L.

Cross	Scaling test			
	A	B	C	D
Tori 7 × SAU Sarisha 1	-2.00±0.00	0.66±0.01	-19.44±1.12	-9.05±0.56
Tori 7 × SAU Sarisha 2	-2.00±0.00**	0.66±0.01**	-19.44±1.12**	-9.05±0.56**
Tori 7 × SAU Sarisha 3	2.29±0.22**	0.39±0.28	-5.54±1.11**	-4.11±0.50**
Tori 7 × BARI Sarisha 6	10.73±0.29**	0.13±0.44	-3.22±1.09**	-7.04±0.56**
Tori 7 × BARI Sarisha 15	9.99±0.47**	-1.00±0.48*	5.10±1.39**	-1.94±0.63**
SAU Sarisha 1 × SAU Sarisha 2	0.46±0.34	7.33±0.30**	-6.19±1.26**	-7.00±0.61**
SAU Sarisha 1 × SAU Sarisha 3	11.23±0.61	-0.56±0.66**	-7.35±3.35*	-9.01±1.64
SAU Sarisha 1 × BARI Sarisha 6	11.23±0.61**	-0.56±0.66	-7.35±3.35*	-9.01±1.64**
SAU Sarisha 1 × BARI Sarisha 15	5.73±1.09**	-1.86±1.17	3.69±1.59*	-0.08±0.75
SAU Sarisha 2 × SAU Sarisha 3	3.53±1.29**	2.58±1.13*	11.93±2.21**	2.90±0.68**
SAU Sarisha 2 × BARI Sarisha 6	7.06±1.23**	-0.93±1.12	9.39±1.67**	1.63±0.62**
SAU Sarisha 2 × BARI Sarisha 15	8.53±1.18**	-2.93±1.07**	0.38±1.93	-2.60±0.62**
SAU Sarisha 3 × BARI Sarisha 6	0.03±0.90	0.26±0.97	7.29±1.53**	3.50±0.57**
SAU Sarisha 3 × BARI Sarisha 15	7.76±0.92**	-1.06±1.06	3.65±1.58*	-1.51±0.62*
BARI Sarisha 6 × BARI Sarisha 15	2.71±0.96**	-0.11±0.96	2.30±1.55	-0.14±0.65

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
Tori 7 × SAU Sarisha 1	65.95±15.85**	-7.21±17.71	-41.71±79.66	-62.22±72.64	-6.74±24.55	105.30±115.42	Duplicate	Dominant decreasers
Tori 7 × SAU Sarisha 2	76.30±0.28**	-1.00±0.00**	21.10±1.12**	18.10±1.12**	-1.33±0.00**	-16.77±1.12**	Duplicate	Dominant increasers
Tori 7 × SAU Sarisha 3	79.27±0.25**	0.00±0.01	7.85±1.04**	8.23±1.01**	0.95±0.11**	-10.93±1.11**	Duplicate	Dominant increasers
Tori 7 × BARI Sarisha 6	82.79±0.26**	1.96±0.22**	14.42±1.14**	14.09±1.13**	5.29±0.25**	-24.95±1.41**	Duplicate	Dominant increasers
Tori 7 × BARI Sarisha 15	84.19±0.30**	2.33±0.19**	3.39±1.31**	3.89±1.26**	5.49±0.26**	-12.89±1.59**	Duplicate	Dominant increasers
SAU Sarisha 1 × SAU Sarisha 2	78.83±0.29**	-4.667±0.143**	13.23±1.24**	14.00±1.23**	-3.43±0.20**	-21.80±1.39**	Duplicate	Dominant increasers
SAU Sarisha 1 × SAU Sarisha 3	80.80±0.28**	-0.53±0.43	-0.15±1.67	-1.09±1.43	-0.96±0.60	-2.37±2.70	Complementary	Dominant decreasers
SAU Sarisha 1 × BARI Sarisha 6	82.32±0.81**	2.33±0.26**	20.36±3.31**	18.02±3.28**	5.90±0.39**	-28.69±3.51**	Duplicate	Dominant increasers
SAU Sarisha 1 × BARI Sarisha 15	83.74±0.23**	0.10±0.58	1.94±1.63	0.17±1.50	3.80±0.73**	-4.04±2.81	Duplicate	Dominant increasers
SAU Sarisha 2 × SAU Sarisha 3	83.52±0.25**	2.18±0.44**	-6.50±1.68**	-5.81±1.36**	0.47±0.56	-0.30±2.84	Complementary	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 6	85.96±0.15**	1.09±0.54*	-0.76±1.46	-3.26±1.24**	3.99±0.70**	-2.86±2.73	Complementary	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 15	83.41±0.22**	1.50±0.43**	8.84±1.51**	5.21±1.25**	5.73±0.60**	-10.80±2.59**	Duplicate	Dominant increasers
SAU Sarisha 3 × BARI Sarisha 6	87.89±0.20**	0.23±0.40	-5.88±1.31**	-7.00±1.14**	-0.11±0.54	6.70±2.23**	Duplicate	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 15	83.44±0.22**	1.06±0.42*	7.25±1.40**	3.03±1.24*	4.41±0.62**	-9.73±2.32**	Duplicate	Dominant increasers
BARI Sarisha 6 × BARI Sarisha 15	84.78±0.23**	0.09±0.44	1.81±1.43	0.29±1.30	1.41±0.60*	-2.90±2.34	Duplicate	Dominant increasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

The estimated j (additive × dominance) was positive and highly significant for Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15, SAUSarisha 1 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. On the other hand, Tori 7 × SAU Sarisha 2 and SAU Sarisha 1 × SAU Sarisha 2 showed highly significant and negative additive × dominance type of gene interaction.

The value of l was negative and highly significant for Tori 7 × SAU Sarisha 2, Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. Only the cross SAU Sarisha 3 × BARI Sarisha 15, the estimated value of l was positive and highly significant. The rest of the crosses showed insignificant dominance × dominance type of gene interaction.

Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect will produce new recombinants capable of improving the character. Therefore, the improving of this character could be achieved through hybrid breeding method.

4.4.8 Estimates of scaling test and gene action of yield per plant

Scaling test

All the scales were significant in Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, Tori 7 × SAU Sarisha 3 and Tori 7 × BARI Sarisha 6 but in SAU Sarisha 3 × BARI Sarisha 6 where all the scales were insignificant (Table 22). Only B scale was insignificant for the cross Tori 7 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. However, in the cross SAU Sarisha 1 ×

Table 22: Estimates of scaling test and gene effects for yield per plant in different crosses of *Brassica rapa L* .

Cross	Scaling test			
	A	B	C	D
Tori 7 × SAU Sarisha 1	-4.70±1.60**	-5.61±1.67**	-6.54±2.95*	1.88±0.80*
Tori 7 × SAU Sarisha 2	-4.70±1.60**	-5.61±1.67**	-6.54±2.95*	1.88±0.80*
Tori 7 × SAU Sarisha 3	4.09±1.21**	-3.09±1.07**	-9.82±1.86**	-1.31±0.61*
Tori 7 × BARI Sarisha 6	2.54±1.23*	-2.33±1.15*	-8.35±1.68**	-1.74±0.69*
Tori 7 × BARI Sarisha 15	-4.04±1.15**	0.06±1.20	-6.35±1.99**	-1.18±0.60*
SAU Sarisha 1 × SAU Sarisha 2	3.65±0.78**	-2.76±0.95**	-7.19±1.43**	-0.38±0.45
SAU Sarisha 1 × SAU Sarisha 3	1.50±1.12**	-2.86±1.04**	-6.47±0.97**	-1.05±0.76
SAU Sarisha 1 × BARI Sarisha 6	1.50±1.12	-2.86±1.04**	-6.47±0.97**	-1.05±0.76
SAU Sarisha 1 × BARI Sarisha 15	-0.51±0.91	3.31±0.79**	4.68±1.00**	0.94±0.72
SAU Sarisha 2 × SAU Sarisha 3	-3.38±0.99**	-1.08±1.16	-3.83±1.79*	0.31±0.61
SAU Sarisha 2 × BARI Sarisha 6	3.01±0.92**	-3.38±0.85**	-8.41±1.64**	-1.00±0.56
SAU Sarisha 2 × BARI Sarisha 15	5.62±1.22**	-2.21±1.30	-11.39±2.31**	-1.77±0.57**
SAU Sarisha 3 × BARI Sarisha 6	-1.25±0.78	0.12±1.14	-1.25±1.41	-0.06±0.67
SAU Sarisha 3 × BARI Sarisha 15	5.50±1.27**	-1.33±1.42	-9.89±2.48**	-1.52±0.64*
BARI Sarisha 6 × BARI Sarisha 15	-3.17±1.08**	0.32±1.19	-6.39±1.97**	-1.77±0.59**

