GENE ACTION AND HETEROSIS THROUGH LINE x TESTER ANALYSIS IN *Brassica napus* L.

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CERTIFICATE

This is to certify that the thesis entitled, "GENE ACTION AND HETEROSIS THROUGH LINE **X** *TESTER ANALYSIS IN BRASSICA NAPUS L." submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING, embodies the result of a piece of bona fide research work carried out by* ***Rashma Afrose****, Registration No.* **06-02073** *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 2012
Place: Dhaka, Bangladesh

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(Prof. Dr. Firoz Mahmud)
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DEDICATED TO MY

BELOVED

PARENTS

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LIST OF SOME COMMONLY USED ABBREVIATIONS

ABBREVIATION	FULL MEANING
AEZ	Agro-Ecological Zone
BARI	Bangladesh Agricultural Research Institute
Cm	Centimeter
^{0}C	Degree Celsius
CV	Co-efficient variation
CMS	Cytoplasmic Male Sterility
DAE	Days after Emergence
df	degree of freedom
et al	and others
etc	Etcetera
e.g.	For Example
FAO	Food and Agriculture Organization
GCA	General Combining Ability
g	Gram(s)
H	High
L	Low
i.e.	That is
SAU	Sher-e-Bangla Agricultural University
Agric	Agriculture
Agril.	Agricultural
j	Journal
Sci	Science

GENE ACTION AND HETEROSIS THROUGH LINE x TESTER ANALYSIS IN *Brassica napus* L.

BY

RASHMA AFROSE

ABSTRACT

The study was conducted to evaluate five female parents (lines) and eight male parents (testers) in a line x tester mating design at the research field of Sher-e-Bangla Agricultural University, Dhaka during November 2011 to April 2012 to estimate their gene action and heterosis. The data recorded on 40 F_1's and their parents for their combining ability indicated that GCA effect was significant for plant height, primary branches and secondary branches per plant, days to fifty percent flowering, days to fifty percent maturity, no. of siliqua per plant, length of siliqua, seeds per siliqua, thousand seed weight and seed yield per plant. High ratio of GCA and SCA variance was observed indicating preponderance of non additive gene effects in the inheritance of the yield and yield contributing characters under study. Among the lines Nap 9908 and Nap 94006 were found as good general combiners. Among 40 hybrids 16 were found as good specific combiner for yield and other characters. Different types of heterosis i.e. heterosis over mid parent (Hm), heterosis over better parent (Hb) and heterosis over standard check (Hc) were estimated to evaluate forty hybrids for seed yield and yield contributing characters. The average heterosis for seed yield of forty hybrids over mid parent was 3.27% and that of better parent and standard check was -9.72% and 5.60% respectively.

Chapter I

Introduction

CHAPTER 1

INTRODUCTION

Rapeseed (*Brassica napus* L.), known as rape, oilseed rape, rapa, rapeseed and it is the most important oilseed crop in Bangladesh but its national average seed yield is 902 kg/ha only (BBS, 2010) It is ranked as the third most important oilseed crop after soybean and palm. It is originated in either the Mediterranean area or Northern Europe. Approximately 70% of the total cultivated mustard in Bangladesh is the variety of either *Brassica rapa* or *Brassica napus*.

Oil seed rape (*B. napus* L) is usually classified as a largely self-pollinated species and it is a bright yellow flowering member of the family Brassicaceae (Cruciferae). It is an amphidiploid containing 2n = 38 Chromosomes with AACC genomic constituents developed from *Brassica rapa (AA)* and *Brassica oleracea* (CC). Some botanists include the closely related *Brassica campestris* with in *B. napus* (Triangle of U).

Mustard and rapeseed seeds contain 42% oil, 25% protein (Khaleque, 1985). The oil is mainly used as edible product. Oil and fat are not only the source of energy (9-k.cal.g -1) but also contain fat-soluble vitamins A, D, E and K. Rapeseed (*B. napus* L) play a vital role in human diet but the consumption rate of oil in Bangladesh is far below than that of balanced diet (6 g oil per day per capita).

According to Mondal et al., 2001, oil crops produce 0.16 million tons of edible oil every year as against the total requirements of 0.5 million tons for a population of 130 million in Bangladesh. The shortage of edible oil has become a chronic problem for the nation. The present seed yield per hectare of mustard in Bangladesh is far below the level attained in the developed countries of the world (BBS, 2008).

The main reasons behind these are use of low yielding local indigenous cultivars, unavailability of locally developed hybrids and low management practices. Also this crop is mostly grown under residual soil moisture in winter season as well as poor cultural practices, the average yield is quite lower than that in the developed countries (Hasanuzzaman and Karim, 2007).

The yield of rape seed can be increased by expansion of cultivated area (Skipping of fallow period, cultivation of marginal soils, cultivation of hillside locations), development of high-yielding and resistant varieties, use of optimum fertilizer and plant protection, irrigation mechanization, multiple cropping and reduction of postharvest losses (quantitative and qualitative losses).

Development of high-yielding and resistant variety is the direct ways to increase production and the major research thrust in the oilseed *Brassica sp.* improvement in Bangladesh has been to develope high yielding varieties with early to medium maturity, non-shattering ability, shorter plant with stronger stem, a better harvesting index, responsiveness to good management, resistance to diseases and pests, and improved oil and meal quality.

Meanwhile, 26 mustard and rapeseed variety have been released in Bangladesh by different organization like Bangladesh Agricultural Research Institute (BARI), Bangladesh Institute of Nuclear Agriculture (BINA), Bangladesh Agricultural University (BAU) Sher-e-Bangla Agricultural University (SAU), Bangladesh Agricultural Development Corporation (BADC) but most of them are not popular among the farming community due to their long duration, low to moderate yield and susceptibility to biotic and abiotic stresses.