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
Tori 7 × SAU Sarisha 1	5.09±0.26**	0.24±0.59	-2.480±2.11	-3.77±1.60*	0.45±0.66	14.10±3.80**	Duplicate	Dominant decreasers
Tori 7 × SAU Sarisha 2	5.09±0.26**	0.24±0.59	-2.48±2.11	-3.77±1.60*	0.45±0.66	14.10±3.80**	Duplicate	Dominant decreasers
Tori 7 × SAU Sarisha 3	3.70±0.18**	-0.37±0.49	3.47±1..50*	2.63±1.23*	-0.50±0.57	4.54±2.72	Complementary	Dominant increasers
Tori 7 × BARI Sarisha 6	4.27±0.16**	0.11±0.61	4.92±1.59**	3.48±1.39*	-0.10±0.67	1.39±2.97	Complementary	Dominant increasers
Tori 7 × BARI Sarisha 15	3.84±0.17**	-1.06±0.48*	3.48±1.52*	2.37±1.20*	-2.05±0.543**	1.59±2.78	Complementary	Dominant increasers
SAU 1 × SAU Sarisha 2	3.36±0.13**	-0.11±0.36	-0.81±1.12	0.77±0.91	-0.44±0.45	5.63±2.03**	Duplicate	Dominant decreasers
SAU Sarisha 1 × SAU Sarisha 3	3.33±0.17**	-0.97±0.41*	-1.74±1.34	-0.64±1.09	-1.13±0.51*	10.26±2.40**	Duplicate	Dominant decreasers
SAU Sarisha 1 × BARI Sarisha 6	3.70±0.15**	1.11±0.69	1.02±1.57	2.10±1.52	0.68±0.74	2.26±2.94	Complementary	Dominant increasers
SAU Sarisha 1 × BARI Sarisha 15	5.33±0.22**	-0.71±0.56	-3.75±1.45**	-1.88±1.44	-1.91±0.60**	-0.90±2.47	Complementary	Dominant decreasers
SAU Sarisha 2 × SAU Sarisha 3	6.42±1.26**	-0.17±0.31**	-6.74±3.42	-0.62±1.22	-1.15±0.55*	5.09±2.58*	Duplicate	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 6	3.87±0.22**	0.46±0.34	2.56±1.32	2.01±1.12	0.18±0.45	4.38±2.13*	Complementary	Dominant increasers
SAU Sarisha 2 × BARI Sarisha 15	3.57±0.20**	-0.66±0.41	6.52±1.58**	3.55±1.15**	-1.70±0.49**	4.29±2.85	Complementary	Dominant increasers
SAU Sarisha 3 × BARI Sarisha 6	4.19±0.20**	0.07±0.54	-0.17±1.46	0.12±1.34	-0.69±0.58	1.00±2.58	Duplicate	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 15	3.72±0.22**	-0.94±0.46*	5.37±1.73**	3.05±1.28*	-2.0±0.51**	3.77±3.10	Complementary	Dominant increasers
BARI Sarisha 6 × BARI Sarisha 15	3.90±0.21**	-1.43±0.41**	4.50±1.49**	3.54±1.19**	-1.75±0.59**	-0.69±2.57	Duplicate	Dominant increasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 2 × BARI Sarisha 6 the scale A was highly significant and negative where as both the scale B and C was highly significant and negative for the same crosses. In SAU Sarisha 1 × BARI Sarisha 6, the scale B and C was highly significant and negative; and positive and highly significant relationship in the same scale was found in SAU Sarisha 1 × BARI Sarisha 15. On the other hand, cross SAU Sarisha 2 × SAU Sarisha 3 showed highly significant and negative data in the scale A and C.

Gene action

The highly significant effect of parameter m was found for yield per plant in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited.

The estimated d (additive component) was negative and significant for Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. The rest of the crosses showed insignificant result.

Significant and positive value of h was obtained in Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. Only the SAU Sarisha 1 × BARI Sarisha 15 showed highly significant and negative dominance effect. Mean while, the rest of the crosses showed insignificant result.

With regards to the additive × additive type gene interaction, the highly significant and positive effect was found in SAU Sarisha 2 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. On the other hand, significant and positive effect was found in Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 6, Tori 7 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15. Meanwhile, the significant and negative value of i was observed in Tori 7 × SAU Sarisha 1 and Tori 7 × SAU Sarisha 2.

The estimated j (additive × dominance) was negative and highly significant for Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. On the other

hand, the negative and significant value of j was observed in SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 2 × SAU Sarisha 3.

The value of l was positive and highly significant for Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 2 and SAU Sarisha 1 × SAU Sarisha 3. In the cross SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 2 × BARI Sarisha 6, the estimated value of l was positive and significant. The rest of the crosses showed insignificant dominance × dominance type of gene interaction.

Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect will produce new recombinants capable of improving the character. Therefore, the improving of this character could be achieved through hybrid breeding method.

4.4.9 Estimates of scaling test and gene action of 1000 seed weight

Scaling test

Scaling test for 1000 seed weight for the fifteen crosses is presented in the Table 23. The scale test results revealed that SAU Sarisha 2 × BARI Sarisha 15 and SAU Sarisha 3 × BARI Sarisha 15 was insignificant for all the scales where as Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2 and Tori 7 × SAU Sarisha 3 were showed significant score for these crosses. Only the C scales was positive and insignificant for Tori 7 × BARI Sarisha 6, SAU Sarisha 1× SAU Sarisha 2 and BARI Sarisha 6 × BARI Sarisha 15. On the contrary, the B scale was insignificant and negative in the cross Tori 7 × BARI Sarisha 15 where as the rest of the scales were highly significant. Both the cross SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 1 × BARI Sarisha 6, only the D scale was positive and insignificant. The D scale was highly significant and positive for both the crosses SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6. On the other hand, the scale B and C was significant for the crosses SAU Sarisha 1 × BARI Sarisha 15 and SAU Sarisha 2 × BARI Sarisha 6.

Table 23: Estimates of scaling test and gene effects for 1000 seed weight in different crosses of *Brassica rapa* L .

Cross	Scaling test			
	A	B	C	D
TORI 7 × SAU Sarisha 1	-1.15±0.24**	-1.10±0.23**	-1.31±0.41**	0.47±0.15**
TORI 7 × SAU Sarisha 2	-1.15±0.24**	-1.10±0.23**	-1.31±0.41**	0.47±0.15**
TORI 7 × SAU Sarisha 3	0.83±0.18**	-0.54±0.19**	-1.96±0.30**	-0.29±0.13*
TORI 7 × BARI Sarisha 6	-0.84±0.18**	-0.43±0.17*	0.14±0.31	0.71±0.14**
TORI 7 × BARI Sarisha 15	1.19±0.19**	-0.20±0.20	-2.04±0.30**	-0.33±0.12**
SAU Sarisha 1 × SAU Sarisha 2	-0.58±0.20**	-0.81±0.22**	0.11±0.42	0.75±0.16**
SAU Sarisha 1 × SAU Sarisha 3	-0.90±0.21**	-1.03±0.21**	-1.55±0.29**	0.19±0.16
SAU Sarisha 1 × BARI Sarisha 6	-0.90±0.21**	-1.03±0.21**	-1.55±0.29**	0.19±0.16
SAU Sarisha 1 × BARI Sarisha 15	0.02±0.17	-0.77±0.17**	1.33±0.22**	0.27±0.14
SAU Sarisha 2 × SAU Sarisha 3	-0.72±0.22**	-0.21±0.22	-0.20±0.35	0.37±0.14**
SAU Sarisha 2 × BARI Sarisha 6	0.27±0.17	-0.61±0.16**	-0.66±0.31*	-0.16±0.12
SAU Sarisha 2 × BARI Sarisha 15	0.04±0.20	-0.02±0.22	-0.55±0.36	-0.24±0.14
SAU Sarisha 3 × BARI Sarisha 6	-0.19±0.21	-0.24±0.24	1.19±0.41**	0.81±0.13**
SAU Sarisha 3 × BARI Sarisha 15	-0.03±0.22	0.11±0.23	-0.29±0.40	0.18±0.14
BARI Sarisha 6 × BARI Sarisha 15	0.95±0.33**	0.86±0.32**	0.30±0.39	-0.76±0.25**