Commercial hybrid cultivars become increasingly important for oilseed crops. Because mutation breeding, marker assistant breeding, genetic engineering and protoplast fusion contribute only a little in the production of disease and pest resistant plants. For commercial exploitation of hybrid technology in mustard, a cytoplasmic male sterile line (A), a maintainer line (B) and a restorer line (R) are required.

In rapeseed breeding program for hybrid and open pollinated varieties, general and specific combining ability effects (GCA and SCA) are 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 inbreds 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).

In F_1 hybrids of *B. napus,* the levels of heterosis were reported to be about 20 percent above the better parent (Sernyk and Stefansson, 1983, Grant and Beversdorf, 1985, Lefort-Buson and Dattee, 1982). With good management and hybrid varieties, the present yield level could be increased.

Combining ability concepts are the basic tools for improved production of crops in the form of F_1 hybrids. Identifying parental combinations with strong heterosis for yield and obtain genetic parameters are the most important steps in the development of new cultivars (Diers *et al.,* 1996; Becker *et al.,* 1999; Melchinger 1999), and heterosis effects are generally more pronounced in crosses between genetically distinct materials.

Development of hybrid varieties requires the testing of inbred lines for general combining ability (GCA), making their all possible cross combinations, predicting F_1 performance constituting a number of experimental synthetics. Many workers have reported GCA and SCA effects for yield and yield components in different crops (Muraya *et al.,* 2006. Jan *et al.,* 2005; Jurna *et al., 1999;* Islam *et al.,* 1999) whereas critical studies on gene action on yield and yield components in *Brassica* are very few. However, studies, on combining ability in relation to combining ability in other traits have been reported by Abercrombie *et al.,* (2005), Satwinder *el al.,* (2000), Kumar *et al.,* (1997), Thakur and Bhateria (1993). These data suggested that there is few works to understand the nature of gene effects and the inheritance of yield and yield components in *Brassica napus* under Bangladesh condition. Therefore the knowledge about the combining ability and heterosis are important in selecting suitable parents for hybridization, proper understanding of inheritance of quantitative traits and also in identifying the promising crosses for further use in breeding programme. The present investigation was carried out to fulfill the following objectives:

- To estimate the nature and extent the combining ability of selected parents and their hybrid,

- To determine the mode of gene action in governing different characters and

- To estimate the magnitude and direction of heterosis.

Chapter II

Review of Literature

CHAPTER 2

REVIEW OF LITERATURE

In undertaking the present piece of research work (Line × Tester analysis) on thirteen genotypes among them five lines and eight testers of *Brassica napus*, a number of literatures on *Brassica spp* had to be studied. The important prerequisites for development of high yielding varieties are to identification of superior parents, promising cross combination(s) and suitable breeding method. The estimation of gene action, combining ability, magnitude of heterosis is an important factor in developing an effective breeding programme. The review and literature concerning the studies is outlined under the following points:

2.1 Combining ability

2.2 Heterosis

2.1 Combining ability

A good number of literatures concerning the Combining ability in the *Brassica spp* available. These literatures are outlined here.

V. Rameeh (2011) conducted an experiment on Line × tester analysis for seed yield and yield components in spring and winter type varieties of oil seed rape. Line × tester analysis of two testers of spring type and six lines of winter type oil seed rape varieties were used to estimate combining ability and heterosis of yield components and seed yield. Significant mean squares of treatments for yield components and seed yield, indicating significant genetic variations among the genotypes including parents and their crosses. Parents vs crosses mean square which indicate average heterosis was significant for all the traits except pods per plant. Line × tester mean square was significant estimate for 1000-seed weight indicating the prime importance of additive genetic effects for this trait. Significant positive general combining ability (GCA) effects of seed yield were observed for parents which had positive GCA effects of pods per plant. Most of the crosses with significant for all the traits except pods per plant. High narrow sense heritability positive specific combining ability (SCA) effects for pods per plant had significant positive SCA effects of seed yield. Most of the crosses had significant positive over spring parent heterosis of seed yield, indicating winter type of oil seed rape varieties are suitable candidates for improving this trait using combination method.

Priti Gupta *et al.*, (2011) conducted an experiment on heterosis and combining ability for yields and its components in Indian mustard (*Brassica juncea* (L.) Czern & Cass.). Half diallel analysis of eight parents was carried out to identify the high heteritic crosses and their relationship in terms of general and specific combining ability (GCA and SCA) in *Brassica juncea* (L.) Czern & Cass at IARI, New Delhi during 2007-08 and 2008-09. The relative heterosis and heterobeltiosis was observed to be highest with to seed yield per 100 siliquae and days to 50% flowering in case of cross IC-199715 X IC-199714, EC-289602 X Prakash for number of primary brances per plant and harvest index, Agra Local X Pusa Bahar for length of main axis, Poorbijaya X Agra Local for nuber of siliquae per main axis, EC-289602 X Pusa Bahar for biological yield and seed yield per plant. It was found that different cross combinations exhibit maximum value for better and mid-parent heterosis for remaining traits viz days to maturity, number of secondary branches per plant and 1000 seed weight. GCA and SCA variances significant for all the characters. Variance for gca (σ^2g) was observed to be higher for days to 50% flowering, days to maturity, plant height and 1000 seed weight, whereas variance for sca (σ^2s) was higher for seed yield and other remaining parameters.

Aghao *et al.*, (2010) conducted an experiment on diallel analysis for yield and yield contributing characters in Indian mustard (*Brassica juncea*). Diallel analysis in mustard involving ten parents and forty five crosses was performed to estimate the general (gca) and specific combining ability (sca) of parents and crosses respectively. The gca and sca effects showed wide variation in the level of significance for various yield contributing characters. The parents Seeta, Varuna and Laxmi were identified as best general combiners for yield and yield contributing characters on the basis of high mean performance and significant gca effects. Among the crosses Varuna x Seeta was identified as best F_1 cross, which can be forwarded to the next generation by single seed descent method with an aim of getting useful segregants in the succeeding generation.

Marijanovic-Jeromela *et al.,* (2007) conducted an experiment on Combining abilities of rapeseed (*Brassica napus* L.) varieties. The global acreage under rapeseed increases steadily. Rapeseed is grown for oil for human consumption, feed and biodiesel production. For faster advances in breeding, it is necessary to know variability and combining ability of selection material i.e. modes of inheritance of certain traits. General (GCA) and specific combining abilities (SCA) of five rapeseed varieties as well as the mode of inheritance of plant height, height to the first lateral branch, number of lateral branches and seed yield per plant were analyzed in this paper. Positive heterosis for plant height was found in five cross combinations, for the height to the first lateral branch in two combinations and for the number of lateral branches in only one combination and for seed yield in three cross combinations.

A study in Haryana, India, was conducted by Goswami *et al.,*(2005) to estimate the combining ability and gene action for yield and yield contributing characters in breeding lines of Indian mustard (consisting of 30 crosses and 13 parents). In the line x tester analysis of Indian mustard, both GCA and SCA variances were found highly significant for yield and yield contributing characters. Analysis revealed a significant role of non-significant gene action for all the traits.

Forty-five F_1s was derived by Singh *et al.,* (2005) from crossing between six indigenous and four exotic genotypes of Indian mustard in a diallel fashion excluding reciprocals and parents were evaluated. Observations were recorded for days to 50% flowering, days to maturity, plant height, length of main shoot, primary and secondary branches per plant, siliqua on main shoot, siliqua length, seeds per siliqua, seed yield per plant, 1000-seed weight, oil content and harvest index. The results revealed the importance of additive and non-additive genetic variances for most of the characters.

To study the combining ability and heterosis for seed yield, its components and oil content, Shweta *et al.,* (2005) crossed diverse lines of Indian mustard *(Brassica juncea).* Forty-eight F_1 crosses obtained by crossing twelve lines and four testers in a line x tester fashion along with their parents were used in the experiment. Analysis of variance for combining ability revealed the presence of genetic variability due to general combining ability among the parents and due to specific combining ability among the crosses for all the traits studied. This result indicated the predominance of non-additive gene action along with over dominance for all the characters, except oil content where it was additive and dominance as partial.

Panja *et al.,* (2005) performed an experiment by crossing Indian mustard cultivars Vardhan, NDR-8501, MCN-20, Rohini, RH-30, Varuna, Seeta and Kranti in half-diallel mating system without reciprocals. Parents and F_1s were grown in inter row and plant to plant spacing of 45 and 15 cm, respectively. Prakash, leaf blight (Alternaria brassicae)-susceptible, was interplanted as an infector row after every fourth test entry and all around the experimental plot. The mean percent disease index (PDI) of the genotypes ranged from 10.1 in Kranti to 16.9 in RH-30. Kranti was resistant to leaf blight followed by Varuna while RH-30 was susceptible. The PDI of the hybrids ranged from 10.4 in Vardhan x Kranti to 21.8% in Varuna x Seeta. The majority of crosses exhibited lower PDI value compared to mid-parental value indicating dominance for disease inheritance. General and specific combining abilities were significant indicating the importance of both additive and non-additive gene actions in controlling leaf blight resistance. Analysis of variance for heterosis revealed that the differences among combining abilities of parents and differences for heterosis among individual crosses were significant.

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

The estimates of specific combining ability variances were considerably higher than general combining ability (average) for all the characters studied, indicating dominance of non-additive type of gene action in the inheritance of the traits. (Yadav *et al.,* 2004).

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

Sharief *et al.,* (2002) conducted an experiment on Combining ability of some canola (*Brassica napus, L*) Inbred lines and their hybrids under different plant population density. Two field experiments were carried out at the Experimental Station, Fac. of Agric., Mansoura Univ. during the growing seasons of 1997/98 and 1998/99.The objectives of this investigation was aimed to evaluate combining ability of some canola inbred lines and their hybrids under different plant population density. The genetic materials were the four lines of Drakkar, Fido, Serw 4 and Serw 6 as well as all possible combinations among them according to a complete diallel matting design. A split plot design with three replicates was used. Test of significance of the mean squares for general combining ability (GCA) and specific combining ability (SCA) cleared that GCA and SCA were highly significant for most of studied traits. In addition, the magnitudes of SCA were larger than the corresponding values of GCA in most studied traits and this finding suggested that these traits were mainly controlled by dominance genes, indicating that the non-additive genetic variance played a major role in the inheritance of these traits. On the other hand, the mean squares of reciprocal effects were significant of most of cases but their values were less than the corresponding values of GCA and SCA. This indicates that maternal effect played a minor role in the expression of these traits. For GCA effects, the parents S 30 and S 32 could be utilized in a breeding program for improving most of studied traits to pass favorable genes for improving hybrids. For SCA effects, the two combinations of P1 f^3 P3 and P2 f^3 P4 showed the highest positive and significant values for most of studied traits.