Cross	Gene effect							
	m	d	h	i	j	l	Epistatic gene action	Comments
TORI 7 × SAU Sarisha 1	3.64±0.05**	0.08±0.10	-0.96±0.34**	-0.94±0.29**	-0.02±0.11	3.19±0.58**	Duplicate	Dominant decreasers
TORI 7 × SAU Sarisha 2	3.64±0.05**	0.08±0.10	-0.95±0.34**	-0.94±0.29**	-0.02±0.11	3.19±0.58**	Duplicate	Dominant decreasers
TORI 7 × SAU Sarisha 3	3.39±0.04**	-0.01±0.09	0.41±0.28	0.58±0.25*	-0.14±0.10	0.79±0.46	Complementary	Dominant increasers
TORI 7 × BARI Sarisha 6	3.99±0.05**	-0.05±0.09	-1.40±0.30**	-1.41±0.28**	-0.20±0.10	2.69±0.47**	Duplicate	Dominant decreasers
TORI 7 × BARI Sarisha 15	3.34±0.03**	-0.13±0.09	0.87±0.27**	0.65±0.23**	-0.49±0.10**	0.72±0.47	Complementary	Dominant increasers
SAU Sarisha 1 × SAU Sarisha 2	3.75±0.06**	0.13±0.08	-1.75±0.35**	-1.50±0.32**	0.11±0.10	2.89±0.55**	Duplicate	Dominant decreasers
SAU Sarisha 1 × SAU Sarisha 3	3.44±0.05**	-0.46±0.07**	0.08±0.34	-0.36±0.26	-0.55±0.09**	2.97±0.57**	Complementary	Dominant increasers
SAU Sarisha 1 × BARI Sarisha 6	3.61±0.04**	0.10±0.12	-0.05±0.33	-0.38±0.31	0.06±0.13	2.32±0.57**	Duplicate	Dominant decreasers
SAU Sarisha 1 × BARI Sarisha 15	3.80±0.04**	-0.12±0.10	-0.82±0.29**	-0.53±0.28	-0.37±0.11**	-0.25±0.48	Complementary	Dominant decreasers
SAU Sarisha 2 × SAU Sarisha 3	3.63±0.04**	-0.18±0.10	-0.90±0.31**	-0.73±0.27**	-0.25±0.12*	1.66±0.54**	Duplicate	Dominant decreasers
SAU Sarisha 2 × BARI Sarisha 6	3.56±0.04**	0.38±0.06**	0.26±0.26	0.31±0.23	0.43±0.09**	0.02±0.41	Complementary	Dominant increasers
SAU Sarisha 2 × BARI Sarisha 15	3.61±0.05**	0.15±0.09	0.91±0.32**	0.48±0.28	-0.01±0.11	-0.41±0.53	Duplicate	Dominant increasers
SAU Sarisha 3 × BARI Sarisha 6	3.97±0.04**	0.24±0.09**	-1.44±0.31**	-1.62±0.25**	0.02±0.10	2.05±0.55**	Duplicate	Dominant decreasers
SAU Sarisha 3 × BARI Sarisha 15	3.63±0.05**	0.07±0.10	0.69±0.34*	0.37±0.29	-0.07±0.11	-0.45±0.57	Duplicate	Dominant increasers
BARI Sarisha 6 × BARI Sarisha 15	3.83±0.07**	0.19±0.20	1.79±0.51**	1.51±0.49**	0.04±0.21	-3.32±0.89**	Duplicate	Dominant increasers

*P<0.05, **P<0.01 respectively. All the numerical data contain gene effect + standard error, m=mean, d= additive effect, h= dominance effect, i= additive × additive type gene interaction, j= additive × dominance type gene interaction and l= dominance × dominance type gene interaction

Gene action

The highly significant effect of parameter m was found for yield per plant in all the crosses. Initially, it is clear that all studied traits were quantitatively inherited.

The estimated d (additive component) was negative and highly significant for SAU Sarisha 1 × SAU Sarisha 3 but the positive and highly significant value of d was found in SAU Sarisha 2 × BARI Sarisha 6 and SAU Sarisha 3 × BARI Sarisha 6. The rest of the crosses showed insignificant result.

Significant and positive value of h was obtained in Tori 7 × BARI Sarisha 15, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. On the other hand, highly significant and negative value of dominance effect was found in Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × BARI Sarisha 15, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6.

With regards to the additive × additive type gene interaction, the significant and positive effect was found in Tori 7 × SAU Sarisha 3, Tori 7 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15.

Meanwhile, the significant and negative value of i was observed in Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6.

The estimated j(additive × dominance) was negative and significant for Tori 7 × BARI Sarisha 15, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 15 and SAU Sarisha 2 × SAU Sarisha 3. The only cross SAU Sarisha 2 × BARI Sarisha 6 showed positive and highly significant additive × dominance type of gene interaction.

The value of l was positive and highly significant for Tori 7 × SAU Sarisha 1, Tori 7 × SAU Sarisha 2, Tori 7 × BARI Sarisha 6, SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × SAU Sarisha 3 and SAU Sarisha 3 × BARI Sarisha 6. The only cross BARI Sarisha 6 × BARI Sarisha 15 showed negative and highly significant dominance × dominance type of gene interaction.

Opposite marks in the estimated values of effects (-h) and (+l) indicated duplicate epistasis but dominant decreasers which is not favorable since it decreases the value of dominant genes effect. On the other hand, the same marks in the estimated values of (+h and +l) or (-h and -l) indicated complementary epistasis. The complementary effect will produce new recombinants capable of improving the character. Therefore, the improving of this character could be achieved through hybrid breeding method.

4.5 Heritability and Genetic advance

The heritability estimates for different characters depend on the genetic makeup of the breeding materials studied. Therefore, knowledge about these values in the materials breeders' interest is of great significance. High heritability will be effective beinSg less influenced by environmental useful in indicating the relative value of selection based on phenotypic expression of different characters. Johnson *et al*. (1955) impressed that heritability values along with estimates of genetic gain were more useful than heritability alone in predicting the effect of selection. Moderately high heritability estimates associated with high genetic advance and moderate genetic gain indicated the possibility of additive genes effect for the expression of the character, therefore selection for this character would be more effective. Moderate heritability with high genetic advance and genetic gain indicated that the character was governed by additive gene and selection for this character would also be effective. Moderate heritability along with moderate genetic gain indicated that the character was influenced by environmental effect and selection for such trait might not be rewarding (Uddin *et al*. 2013).

Heritability estimates and genetic potential studies of genotypes in terms of their expression for yield and seed quality traits are very much important for selection of best lines for successful and upcoming breeding programs (Junaid *et al*. 2014). In order to estimate the selection effects, heritability along with selection response is much more useful than the heritability alone. In the present study broad sense heritability and expected response to selection and its percentage for yield and yield contributing traits were determined. The broad and narrow sense heritability and expected genetic gain and its

Table 24: Estimation of broad sense heritability of different morphological characters of *Brassica rapa* L. genotypes

Character	Broad sense heritability (%)														
	P1×P2	**P1×P3**	**P1×P4**	**P1×P5**	**P1×P6**	**P2×P3**	**P2×P4**	**P2×P5**	**P2×P6**	**P3×P4**	**P3×P5**	**P3×P6**	**P4×P5**	**P4×P6**	**P5×P6**
PH	87.61	87.61	70.98	64.86	92.87	44.52	93.73	97.52	99.93	80.06	56.55	90.53	93.61	87.40	99.86
PB	69.61	69.61	97.91	92.72	94.54	80.13	79.06	94.17	89.88	74.76	85.60	89.40	67.57	88.73	59.95
NSP	77.45	77.45	85.02	91.18	91.52	66.65	61.16	98.36	89.07	58.01	76.04	80.82	98.63	64.90	75.96
NSS	50.83	64.91	83.87	34.79	77.60	67.67	34.57	60.29	85.25	77.39	81.02	89.11	89.71	72.83	42.00
LS	58.06	58.06	99.83	82.53	76.19	82.40	69.42	69.29	85.50	71.54	80.55	70.09	55.55	77.95	95.21
DF	91.86	99.77	99.21	67.36	94.14	85.61	75.85	74.10	23.00	63.59	87.47	81.01	82.51	85.08	70.59
DM	89.04	99.99	98.94	98.77	97.78	98.96	79.15	99.42	87.66	65.78	86.79	56.99	50.91	49.43	6.64
YP	51.86	51.76	84.01	94.22	82.10	76.70	70.56	97.10	98.18	77.37	78.67	63.54	95.02	58.62	63.38
1000SW	73.91	73.91	82.50	80.00	89.61	88.37	79.34	98.47	97.39	86.25	84.90	56.52	63.63	59.37	97.92

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight

the hybrid P2×P3 showed medium heritability (44.52%). The hybrid P2×P4 and P5×P6 demonstrated medium heritability for number of seeds per siliqua. The figure was 34.57% and 42%, respectively. On the other hand, medium heritability (49.43%) was observed in P4×P6 considering the character days to maturity. Low heritability was observed in the hybrid P2×P6 (23%) for days to 50% flowering and P5×P6 (6.64%) for days to maturity. The highest heritability was recorded by days to maturity (99.99%) in the hybrid P1×P3 followed by plant height (99.93%) in P2×P6 and length of siliqua (99.83%) in P1×P4. Broad sense heritability estimates ranged from 99.99% to 6.64% for all mentioned traits.