Rao *et al.,* (2001) studied on combining ability of F< sub>1</ sub> and F< sub>2</ sub> diallels revealed a predominance of the non-additive component for a majority of the yield contributing characters. Estimates of narrow sense heritability were classified as low, medium and high in two generations, and showed shifts in the magnitudes of heritability from F< sub>1</ sub> to F< sub>2</ sub> in low to medium, medium to high, high to medium and medium to low directions. It was low to medium for number of secondary branches, medium to high for number of primary branches and 1000-seed weight, high to medium for plant height and oil content, and medium to low for seed yield/plant. For the remaining traits, namely, days to 50% flowering, days to maturity and number of seeds per siliqua, the magnitudes of heritability were medium and remained unchanged in both the generations.

A study was undertaken by Pietka *et al.,* (2001) to establish the relationship of general (GCA) and specific combining abilities (SCA) with glucosinolate content in seeds collected from F_1 and F_2 hybrid generations of winter double low rapeseed. Hybrids produced by crossing cultivars Mar, Polo, Silvia, Lirajet and Wotan with inbred lines extremely low in glucosinolate content were grown in the field. Harvested seeds were analysed for glucosinolate content and composition using gas-liquid chromatography of sililated desulfoglucosinolates. Calculations of GCA and SCA were performed in North Caroline's II (N II) design. GCA and SCA values and statistical tests of their significance were calculated separately for F_1 and for F_2 generations and compared. Calculated GCA values showed that both inbred lines and cultivars were highly and significantly differentiated in terms of glucosinolate content and composition, suggesting that an effective selection for low glucosinolate content is possible for segregating hybrid populations. The possibility of using SCA in improving glucosinolate content was smaller than that of GCA. Calculated values were significantly different from zero only for a few combinations and in many cases, positive values found in F_1 became negative in the F_2 generation or vice-versa. Examined cultivars and inbred lines were not differentiated genetically according to 4-hydroxybrassicin content.

Combining ability on nine characters in brown sarson using a (9 x 3) line x tester set was studied by Sheoran *et al.,* (2000). Both general combining ability (GCA) and specific combining ability (SCA) components were significant for all the evaluated characters, viz., plant height, main shoot length, number of primary branches, number of secondary branches, number of siliqua on main shoot, siliqua length, seeds per siliqua, 1000-seed weight and seed yield per plant. Both additive and non-additive gene effects played role in the inheritance of different traits.

Sood *et al.,* (2000) crossed eleven *B. juncea* lines as females with testers Vardan, RLM619 and P17, the last having, been developed by crossing *B. camestris* cv. Candle with a *B. nigra* landrace. The 33 hybrids obtained from the line x tester mating design, together with the parents, were grown at Kangra, Himachal Pradesh, and evaluated for six quantitative traits. P17 was a good general combiner for siliquas/plant but not for seed yield. RLM619, CSR83-268, RCC15 and NDR8602 were good or average general combiners for the traits studied. None of the hybrids was consistently good with regard to high heterosis and SCA effects. The highest heterosis for seed yield was observed in the cross NDR860 x RLM619 (141%).

The information on heterosis and combining ability on seed yield and three yield components in six lines,16 testers and their 96 F_1 hybrids of Indian mustard was reported by Katiyar *et al*., (2000), from a line x tester mating design. Of the hybrids, 64 and 38 showed heterosis for seed yield over the better parent and standard cv. Varuna, respectively.

A laboratory experiments was conducted by Tak and Khan (2000) 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.

General combining ability (GCA) and specific combining ability (SCA) for 23 winter oilseed rape cytoplasmic male sterility (CMS) Ogura lines was reported by Wos *et al.*, (1999). 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 3 pollinator cultivars Kana, Marisa and MAH 1592. Obtained results were used to find the best combinations for hybrid production.

Krzymanski *et al.,* (1997) examined combining ability and heterosis for selected 11 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.

Line x tester analysis involving 40 females and three males from diverse origins was studied by Chaudhary *et al.,* (1997) and they revealed that both additive and non-additive gene actions were important in controlling most of the characters. However, additive gene action was predominant.

Sheoran *et al.* (1997) conducted an experiment with nine female and three male parents of *B. campestris* using line x tester design under two environments (sowing dates) with water stress conditions at Hisar. Data were recorded on six yield components. Pooled analysis of variance for combining ability revealed that mean squares due to males, females and males x females were significant for most of the characters, indicating the importance of both additive and non-additive gene effects.

Chaudhary *et al.,* (1996) conducted an experiment on Line x tester analysis in Indian mustard [*Brassica juncea* (L.) Czern & Cass.]. Line X tester analysis involving 40 females and 3 males from diverse origin revealed that both additive and non additive gene actions were important in controlling most of the characters studied. However, additive gene action was predominant. Variety Varuna, among the male parents, was the best general combiner for seed yield, oil content and most other important traits. Among the female parents, Pusa Bold and P 26/21 for seed yield and oil content; Laha Dholpur and No.6 for oil content; TM-11 and Keshri for earliness and dwarfness were the good general combiners. The cross Yellow Appressed X RL-18 was best for seed yield and oil content. Hybridization systems, such as a multiple or reciprocal recurrent crossing, which exploit both additive and non additive gene effects, simultaneously, could be useful in the genetic improvement of the characters studied.

Bhateria *et al.,* (1995) stated that a line x tester analysis of Indian mustard among 15 lines and three testers revealed the preponderance of non-additive type of gene action, thus indicating the scope for exploitation of heterosis by making suitable crosses.

Nine maternal lines (5S3 and 4S4), their pollinator (tester) Taplidor and 9 F1 hybrids derived by top crossing in *Brassica napus* studied by Kudla (1993).In their study they found that 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.