In the cross P1×P2, length of siliqua showed high (58.06%) narrow sense heritability with very low genetic gain (0.65). Medium narrow sense heritability and medium genetic gain was observed in days to maturity i.e. 39.49% and 10.83, respectively. A trait having high heritability and high genetic advance is considered under control of additive genes which highlights the usefulness of plant selection based on phenotypic performance.

In the cross P1×P3, length of siliqua showed high (58.06%) narrow sense heritability with very low genetic gain (0.65). On the other hand, moderate narrow sense heritability was found in days to maturity (50%) and yield per plant (49.04%) whereas days to maturity and yield per plant demonstrated moderate (11.59) and low (4.02) genetic gain, respectively.

In the cross P1×P4, primary branches per plant showed high narrow sense heritability (51.84%) along with moderate genetic gain (12.82). Moderate narrow sense heritability was calculated in number of siliqua per plant (40.22%), number of seed per siliqua (30.40%), length of siliqua (33.22%), days to maturity (47.29%) and yield per plant (38.33%). The high and low genetic gain was observed in number of siliqua per plant (304.37) and yield per plant (7.85), respectively.

In the cross P1×P5, the highest narrow sense heritability was found in days to maturity (54.52%) followed by number of primary branches per plant (39.75%) and days to 50% flowering (39.04%). On the other hand, the highest genetic gain was observed in number of siliqua per plant (360.14).

In the cross P1×P6, the high narrow sense heritability (65.81%) and the low genetic gain (8.19) was observed in number of primary branches per plant. Moderate narrow sense heritability was demonstrated in number of siliqua per plant (36.65%), days to 50% flowering (37.60%), days to maturity (47.75%) and yield per plant (40.24%). On the other hand, length of siliqua demonstrated the lowest narrow sense heritability. Genetic gain was the highest 396.55 for number of siliqua per plant.

In the cross P2×P3, no hybrid combinations showed the high narrow sense heritability. The highest narrow sense heritability was observed in days to maturity (49.21%) with high genetic gain (41.74). The highest genetic gain was observed in number of siliqua per plant (155.53).In the cross P2×P4, moderate narrow sense heritability (45.96%) and the high expected genetic gain (144.84) was observed in number of siliqua per plant. Days to 50% flowering and yield per plant demonstrated moderate narrow sense heritability along with low expected genetic gain i.e. (46.40%, 4.49) and (42.51%, 4.57), respectively.

In the cross P2×P5, days to 50% flowering showed high narrow sense heritability (51.39%) along with low expected genetic gain (8.75). On the other hand, number of siliqua per plant showed the high genetic gain (695.61) along with moderate narrow sense heritability (34.40%).

In the cross P2×P6, the high narrow sense heritability (49.35%) along with high expected genetic gain (311.80) was observed in plant height. On the other hand, the high expected genetic gain (239.82) along with low narrow sense heritability (7.45%) was in number of siliqua per plant. In the cross P3×P4, the high narrow sense heritability (58.79%) along with low expected genetic gain (3.15) was observed in number of primary branches per plant. On the other hand, the high expected genetic gain (122.06) along with low narrow sense heritability (11.53%) was observed in number of siliqua per plant.

In the cross P3×P5, the high expected genetic gain (123.74) along with low narrow sense heritability (23.33%) was observed in number of siliqua per plant. Days to maturity showed medium narrow sense heritability (41.29%) along with low expected genetic gain (9.79).

Table 25: Estimation of narrow sense heritability of different morphological characters of *Brassica rapa* L. genotypes

Character	Narrow sense heritability (%)														
	P1×P2	**P1×P3**	**P1×P4**	**P1×P5**	**P1×P6**	**P2×P3**	**P2×P4**	**P2×P5**	**P2×P6**	**P3×P4**	**P3×P5**	**P3×P6**	**P4×P5**	**P4×P6**	**P5×P6**
PH	25.49	25.49	5.02	0.90	21.61	11.95	26.35	31.20	49.35	4.33	11.61	35.47	27.96	38.14	50.08
PB	20.44	20.44	51.84	39.75	65.81	43.76	3.24	25.84	35.51	58.79	26.01	24.93	19.14	24.44	44.46
NSP	16.49	16.49	40.22	33.91	36.65	48.03	45.96	34.40	7.45	11.53	23.33	39.77	26.02	4.80	2.40
NSS	7.22	19.47	30.40	2.19	22.13	21.91	4.14	18.00	32.19	41.98	36.55	21.04	32.00	30.82	7.36
LS	58.06	58.06	33.22	20.63	0.00	30.55	17.35	28.30	33.33	1.62	13.88	12.14	16.66	2.60	33.51
DF	39.49	26.73	5.59	39.04	37.60	49.17	46.40	51.39	16.63	3.70	21.67	47.30	10.34	26.32	28.89
DM	27.79	50.00	47.29	54.52	47.75	49.21	24.95	49.39	32.19	11.09	41.29	10.18	32.53	5.98	6.32
YP	49.08	49.04	38.33	35.33	40.24	42.73	42.51	27.74	25.67	36.64	26.68	19.13	29.74	23.54	5.00
1000SW	21.73	21.73	20.00	36.66	32.46	46.51	17.39	32.60	23.47	32.50	37.73	0.00	33.33	18.75	28.36

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight

In the cross P3×P6, the lowest narrow sense heritability was observed in 1000 seed weight. In this hybrid, no characters showed high narrow sense heritability. The high expected genetic gain (213.61) was demonstrated for number of siliqua per plant. The poor narrow sense heritability along with poor genetic gain suggested that these characters were predominately controlled by non-additive gene action.

In the cross P4×P5, the low narrow sense heritability along with high expected genetic gain was observed in plant height (27.96%, 40.82) and number of siliqua per plant (26.02%, 353.06). Narrow sense heritability was poor which resulted due to low fixable genetic variance.

In the cross P4×P6, no characters showed high narrow sense heritability. High expected genetic gain (146.47) along with very low narrow sense heritability (4.80) was observed in number of siliqua per plant. In this hybrid, plant height showed high broad sense heritability along with considerable narrow sense heritability indicated the presence of additive gene action for controlling the character.

In the cross P5×P6, the high narrow sense heritability (50.08%) along with high expected genetic gain (236.04) was observed in plant height that indicated additive effects. On the other hand, the low narrow sense heritability (2.40%) along with high expected genetic gain (317.11) was observed in number of siliqua per plant. High narrow sense heritability with high expected genetic gain shows better selection in early segregating generations leading to substantial improvement of the character. In this hybrid, yield per plant showed high broad sense heritability but the narrow sense heritability was poor which might be due to presence of non allelic interaction and sampling for this character.

Hussain *et al*. (1998) observed high estimates for heritability and genetic advance for number of secondary branches, biological yield per plant, 1000-seed weight, plant height and number of seeds per plant. Das *et al*. (1998) also noted high heritability coupled with high genetic advance for siliquae per plant, number of secondary branches per plant, 1000-seed weight and plant height. Larik and Rajput (2000) estimated low genetic advance for

Table 26: Estimation of expected genetic gain of different morphological characters of *Brassica rapa* L. genotypes

Character	Expected genetic gain (k=2.06)														
	P1×P2	**P1×P3**	**P1×P4**	**P1×P5**	**P1×P6**	**P2×P3**	**P2×P4**	**P2×P5**	**P2×P6**	**P3×P4**	**P3×P5**	**P3×P6**	**P4×P5**	**P4×P6**	**P5×P6**
PH	29.85	29.85	13.03	13.23	35.76	6.85	34.06	63.64	311.80	47.41	9.15	43.62	40.82	40.89	236.04
PB	3.31	3.31	12.82	5.15	8.19	4.84	3.82	8.21	5.20	3.15	3.46	6.41	5.72	6.29	2.68
NSP	344.01	344.01	304.37	360.14	396.55	155.53	144.84	695.61	239.82	122.06	123.74	213.61	353.06	146.47	317.11
NSS	3.90	5.91	10.07	1.89	6.97	6.04	1.87	4.54	8.75	6.34	5.45	9.18	8.94	6.57	2.98
LS	0.65	0.65	15.07	1.33	0.70	1.73	1.56	1.02	1.45	1.60	2.20	1.48	0.47	3.53	2.68
DF	7.27	21.04	10.01	6.83	9.75	6.68	4.49	8.75	1.62	6.25	9.19	6.85	11.92	12.27	4.03
DM	10.83	11.59	10.55	8.92	11.52	41.74	7.38	32.73	9.46	4.78	9.79	3.58	2.39	2.66	0.27
YP	4.02	4.02	7.85	13.41	7.41	5.47	4.57	2.61	11.99	5.86	5.46	4.62	11.01	4.14	4.51
1000SW	1.00	1.00	1.06	0.88	1.59	1.66	1.54	17.30	2.13	1.57	1.24	0.54	0.73	0.68	4.37

Here, PH = Plant height, PB = Number of primary branches per plant, SB = Number of secondary branches per plant, NSP = Number of siliquae per plant, NSS = Number of seeds per siliqua, LS = Length of siliqua, DF = Days to 50% flowering, DM = Days to 80% maturity, YP = Yield per plant and SW = Seed weight

dry matter yield, seeds per siliqua and plant height irrespective of their high heritability. Shalini *et al*. (2001) found that the values for heritability and genetic gain were moderate to high for 1000-seed weight, number of silliquae per plant and number of secondary branches per plant. Khan *et al*. (1992), Mahmood *et al*. (2003), Akbar *et al*. (2007), Kumar *et al*. (2007) Sheetal *et al*. (2007) and Acharya and Pati (2008) also presented supporting results to the present findings. However, contradictions in results for some traits might de due to differences in genetic material studied or due to different environmental conditions under which experiments were conducted.

CHAPTER 5
SUMMARY AND CONCLUSION

The investigation on *Brassica rapa* genotypes was an attempt to generate genetic variation through hybridization and obtained genetic information on yield and its contributing attributes for different generations at the experimental farm of Sher-e-Bangla Agricultural University during October, 2010 to March, 2013. Six parents (TORI 7, SAU Sarisha 1, SAU Sarisha 2, SAU Sarisha 3, BARI Sarisha 6, BARI Sarisha 15) and half diallel cross hybrids were evaluated for estimating the different genetic parameters viz. variability, combining ability effects, generation mean analysis, heterosis, inbreeding depression, heritability and genetic advance. The parents were crossed in all possible combinations under half diallel fashion through hand emasculations and controlled pollinations in winter season 2010-11 to produce F_1 seed. The 15 F_1 hybrids along with their parents were sown in randomized complete block design with three replications during next crop season 2011-12. During the same crop season, thousand of hybridization was done to generate F_1, F_2 generation, back cross generations i.e, BC_1 and BC_2. The seeds of six parents, F_1, F_2, BC_1 and BC_2 were sown during crop season 2012-13. Data was recorded for plant height, primary branches per plant, secondary branches per plant, siliquae per plant, seeds per siliqua, Siliqua length, days to 50% flowering, days to 80% maturity, seed yield per plant,1000-seed weight and oil content percentage.

The results suggested the presence of inherent genetic differences with respect of various traits among the genotypes which can be exploited through selection. The life span of the parent SAU Sarisha 3 was the lowest but the yield was moderate considering the other parents. On the other hand, the highest yield and 1000-seed weight was noticed in TORI 7 and its 80% maturity was observed in 81 days. In case of hybrids, the lowest duration of 80% maturity was found in 79 days in SAU Sarisha 3 X TORI 7. On the other hand, the highest yield per plant and 1000-seed weight was observed in BARI Sarisha 6 X SAU Sarisha 2 and BARI Sarisha 6 X SAU Sarisha 1, respectively. Considering the yield contributing attributes, TORI 7 was the best parent followed by SAU Sarisha 1, SAU

Sarisha 2 and SAU Sarisha 3 and TORI Sarisha 6 X SAU Sarisha 1 was the best hybrid combination followed by BARI Sarisha 6 X SAU Sarisha 1 and BARI Sarisha 6 X TORI 7.

The ANOVA carried out for ten characters which indicated that the genotypes are differed significantly for all the characters under studied except plant height, number of siliquae per plant and 1000 seed weight. Parents and crosses showed highly significant variances for days to 50% flowering and days to 80% maturity. Parents demonstrated highly significant variances for primary branches per plant and cross noticed highly significant variances for secondary branches per plant, number of seed per siliquae and length of siliquae. Variances due to parent vs cross interaction was also observed highly significant for most of the traits except plant height, days to 50% flowering and yield per plant. The mean sum of square due to GCA was significant for all the traits except number of siliqua per plant, yield per plant and 1000 seed weight indicating that the additive gene action was predominant for the expression of these characters. The significant mean sum of square due to SCA was found for number of primary branches per plant, number of seed per siliqua, length of siliqua, days to 50% flowering and days to 80% maturity indicating that the non-additive gene actions were predominant for the expression of these characters. The higher magnitude of GCA variance was observed than that of SCA variance for all the traits under study except length of siliqua.

The D and H components which measure additive and dominance variation respectively were significant for all the traits under study suggesting the importance of both additive and dominance components for the inheritance of all the traits in *B. rapa*. However, the magnitude of dominance was higher than the additive component for all the traits except for primary branches per plant, number of seeds per siliqua, days to 50% flowering and days to 80% maturity which indicated that dominance component had a predominant role in the inheritance of these traits. The H_2 representing dominance deviation due to relative frequency of positive and negative genes was significant for all the characters. The h^2 was highly significant for all the studied characters implied that substantial contribution of dominance effects was due to heterogeneity of the loci in all the characters.

Primary branches per plant, secondary branches per plant, days to 80% maturity, yield per plant and 1000-seed weight 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, plant height, number of siliquae per plant, number of seeds per siliqua, length of siliqua and days to 50% flowering exhibited the values in negative direction, implying the excess of recessive gene for these traits. Positive F value for primary branches per plant, days to 50% flowering, days to 80% maturity and yield per plant indicated the high frequency of dominant alleles governing these characters. Negative F value for days to flowering, plant height, secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, length of siliqua and 1000-seed weight exhibited a preponderance of recessive alleles. "E" exhibited highly significant values for all the traits, indicating the influence of environmental factors in the expression of those traits. The magnitude of E for each character was much higher than the respective value of D and H_1 except days to 50% flowering and days to 80% maturity indicating that the characters were influenced much by the environment. The average degree of dominance $(H_1/D)^{0.5}$ was more than unity, suggesting that over dominance was operating in the expression for most of the components of yield. 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 greater than 0.25 for all the characters except number of siliquae per plant studied suggested asymmetrical distribution of alleles. Most of the characters presently studied indicated equal distribution of positive and negative alleles. The estimated numbers of effective factors (h^2/H_2) were less than unity for all oil yielding attributes except for length of siliqua. 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. Heritability in narrow sense was higher for length of siliqua, yield per plant and 1000 seed weight indicating these characters were more or less heritable.

Regression line intersected the Wr-axis below the origin for all the characters except yield per plant 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 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 seed yield in the present study has also been substantiated by the findings of Singh *et al.* (1970, 1971) in *B. campestris*, Rawat (1975) in *B. juncea*, and Trivedi and Mukharjee (1985) in *B. juncea*, Chowdhury *et al*. (2004b) in *B. rapa*.

As non-fixable variation was high for all the attributes except yield per plant, 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.

Analysis of variance and generation mean analysis to derive information on the relative importance of additive effects, dominance deviations and epistasis. Partitioning of epistatic effects was carried out through this technique. Various genetic components of generation mean were estimated with the help of six parameter model presented by Hayman (1958). Significance and non significance of scaling tests indicated presence of digenic epistasis for the trait indicated the absence of non-allelic interactions, respectively. In plant height the highly significant negative scale A was observed for SAU Sarisha 1 × SAU Sarisha 2,

SAU Sarisha 1 × SAU Sarisha 3, SAU Sarisha 2 × SAU Sarisha 3, SAU Sarisha 3 × BARI Sarisha 6 and BARI Sarisha 6 × BARI Sarisha 15 and all the crosses (except SAU Sarisha 1 × BARI Sarisha 6) the contribution of dominance effect is greater than additive effect. There was no evidence of non-allelic interaction for the character plant height which agreed with the conclusion from individual scaling test results. For the remaining crosses at least one of the two (i and l) interaction parameters were significantly different from zero.

In case of primary branches the dominance × dominance effects were greater in magnitudes that additive × additive and additive × dominance in all cases which recorded non-allelic interaction except in the crosses of TORI 7 × BARI Sarisha 6, SAU Sarisha 1 × BARI Sarisha 6, SAU Sarisha 2 × BARI Sarisha 15, SAU Sarisha 3 × BARI Sarisha 15 and BARI Sarisha 6 × BARI Sarisha 15. The dominant gene action for seeds per siliqua indicated the usefulness hybrid program of rapeseed. The highly significant effect of m was found for days to 50% flowering in all the crosses. Only A scale was positive and highly significant in BARI Sarisha 6 × BARI Sarisha 15. In the cross SAU Sarisha 1 × SAU Sarisha 2, SAU Sarisha 1 × SAU Sarisha 3 and SAU Sarisha 2 × BARI Sarisha 6 the scale A was highly significant and negative where as both the scale B and C was highly significant and negative for the same crosses for the trait yield per plant. In case of 1000 seed weight TORI 7 × SAU Sarisha 1, TORI 7 × SAU Sarisha 2 and TORI 7 × SAU Sarisha 3 were showed significant score in scaling test.