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 x 3 tester mating design of *Brassica napus*. The varieties Midas, Regent 3-1 and DB054 were identified as good general combiners and DNA38 x DISNI and N20-1 represent as good specific cross combinations.

An analysis in a (13 x 4) line x tester crosses in Brassica *juncea* was performed by Gupta *et al.*, (1987). Additive gene was relatively more important than non additive for seed yield/plant and most of the five yield components investigated and showed significant GCA and SCA effect for seed yield and plant height.

A line x tester analysis involving 12 females and eight males of *Brassica juncea* of diverse origin was carried out by Rawat *et al.*, (1983). Variance components of GCA and SCA were significant for days to 50% flowering, Number of primary branch, plant height, seed height and seed yield/plant. For secondary branches GCA was important and also showed significant SCA for increased seed yield.

2.2 Heterosis

Fifteen elite genotypes of mustard with two testers was crossed by Beena-Nair (2007) in line x tester fashion, and evaluated F_1's along with parents to estimate the magnitude of heterosis for yield and yield contributing characters in mustard. Highest magnitude of heterosis for seed yield per plant was obtained in crosses vardhan x TM-17, Vardhan x Laxmi and vardhan x RL-1359. Hence, these crosses may be utilized to identify superior recombinants after homozygosity has reached in mustard improvement programme.

Kishor *et al.*, (2006) said that heterosis was exploited in Indian mustard *(Brassica juncea)* using hybrid and line composite (HLC) method by growing blended Population of sterile F_1 and male fertile line. In general, seed yield increased with increasing proportion of heterotic (F_1) plants in blended populations. They suggested absence of a restorer system, a scheme for exploitation of hybrid vigor in Indian mustard.

Genetic distances between three double-low self-incompatible (SI) lines and 22 pure-line varieties of different geographic origins and the performance of the 66 hybrids produced by the three SI lines and these varieties within an NCII mating design for yield-contributing traits were investigated by Shen *et al.*, (2005). The F_1 hybrids of the SI lines and varieties derived from foreign countries showed high mid-parent heterosis for yield/plant, though the genetic differences between the SI lines and the male parents were not great. Primary branches and their siliqua contributed most to seed yield/plant and heterosis of yield/plant. Therefore, in genetic improvement of yield- related traits of rapeseed and in the utilization of heterosis, attention should be focused on the number of primary branches and the number of siliqua on them. Improvement of seed number per siliqua and 1000-seed-weight based on sufficient primary branches and siliqua will be an effective approach to yield improvement.

A field study was conducted by Saurabh *et. al.*, (2005) to estimate heterosis in Indian mustard for different quantitative characters, i.e. days to 50% flowering, days to maturity, plant height, primary branches, secondary branches, siliqua length, seeds per siliqua, 1000-seed weight, yield per plant and oil content. The experimental material consisted of sixty F_1's derived in a line x tester mating fashion (4 lines + 15 testers) and the standard cultivar as control. The crosses showed heterobeltiosis for seed yield with significant and positive specific combining ability (SCA) effects.

Four cytoplasmic male sterile lines of cabbage were crossed by (Chander and Verma, 2004).with line testers in a line x tester design. The resulting 20 F_1 hybrids were evaluated along with their parents. Heterosis over better parent (BP) and mid parent (MP) were calculated for days to first harvest, stalk size index, number of outer leaves, head size index, gross weight per plant and yield per plant. A wide range of heterosis over both BP and MP were observed for all characters.

Satyendra *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 (%). High heterosis (15.99, 15.51 and 12.37%) was obtained for seed yield in the crosses.

The study was carried out by Katiyar *et al.*, (2004) in 2002-03 in New Delhi, India on the combining ability effects and heterosis for the seed yield in ninety intervarietal crosses of *B. campestris*. Existence of significant variation among parents and crosses indicated the presence of adequate genetic variance between parents which reflected in differential performance of individual cross combinations. Twenty one crosses (23.3%) showed significant +ve heterosis over better parent while only four crosses (4.4%) were so over the best commercial variety. The presence of both additive and non-additive genetic variance and adequate heterosis provided the possibility of improvement of this crop not only by hybridization and selection but also by developing hybrids.

An investigation involving 45 genotypes (9 parents and their diallels, excluding reciprocals) was performed by Mahto *et al.*, (2004) to identify the high heterotic crosses in Brassica juncea was undertaken during the winter seasons of 1995/96 and 1996/97 at Ranchi, Bihar, India. Data were recorded for days to 50% flowering, primary and secondary branches per plant, plant height, siliqua per plant, seeds per siliqua, days to maturity, harvest index, 1000-seed weight, seed yield per plant, and oil content. The cross combinations RH 843 x RH 851 and PR 18 x BR 40 showed high relative heterosis and heterobeltiosis, respectively, for most characters. Overall, crosses PR 18 x BR 40, PR 830 x RH 851 and RH 843 x RH 851 were superior to others in heterotic effects.

Twenty-one Indian mustard hybrids and their parents (Varuna, Pusa Bold, Basanti, Maya NRD 8501, RH 30 and Kanti) evaluated by Singh *et al.*, (2004) for 8 quantitative traits: days to flowering, days to maturity, plant height, number of primary branches, length of the main raceme, seed yield, 1000-seed weight and oil content percentage, in an experiment conducted in Uttar Pradesh, India during the rabi season of 2002-03. High heterosis (15.99, 15.51 and 12.37%) was obtained for seed yield in the crosses Basanti x NDR 8501, Basanti x Kanti and Basanti x RH 30, respectively. These hybrids showed high heterosis over the best cultivar. Among the crosses, Basanti x Kranti may be used for selecting for seed yield and quality traits.