Early flowering and maturity type genotypes in *Brassica* is preferred over late flowering and maturing because earliness might certainly help to get early maturing lines that could not only tolerate or escape heat stress but could also provide sufficient time for the cultivation of next crop. In addition it would help to reduces losses occurred due to shattering that would ultimately enhance yields. Keeping in view the importance of early flowering and maturity and shorter plant height, emphasis was focused on negative heterosis for these characteristics (Turi *et al*., 2006). Significant and negative heterosis for 50% flowering was observed in the hybrid P1×P4 and P2×P6 considering the better parent. On the other hand, there was no cross combinations expressed significant negative heterosis over mid parent. Crosses showing significant negative values suggested that these crosses could be used to develop new early maturing lines. Hybrid P2×P5 expressed

significant negative better parent heterosis on plant height. None of the hybrids showed significant negative heterosis over mid parent for the trait except P4×P6 (significant and positive heterosis). Hybrid demonstrated significant negative value suggested that P2×P5 could be used to develop short stature of plant. Significant negative heterosis over better parent for days to 80% maturity was found in the hybrid P1×P3, P1×P5 and P1×P6. None of the hybrids showed significant negative heterosis over mid parent for the trait.

Positive heterosis for number of primary branches is desirable, because plants with vigorous stature containing more branches provided opportunity for higher yields. The presence of significantly positive heterosis for branches per plant in F_1 crosses indicates the potential of their use for developing high-yielding genotypes. The presence of high levels of better and mid parent heterosis indicates a considerable potential to embrace on breeding of hybrid cultivars in *B. rapa*. P4×P5 and P2×P6 showed highly significant positive and negative heterosis over better and mid parent, respectively. Hybrid P4×P5 could be used to develop more branches in rape seed. P2×P6 showed significant positive heterosis over better on number siliquae per plant. On the other hand, P3×P5, P3×P6 and P4×P6 expressed significant positive heterosis considering mid parent for the trait. P3×P6 showed the best performance on heterosis considering both the parents. So, the hybrid P3×P6 found the best to develop more number of siliquae per plant.

None of the hybrids showed significant positive heterosis considering better and mid parent for number of seeds per siliqua and length of siliqua. So, none of the hybrids could be well fit to develop more number of seeds per siliqua and tall siliqua length. P4×P6 showed significant positive heterosis on mid parent only for yield per plant and 1000 seed weight. P2×P5, P3×P4 and P4×P6 (0.45) showed highly significant positive heterosis for better parent and P2×P4 showed significant positive heterosis over mid parent for oil content percentage. So, this cross combination is important for developing high yielding *B. rapa* genotypes. From the present study the high yielding cross combinations can be utilized in future breeding programmes for developing high yielding genotypes; parents used in developing heterotic hybrids shall be converted to well adapted cytoplasmic male sterile or restorer lines.

Higher estimates for heritability and genetic advance for a certain trait indicate its excellent potential for use in future breeding programs. High broad sense heritability estimates were observed for all the traits. Maximum heritability value was noticed for days to 80% maturity in P1×P3 (99.99%) followed by plant height in P2×P6 (99.93%), siliqua length in P1×P4 (99.83%) and days to 50% flowering in P1×P3 (99.77%). Broad sense heritability estimates ranged from 99.99% to 6.64% for all mentioned traits. In the cross P1×P6, Number of primary branches showed high (65.81%) narrow sense heritability followed by length of siliqua (58.06%) in P1×P2 and days to 50% flowering (51.39%) in P2×P5. Narrow sense heritability estimates ranged from 65.81% to 0.90% for all mentioned traits.
The estimates for genetic advance were moderate to high for all the traits. The lowest value was noted for days to maturity in P5×P6 (0.27%) while the highest value was found for Number of seed per plant (695.61) in P2×P5 followed by plant height (311.80) in P2×P6. High values for heritability and genetic advance for various traits indicated good genetic potential for selection. A trait having high heritability and high genetic advance is considered under control of additive genes which highlights the usefulness of plant selection based on phenotypic performance.

The main conclusions drawn from present work were as follows:

The results of present studied indicated that from the developed segregating generations, combinations have been identified for the breeding of early maturing, high yielding and information regarding genetic control of all these traits were derived simultaneously from same genetic material. Considering the yield contributing traits, the parent TORI 7 was the best parent and BARI Sarisha 6 × SAU Sarisha 1 was the best hybrid combination. The hybrid TORI 7 × SAU Sarisha 3 showed significant negative values for 50% flowering and high yield suggested that these crosses could be used to developed new early maturing lines.

Gene action and type of epistasis involved in *Brassica rapa* genotypes were estimated, which might be useful for other researchers.

RECOMMENDATION

The following recommendations can be made for future research:

1. Plants selected from F_2 populations may be grown for further generations to select promising plants if any.

2. Hybrids may be evaluated further for identifying the best specific combiners for yield as well as shorter duration.

3. More backcrosses can be carried out to develop short duration variety with higher yield potential.

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APPENDICES

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

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

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

Appendix II. A. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from October, 2010 to April, 2011

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
October, 2010	34.8	18.0	77	227	5.8
November, 2010	32.3	16.3	69	0	7.9
December, 2010	29.0	13.0	79	0	3.9
January, 2011	28.1	11.1	72	1	5.7
February, 2011	33.9	12.2	55	1	8.7
March, 2011	34.6	16.5	67	45	7.3
April, 2011	35.8	20.3	65	88	8.3

Source: Bangladesh Metrological Department (Climate division), Agargaon, Dhaka-1212.

Appendix II. B. Monthly average temperature, relative humidity and total rainfall of the experimental site during the November 2011 to February 2012

Month	Air temperature (°c)		Relative humidity (%)	Total Rainfall (mm)
	Maximum	Minimum		
November, 2011	28.1	6.88	15.6	58.18
December, 2011	28.1	6.88	15.6	58.18
January, 2012	25.36	6.12	0.62	54.3
February, 2012	25.0	12	18	46

Source: Weather station, Sher-e-Bangla Agricultural University, Dhaka-1207.

Appendix II. C. Monthly average temperature, relative humidity and total rainfall of the experimental site during the November 2012 to February 2013

Month	Air temperature (°C)		Relative humidity (%)	Total rainfall (mm)
	Maximum	Minimum		
November, 2012	29.1	6.58	16.6	59.10
December, 2012	28.1	6.78	15.75	57.88
January, 2013	26.11	6.12	0.72	54.3
February, 2013	26.50	11	18	46

Source: Weather station, Sher-e-Bangla Agricultural University, Dhaka-1207.

Appendix III.

Table A: Analysis of variance for plant height in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	53.79	17.93
	Generation	3	145.86	72.93
	Error	6	109.02	18.17
Tori 7 × SAU 2	Replication	2	32.01	10.67
	Generation	3	168.10	84.05
	Error	6	910.54	151.75
Tori 7 × SAU 3	Replication	2	138.15	46.05
	Generation	3	184.83	92.41
	Error	6	644.51	107.41
Tori 7 × BARI 6	Replication	2	180.47	60.15
	Generation	3	1450.28	725.14
	Error	6	1048.29	174.71
Tori 7 × BARI 15	Replication	2	28.77	9.59
	Generation	3	578.28	289.14
	Error	6	1150.99	191.83
SAU 1 × SAU 2	Replication	2	665.58	221.86
	Generation	3	1706.19	853.09
	Error	6	149.48	24.91
SAU 1 × SAU 3	Replication	2	343.07	114.35
	Generation	3	1057.81	528.90
	Error	6	210.85	35.14
SAU 1× BARI 6	Replication	2	238.32	79.44
	Generation	3	845.73	422.86
	Error	6	421.74	70.29
SAU 1× BARI 15	Replication	2	26.52	8.84
	Generation	3	198.50	99.25
	Error	6	552.44	92.07
SAU 2 × SAU 3	Replication	2	35.88	11.96
	Generation	3	88.43	44.21
	Error	6	727.81	121.30
SAU 2 × BARI 6	Replication	2	301.61	100.53
	Generation	3	675.62	337.81
	Error	6	492.34	82.05
SAU 2 × BARI 15	Replication	2	1097.61	365.87
	Generation	3	347.39	173.69
	Error	6	595.85	99.30
SAU 3 × BARI 6	Replication	2	30.14	10.04
	Generation	3	671.69	335.84
	Error	6	1130.15	188.35
SAU 3 × BARI 15	Replication	2	154.43	51.47
	Generation	3	483.66	241.83
	Error	6	285.06	47.51
BARI 6 × BARI 15	Replication	2	349.47	116.49
	Generation	3	859.42	429.71
	Error	6	379.99	63.33

,** significant at 5% probability level; *,** significant at 1% probability level.

Table B: Analysis of variance for primary branches per plant in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	5.51	1.83
	Generation	3	3.93	1.96
	Error	6	4.57	0.76
Tori 7 × SAU 2	Replication	2	5.81	1.93
	Generation	3	3.57	1.78
	Error	6	2.75	0.46
Tori 7 × SAU 3	Replication	2	0.82	0.27
	Generation	3	2.17	1.08
	Error	6	7.25	1.20
Tori 7 × BARI 6	Replication	2	0.07	0.02
	Generation	3	2.82	1.41
	Error	6	8.56	1.42
Tori 7 × BARI 15	Replication	2	2.96	0.98
	Generation	3	0.78	0.39
	Error	6	7.13	1.18
SAU 1 × SAU 2	Replication	2	1.68	0.56
	Generation	3	7.96	3.98
	Error	6	3.34	0.55
SAU 1 × SAU 3	Replication	2	0.22	0.07
	Generation	3	7.42	3.71
	Error	6	2.93	0.48
SAU 1× BARI 6	Replication	2	0.18	0.06
	Generation	3	8.00	4.00
	Error	6	20.16	3.36
SAU 1× BARI 15	Replication	2	1.55	0.51
	Generation	3	9.14	4.57
	Error	6	4.8	0.80
SAU 2 × SAU 3	Replication	2	0.04	0.01
	Generation	3	1.52	0.76
	Error	6	5.11	0.85
SAU 2 × BARI 6	Replication	2	1.28	0.42
	Generation	3	4.67	2.33
	Error	6	6.63	1.10
SAU 2 × BARI 15	Replication	2	4.01	1.33
	Generation	3	14.47	7.23
	Error	6	9.88	1.64
SAU 3 × BARI 6	Replication	2	1.50	0.50
	Generation	3	3.53	1.76
	Error	6	1.29	0.21
SAU 3 × BARI 15	Replication	2	0.95	0.31
	Generation	3	7.82	3.91
	Error	6	3.78	0.63
BARI 6 × BARI 15	Replication	2	0.21	0.07
	Generation	3	3.01	1.50
	Error	6	4.05	0.67

,** significant at 5% probability level; *,** significant at 1% probability level.

Table C: Analysis of variance for Number of siliqua per plant in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	35660.79	11886.93
	Generation	3	10710.79	5355.39
	Error	6	55378.20	9229.70
Tori 7 × SAU 2	Replication	2	27993.69	9331.23
	Generation	3	31272.19	15636.09
	Error	6	32847.40	5474.56
Tori 7 × SAU 3	Replication	2	8690.96	2896.98
	Generation	3	21654.04	10827.02
	Error	6	68678.90	11446.48
Tori 7 × BARI 6	Replication	2	6753.32	2251.10
	Generation	3	33237.57	16618.78
	Error	6	57422.07	9570.34
Tori 7 × BARI 15	Replication	2	20671.37	6890.45
	Generation	3	44282.45	22141.22
	Error	6	47231.56	7871.92
SAU 1 × SAU 2	Replication	2	4516.42	1505.47
	Generation	3	39040.03	19520.01
	Error	6	16275.71	2712.61
SAU 1 × SAU 3	Replication	2	6122.22	2040.74
	Generation	3	34336.80	17168.40
	Error	6	19862.14	3310.35
SAU 1× BARI 6	Replication	2	6454.99	2151.66
	Generation	3	43910.44	21955.22
	Error	6	13845.70	2307.61
SAU 1× BARI 15	Replication	2	9090.76	3030.25
	Generation	3	47013.52	23506.76
	Error	6	22604.77	3767.46
SAU 2 × SAU 3	Replication	2	18641.39	6213.79
	Generation	3	9084.21	4542.10
	Error	6	16798.13	2799.68
SAU 2 × BARI 6	Replication	2	3731.59	1243.86
	Generation	3	16257.49	8128.74
	Error	6	11115.80	1852.63
SAU 2 × BARI 15	Replication	2	942.76	314.25
	Generation	3	43459.85	21729.92
	Error	6	8053.17	1342.19
SAU 3 × BARI 6	Replication	2	1334.73	444.91
	Generation	3	2374.20	1187.10
	Error	6	2248.87	374.81
SAU 3 × BARI 15	Replication	2	5111.18	1703.72
	Generation	3	11056.45	5528.22
	Error	6	9225.81	1537.63
BARI 6 × BARI 15	Replication	2	18726.88	6242.29
	Generation	3	9193.84	4596.92
	Error	6	24300.78	4050.13

,** significant at 5% probability level; *,** significant at 1% probability level.

Table D: Analysis of variance for Number of seed per siliqua in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	0.74	0.24
	Generation	3	13.38	6.69
	Error	6	52.67	8.77
Tori 7 × SAU 2	Replication	2	15.77	5.25
	Generation	3	61.33	30.66
	Error	6	22.68	3.78
Tori 7 × SAU 3	Replication	2	33.98	11.32
	Generation	3	17.09	8.54
	Error	6	31.52	5.25
Tori 7 × BARI 6	Replication	2	34.80	11.60
	Generation	3	91.21	45.60
	Error	6	26.30	4.38
Tori 7 × BARI 15	Replication	2	3.41	1.13
	Generation	3	136.09	68.04
	Error	6	40.74	6.79
SAU 1 × SAU 2	Replication	2	0.61	0.20
	Generation	3	72.83	36.41
	Error	6	12.39	2.06
SAU 1 × SAU 3	Replication	2	11.57	3.85
	Generation	3	24.64	12.32
	Error	6	30.98	5.16
SAU 1× BARI 6	Replication	2	6.30	2.10
	Generation	3	117.99	58.99
	Error	6	38.06	6.34
SAU 1× BARI 15	Replication	2	44.15	14.71
	Generation	3	57.40	28.70
	Error	6	55.12	9.18
SAU 2 × SAU 3	Replication	2	20.49	6.81
	Generation	3	81.08	40.54
	Error	6	19.36	3.22
SAU 2 × BARI 6	Replication	2	16.41	5.47
	Generation	3	127.54	63.77
	Error	6	39.37	6.56
SAU 2 × BARI 15	Replication	2	0.40	0.13
	Generation	3	106.21	53.10
	Error	6	88.68	14.78
SAU 3 × BARI 6	Replication	2	1.23	0.41
	Generation	3	97.94	48.97
	Error	6	15.58	2.59
SAU 3 × BARI 15	Replication	2	4.57	1.52
	Generation	3	104.23	52.11
	Error	6	8.18	1.36
BARI 6 × BARI 15	Replication	2	32.03	10.67
	Generation	3	93.77	46.88
	Error	6	7.21	1.20

,** significant at 5% probability level; *,** significant at 1% probability level.

Table E: Analysis of variance for length of siliqua in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	0.30	0.10
	Generation	3	0.26	0.13
	Error	6	0.72	0.12
Tori 7 × SAU 2	Replication	2	0.58	0.19
	Generation	3	0.62	0.31
	Error	6	0.76	0.12
Tori 7 × SAU 3	Replication	2	2.18	0.72
	Generation	3	17.48	8.74
	Error	6	20.56	3.42
Tori 7 × BARI 6	Replication	2	0.86	0.28
	Generation	3	0.28	0.14
	Error	6	23.91	3.98
Tori 7 × BARI 15	Replication	2	1.27	0.42
	Generation	3	0.43	0.21
	Error	6	0.17	0.02
SAU 1 × SAU 2	Replication	2	0.13	0.04
	Generation	3	0.61	0.30
	Error	6	0.04	0.00
SAU 1 × SAU 3	Replication	2	4.17	1.39
	Generation	3	22.14	11.07
	Error	6	22.92	3.82
SAU 1× BARI 6	Replication	2	0.07	0.02
	Generation	3	0.18	0.09
	Error	6	0.14	0.02
SAU 1× BARI 15	Replication	2	0.32	0.10
	Generation	3	0.18	0.09
	Error	6	–0.03	-0.00
SAU 2 × SAU 3	Replication	2	5.20	1.73
	Generation	3	20.32	10.16
	Error	6	21.87	3.64
SAU 2 × BARI 6	Replication	2	8.55	2.85
	Generation	3	26.12	13.06
	Error	6	18.6	3.1
SAU 2 × BARI 15	Replication	2	13.33	4.44
	Generation	3	24.11	12.05
	Error	6	55.48	9.24
SAU 3 × BARI 6	Replication	2	0.03	0.01
	Generation	3	0.58	0.29
	Error	6	0.33	0.05
SAU 3 × BARI 15	Replication	2	0.06	0.02
	Generation	3	0.83	0.41
	Error	6	0.25	0.04
BARI 6 × BARI 15	Replication	2	0.26	0.08
	Generation	3	0.82	0.41
	Error	6	0.20	0.03

,** significant at 5% probability level; *,** significant at 1% probability level.