Heterosis for days to flowering, plant height, number of primary and secondary branches, length of main raceme, days to maturity, 1000-seed weight, harvest index, oil content, protein content, and seed yield was studied by Mahak-Singh *et al.*, (2003) in 10 Indian mustard cultivars (Varuna, Rohini, Vardan, RK 9501, NDR 8501, Pusa Bold, Vaibhav, RRLM 198, R.H. 30, and RC 781), and 45 F< sub>1</ sub> and F< sub>2</ sub> hybrids grown in Kanpur, Uttar Pradesh, India, during the rabi season of 1999/2000. High heterosis for seed yield was observed in Varuna x Rohini (56.74%), Vardan x Rohini (53.43%), Varuna x RK 9501 (52.86%), Vardan x NDR 8501 (36.73%), Pusa Bold x Rohini (37.68%), and Varuna x NDA 8501 (32.54%). The inbreeding depression in these hybrids were very low (11.06, 8.25, 10.04, -16.43, -7.26, and -12.48%, respectively).

An investingation was conducted by Pourdad *el al.,* (2003) to study heterosis in rapeseed *(B. napus, B. napus* var. *oleifera)* and for this they planted 42 F_1 s along with seven parents over three environments. They observed high negative heterobelitiosis for days to 50% flowering and days to maturity, which indicates a suitable hybrid for the development of short duriation cultivars. The highest positive heterobeltiosis for seed yield per plant over three environments were also observed.

Pourdad *et al.,* (2003) conducted an investigation to study heterosis and inbreeding depression in rapeseed (*B. napus [B. napus var. oleifera*]). Seven diverse parents were crossed in all possible combinations. Forty-two F_1s along with seven parents were planted over three environments. Inbreeding depression was calculated for 14 and heterosis for 21 characters. Glucosinolate, oil content and fatty acids were measured by spectrophotometer, NMR and gas chromatograph sets, respectively. TERI(OE)R15 x TERI(OE)R983 showed high negative heterobeltiosis for days to 50% flowering and days to maturity, it is suitable hybrid for development of early cultivars. TERI(OE)R983 x HNS9801 exhibited high negative heterobeltiosis for plant height. Results showed that heterosis breeding was not suitable for development of dwarf cultivars. The highest positive heterobeltiosis for seed yield per plant over three environments was observed in GSC3A00 x HNS9801 with mean performance of 14.3 g. The mean of inbreeding depression was 45.63% in this hybrid. Results showed that heterosis breeding was a suitable method to increase seed yield. In most of the hybrids, oil content showed negative heterobeltiosis over three environments. The mean of inbreeding depression in this character was 2.39%. Selection for high oil content was more effective than hybrid production. The highest negative heterobeltiosis for glucosinolate concentration over three environments was observed in GSC3A00 x NPN02. The lowest glucosinolate concentration was observed in GSC3A00 x TERI(OE)R983, with mean performance of 80.6 micro mol/g. For oleic acid content, there was no cross with positive and significant heterobeltiosis over three environments. The highest negative heterobeltiosis for linolenic acid content was observed in HNS9802 x NPN01, with a mean performance of 10.7%. The highest negative heterobeltiosis for erucic acid content was observed in TERI(OE)R983 x GSC3A00, with a mean performance of 2.3%. Heterosis breeding was not suitable for developing single zero cultivar. Characters with low and high inbreeding depression could be basically controlled by additive and non-additive gene action, respectively.

An experiment was conducted by Shen *et al.,* (2002) and they found that 66 F_1 hybrids, produced by three double low self-incompatible lines and 22 varieties of *B. napus* with a North Carolina II (NCII) crossing design, were tested for their heterosis in China. The results showed that significant differences were found between F_1 s and their parents for yield per plant and seed oil content. Mid-parent heterosis of these two characters ranged from 5.50% to 64.11% and from 1.55% to 7.44%, respectively. Heterosis for seed yield per plant was greater than that of seed oil content. For yield components, heterosis of total number of siliques per plant was the highest, followed by seed per silique and 1000 seeds weight.

A line x tester analysis was carried out by Ghosh *et al.,* (2002) involving 29 promising female and seven male parents for 10 quantitative traits in Indian mustard. The crosses showed high heterosis for seed yield and some of the yield contributing traits.

Kumar *et al.,* (2002) crossed three lines and twelve testers of Indian mustard and the resulting 36 F_1s and 15 parents were grown. Physiological data were determined from five plants per entry and the range of heterosis given for all.

Heterosis of parents was studied by Zhang *et al.,* (2002) for seed yield, oil content and protein content in an 8X8 diallel cross in toria *(Brassica campestris var . toria*). Trait data were recorded on five plants of each of the 28 F_1s and 28 reciprocal F_1s (RF_1s). 24 F_1s and 21 RF_1s showed significant positive heterosis for seed yield over mid parent (MP) and 16 F_1s and 21 RF_1s over the better parent (BP).

Lu *et al. (2001)* reported that heterosis is proportional to genetic divergence between respective parents in many crops. The heterosis in interspecific hybrids was evaluated between *Brassica napus (AACC,* 2n=38) and *Brassica rapa [B. campestris] (AA,* 2n=20) for ten agronomic characteristics and was compared to heterosis in hybrids of *B. napes.* Fifteen interspecific crosses were generally characterized for their, crossability, germination rate, morphology, and pollen fertility and seed production. The crossability 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 was found in the number of secondary branches and pod number per plant. Significant mid-parent heterosis was found in plant height, length of main inflorescence, and the number of primary branches.

An experiment was conducted by Chauhan *et al.,* (2000) to estimate the extent of heterosis for seed yield, related traits and oil content in single and 3-way crosses of Indian mustard. The material, comprising 14 parents and 37 hybrids, was grown during rabi 1994-95. Heterosis was estimated as percentage increase or decrease in single and 3-way crosses over the better parent (heterobeltiosis) and standard variety (economic heterosis).

Girke *et al., (1999)* evaluated twelve simple hybrids from crosses of summer rape cv. Korall with two resynthesized lines at Svalov, Sweden and Dyngby, Denmark in 1995-96. Mean heterosis was 32.3%, with mean yield increases of 9.5% over the better parent. Prerequisite for any successful hybrid breeding programme is the existence of genetically diverse gene pools. As a long time perspective for hybrid oilseed rape breeding, the utilization of artificially resynthesized rapeseed could be of interest. Hybrid performance and heterosis in a series of test crosses between resynthesized lines and the spring rapeseed cultivar 'Korall' in male sterile form were investigated under field conditions for two years at two locations in Sweden and Denmark.

A breeding approach was conducted by Liersch *et al.,* (1999) 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, along with heterosis effect.

Krzymanski *et al.* (1998) examined F_1 generation of diallel cross between 10 lines of double low winter oilseed rape. Specific combining ability effects for seed yield were significant in nine combinations. Significant positive heterosis effects as compared to better parent were observed for 18 cross combination. Average seed yield of hybrids as compared to parent mean was 124.7%.

Starrmer *et al.* (1998) examined the magnitude of heterosis in spring canola to determine the potential advantage of hybrid cultivars. Four inbred cultivars, with diverse geographic origins of development, were hand-pollinated in a diallel design. Positive heterosis was found for yield, oil content and oil quality, with the highest degree of heterosis observed for yield. (Hybrid F_1) progeny produced higher yield than inbred parents because of increased pod number (primarily on the main raceme), larger seeds, and later maturity. However, the magnitude of heterosis observed varied between hybrids.

Crosses of nine female and three male sarson (*Brassica campestris*) parents was studied by Yadav *et al.*, (1998) for seven yield components. Of these, 18 hybrids exhibited significant positive heterosis. Highest heterotic response for seed yield was observed in DBI x Pusa kalyani and BSKI x BSIK2. Singh and Verma (1997) discussed different aspects of heterosis breeding, including prerequisites for the development of hybrids, different existing hybrid systems, and extent of out crossing, recent advances in India and abroad, limitations of hybrids in *Brassica,* and future strategies.

Chapter III

Materials and Methods

CHAPTER 3

MATERIALS AND METHODS

3.1 Experimental site

The Experiment was conducted at research Farm of Sher-e-Bangla Agricultural University, Dhaka-1207 during the period from November 2011 to April 2012. The experiment field is located at $90^{0}33'$ E longitude and $23^{0}77'$ latitude at a height of 9 meter above the sea level (BCA, 2004). The land was medium high and well drained (Plate 1)

3.2 Climate

The annual precipitation and potential evaporation of the site were 2152mm and 1297mm, respectively. The average maximum and minimum temperature was 30.34^{0}C and 21.21^{0} C, respectively with average temperature of 25.77^{0}C.Temperture during the cropping period ranged between12.50^{0}C to 36.20^{0}C. The humidity varied from 47.13% to 68.14%.The day length between 10.5-11.0 hours only there was three times rainfall during experimentation.

3.3 Soil

The soil of the experimental site is belong to the Agro-Ecological Zone of "Madhupur Tract'' (AEZ No.28). It was Deep red Brown Terrace soil and belong to "Nodda" Cultivated series. The top soil is silty clay loam in texture. Organic matter content was very low (0.82%) and soil pH varied from 5.47 to 5.63.

3.4 Experimental materials

Five line such as Nap94006, Nap9908, Nap2037, BARI Sarisha 7, BARI Sarisha 13 and eight tester such as Nap248, Nap179, Nap206, Nap2001, Nap2057, Nap2012, Nap2013, Nap2022 were collected from the department of Genetics and Plant Breeding Sher-e-Bangla Agricultural University, Dhaka-1207 . These thirteen parents were grown in the experimental farm of Sher-e-Bangla Agricultural University during the winter season of 2011 to 2012 to obtain F1 test cross progenies for estimation of combinig ability and heterosis.

3.5 Land Preparation

The land was prepared thoroughly by 3 - 4 ploughing and cross ploughing followed by laddering to attain a good filth. During land preparation, weed and stubble of the previous crops were collected and removed from the field.

3.6 Manure and fertilizer application

Fertilizers were applied at the rate of 270: 170: 100. 150: 5 kg/ ha of Urea, TSP MP. Gypsum and Zinc sulphate respectively. Cowdung was applied at the rate of 10 M ton/ha. Whole amount of cowdung TSP, MP, Gypsum. Zinc sulphate and half of Urea were applied at the time of final land preparation. The remaining urea was top dressed at 30 days after seedlings emergence.

3.7 Sowing of seeds

Seeds of 40 F_1s were grown in separate line in the experimental field on 15 November, 2011. Respective parental genotypes (pollen parents) were also grown in alternate line. The row spacing was 30 cm having plant spacing 15 cm within the row. The seedlings emerged with in four days.