Table F: Analysis of variance for Days to 50% flowering in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	159.99	53.33
	Generation	3	195.91	97.95
	Error	6	–150.83	-25.13
Tori 7 × SAU 2	Replication	2	7.19	2.39
	Generation	3	14.4	7.24
	Error	6	3.73	0.62
Tori 7 × SAU 3	Replication	2	10.78	3.59
	Generation	3	49.84	24.92
	Error	6	–0.27	-0.04
Tori 7 × BARI 6	Replication	2	0.41	0.13
	Generation	3	84.97	42.48
	Error	6	7.74	1.29
Tori 7 × BARI 15	Replication	2	5.29	1.76
	Generation	3	27.00	13.50
	Error	6	32.65	5.44
SAU 1 × SAU 2	Replication	2	0.44	0.14
	Generation	3	41.28	20.64
	Error	6	7.57	1.26
SAU 1 × SAU 3	Replication	2	0.73	0.24
	Generation	3	2.13	1.06
	Error	6	3.35	0.55
SAU 1× BARI 6	Replication	2	3.74	1.24
	Generation	3	182.00	91.00
	Error	6	0.56	0.09
SAU 1× BARI 15	Replication	2	1.53	0.51
	Generation	3	107.15	53.57
	Error	6	2.99	0.49
SAU 2 × SAU 3	Replication	2	0.21	0.07
	Generation	3	35.48	17.74
	Error	6	12.05	2.00
SAU 2 × BARI 6	Replication	2	1.99	0.66
	Generation	3	188.83	94.41
	Error	6	7.47	1.24
SAU 2 × BARI 15	Replication	2	23.40	7.80
	Generation	3	130.61	65.30
	Error	6	41.39	6.89
SAU 3 × BARI 6	Replication	2	1.58	0.52
	Generation	3	19.14	9.57
	Error	6	3.14	0.52
SAU 3 × BARI 15	Replication	2	7.84	2.61
	Generation	3	64.91	32.45
	Error	6	3.28	0.54
BARI 6 × BARI 15	Replication	2	4.99	1.66
	Generation	3	23.58	11.79
	Error	6	3.26	0.54

,** significant at 5% probability level; *,** significant at 1% probability level.

Table G: Analysis of variance for Days to 80% maturity in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	0.15	0.05
	Generation	3	61.45	30.72
	Error	6	5.79	0.96
Tori 7 × SAU 2	Replication	2	6.87	2.29
	Generation	3	12.11	6.05
	Error	6	5.05	0.84
Tori 7 × SAU 3	Replication	2	0.28	0.09
	Generation	3	21.91	10.95
	Error	6	9.72	1.62
Tori 7 × BARI 6	Replication	2	0.69	0.23
	Generation	3	67.83	33.19
	Error	6	4.76	0.79
Tori 7 × BARI 15	Replication	2	0.40	0.13
	Generation	3	63.88	31.94
	Error	6	10.11	1.68
SAU 1 × SAU 2	Replication	2	2.23	0.74
	Generation	3	17.41	8.70
	Error	6	11.27	1.87
SAU 1 × SAU 3	Replication	2	0.42	0.14
	Generation	3	8.41	4.20
	Error	6	9.43	1.57
SAU 1× BARI 6	Replication	2	0.81	0.27
	Generation	3	94.51	47.25
	Error	6	6.31	1.05
SAU 1× BARI 15	Replication	2	2.25	0.75
	Generation	3	76.82	38.41
	Error	6	12.28	2.04
SAU 2 × SAU 3	Replication	2	0.24	0.08
	Generation	3	42.45	21.22
	Error	6	10.86	1.81
SAU 2 × BARI 6	Replication	2	0.98	0.32
	Generation	3	126.02	63.01
	Error	6	5.43	0.90
SAU 2 × BARI 15	Replication	2	0.06	0.02
	Generation	3	97.65	48.82
	Error	6	8.09	1.34
SAU 3 × BARI 6	Replication	2	3.20	1.06
	Generation	3	6.07	3.03
	Error	6	5.24	0.87
SAU 3 × BARI 15	Replication	2	7.61	2.53
	Generation	3	89.13	44.56
	Error	6	4.42	0.73
BARI 6 × BARI 15	Replication	2	0.42	0.14
	Generation	3	22.23	11.11
	Error	6	17.19	2.86

,** significant at 5% probability level; *,** significant at 1% probability level.

Table H: Analysis of variance for Yield per plant in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	38.02	12.67
	Generation	3	8.01	4.00
	Error	6	28.36	4.72
Tori 7 × SAU 2	Replication	2	15.54	5.18
	Generation	3	13.57	6.78
	Error	6	4.54	0.75
Tori 7 × SAU 3	Replication	2	4.71	1.57
	Generation	3	9.55	4.77
	Error	6	49.07	8.17
Tori 7 × BARI 6	Replication	2	5.13	1.71
	Generation	3	12.15	6.07
	Error	6	37.64	6.27
Tori 7 × BARI 15	Replication	2	9.08	3.02
	Generation	3	12.72	6.36
	Error	6	35.19	5.86
SAU 1 × SAU 2	Replication	2	11.44	3.81
	Generation	3	15.36	7.68
	Error	6	6.90	1.15
SAU 1 × SAU 3	Replication	2	2.67	0.89
	Generation	3	15.87	7.93
	Error	6	16.22	2.70
SAU 1× BARI 6	Replication	2	3.19	1.06
	Generation	3	10.73	5.36
	Error	6	14.09	2.34
SAU 1× BARI 15	Replication	2	4.9	1.63
	Generation	3	17.27	8.63
	Error	6	16.62	2.77
SAU 2 × SAU 3	Replication	2	2.73	0.91
	Generation	3	5.17	2.58
	Error	6	11.63	1.93
SAU 2 × BARI 6	Replication	2	2.02	0.67
	Generation	3	10.17	5.08
	Error	6	38.88	6.48
SAU 2 × BARI 15	Replication	2	1.48	0.49
	Generation	3	26.30	13.15
	Error	6	7.25	1.20
SAU 3 × BARI 6	Replication	2	1.51	0.50
	Generation	3	3.98	1.99
	Error	6	5.90	0.98
SAU 3 × BARI 15	Replication	2	3.88	1.29
	Generation	3	13.06	6.53
	Error	6	9.27	1.54
BARI 6 × BARI 15	Replication	2	10.12	3.37
	Generation	3	17.29	8.64
	Error	6	11.52	1.92

,** significant at 5% probability level; *,** significant at 1% probability level.

Table I : Analysis of variance for 1000 seed weight per plant in different crosses of *Brassica rapa* genotypes

Crosses	S.V.	df	SS	MS
Tori 7 × SAU 1	Replication	2	1.44	0.48
	Generation	3	2.32	1.16
	Error	6	–1.32	-0.22
Tori 7 × SAU 2	Replication	2	1.21	0.40
	Generation	3	0.76	0.38
	Error	6	0.82	0.13
Tori 7 × SAU 3	Replication	2	0.22	0.07
	Generation	3	0.26	0.13
	Error	6	1.56	0.26
Tori 7 × BARI 6	Replication	2	0.42	0.14
	Generation	3	0.14	0.07
	Error	6	1.78	0.29
Tori 7 × BARI 15	Replication	2	0.95	0.31
	Generation	3	1.21	0.60
	Error	6	1.23	0.20
SAU 1 × SAU 2	Replication	2	0.11	0.03
	Generation	3	0.06	0.03
	Error	6	0.64	0.10
SAU 1 × SAU 3	Replication	2	0.25	0.08
	Generation	3	0.98	0.49
	Error	6	0.57	0.09
SAU 1× BARI 6	Replication	2	0.01	0.00
	Generation	3	0.47	0.23
	Error	6	1.54	0.25
SAU 1× BARI 15	Replication	2	0.02	0.00
	Generation	3	0.71	0.35
	Error	6	0.76	0.12
SAU 2 × SAU 3	Replication	2	0.03	0.01
	Generation	3	0.09	0.04
	Error	6	0.75	0.12
SAU 2 × BARI 6	Replication	2	0.06	0.02
	Generation	3	0.02	0.01
	Error	6	0.37	0.06
SAU 2 × BARI 15	Replication	2	0.19	0.06
	Generation	3	0.55	0.27
	Error	6	0.13	0.02
SAU 3 × BARI 6	Replication	2	0.06	0.02
	Generation	3	0.59	0.29
	Error	6	0.60	0.10
SAU 3 × BARI 15	Replication	2	0.72	0.24
	Generation	3	0.11	0.05
	Error	6	2.98	0.49
BARI 6 × BARI 15	Replication	2	0.92	0.30
	Generation	3	0.55	0.27
	Error	6	1.04	0.17

,** significant at 5% probability level; *,** significant at 1% probability level.