Plate 1. Sowing of Mustard seeds in the experimental plot at SAU farm (15 Nov 2011)

3.8 Intercultural operations

Necessary intercultural operation was taken during cropping period for proper growth and development of the plants. Thinning and first weeding was done at 10 days after emergence (DAE). The second weeding was done at 30 DAE followed by top dressing of Urea. Irrigation was given at regular interval. For suppression of aphid population Malathion 57 EC was applied three times as foliar spray at an interval of 10-1 5 days after seedling emergence.

Plate 2. A field view of the experimental site at SAU farm (Rabi 2011)

3.9. Crossing among the selected genotypes of rape seed

Five line (Seed parents) were crossed with eight tester (Pollen Parents) of *B.napus* in one direction during December 2011 to January 2012. Removal of sepal and petal from the upper portion of bud of CMS *Brassica* genotypes was done in the evening to expose stigma for pollination. Hand pollination was carried out in the following morning by dusting pollen from the fertile *Brassica napus* genotypes. The crossed buds were bagged and tagged properly. Bagging after pollination was continued for 3-4 clays to avoid unwanted pollination. Thus 40 test cross F_1s were produced. After maturity the siliqua were collected separately from the plant followed by threshing and drying the F_1 and parental seeds were kept in the cold storage for the study in the following year.

Plate 3. (a) Hand pollination and (b) Bagging and tagging in *Brassica napus* genotypes.

3.10 Growing test cross (F_1s) and their parental population

Evaluation of test cross progenies were carried out during November 2011 to April 2012 in the experimental field. Department of Genetics and Plant Breeding, SAU.

3.11 Plant material used

The seeds of thirteen parents (Five line and Eight tester of *B. napus* genotypes and their 40 F_1s obtained from previous year and BARI Sharisha-13 (Check variety) were used as plant materials.

3.12 Layout and design

The seeds of 40 F_1s (hybrids) and 13 parents were grown in Randomized Complete Block Design (RCBD) with three replications. Single row of 5 m each constituted the experimental unit. Treatment was distributed in the experimental Unit through randomization by using the random number from Calculator.

Table 1: List of the line (seed parent), tester (pollen parent) and standard check for combining ability and *heterosis* estimation.

Line (Seed parents)	Standard Check Variety	Tester (Pollen Parents)
Nap 94006	BARI Sharisha-13	Nap 248
Nap 9908		Nap 179
Nap 2037		Nap 206
BARI Sarisha-7		Nap 2001
BARI Sarisha-13		Nap 2057
		Nap 2012
		Nap 2013
		Nap 2022

Table 2. List of F_1 hybrids for combining ability and heterosis estimation

F1Hybrids	F1 Hybrids	F1Hybrids	F1Hybrids	F1Hybrids
Nap 94006 x Nap 248	Nap 9908 xNap 248	Nap 2037 xNap 248	BARI Sarisha-7 xNap 248	BARI Sarisha-13 xNap 248
Nap 94006 x Nap 179	Nap 9908 xNap 179	Nap 2037 xNap 179	BARI Sarisha-7 xNap 179	BARI Sarisha-13 xNap 179
Nap 94006 x Nap 206	Nap 9908 xNap 206	Nap 2037 xNap 206	BARI Sarisha-7 xNap 206	BARI Sarisha-13 xNap 206
Nap 94006 x Nap 2001	Nap 9908 xNap 2001	Nap 2037 xNap 2001	BARI Sarisha-7 xNap 2001	BARI Sarisha-13 xNap 2001
Nap 94006 x Nap 2057	Nap 9908 xNap 2057	Nap 2037 xNap 2057	BARI Sarisha-7 xNap 2057	BARI Sarisha-13 xNap 2057
Nap 94006 x Nap 2012	Nap 9908 xNap 2012	Nap 2037 xNap 2012	BARI Sarisha-7 xNap 2012	BARI Sarisha-13 xNap 2012
Nap 94006 xNap 2013	Nap 9908 xNap 2013	Nap 2037 xNap 2013	BARI Sarisha-7 xNap 2013	BARI Sarisha-13 xNap 2013
Nap 94006 xNap 2022	Nap 9908 xNap 2022	Nap 2037 xNap 2022	BARI Sarisha-7 xNap 2022	BARI Sarisha-13 xNap 2022

3.13 Data collection

Ten randomly selected competitive plants from each of the parents, F_1s were used in each replication for recording data on the following 10 characters:

3.13.1 Plant height

The height of the plant was taken in centimeter (cm) from the ground level to the tip of the inflorescence during harvest.

3.13.2 Number of primary branches per plant

The total number of primary branches of ten plants were measured and averaged.

3.13.3 Number of secondary branches per plant

The total number of secondary branches of ten plants were measured and averaged.

3.13.4 Days to 50% flowering

Determined as the days from sowing of seeds to the days when the flower was opened at 50 percent of the plant in each line.

3.13.5 Days to 50% maturity

Determined as the days from flowering of plant to when the siliqua was matured at 50 percent of the plant in each line.

3.13.6 Number of siliqua per plant

The total number of siliqua of ten plants were counted and average number of siliqua per plant were recorded.

3.13.7 Length of siliqua(cm)

Length taken from the base to the tip of the siliqua. Length of siliqua of (ten siliqua per plant) ten plants was taken and avereged.

3.13.8 No. of seeds per siliqua

All siliqua front the sample plant were collected and 10 siliqua were randomly selected. Seeds obtained from them were counted and recorded average number ofseeds per siliqua.

3.13.9 Seed yield per plant (g)

The weight of seeds harvested from the selected plants was recorded and then seed yield per plant was determined.

3.13.10 Thousand seed weight (g)

Thousand seed from the selected plant were counted and their weight was taken in an electric balance.

3.14 Statistical Analysis

Collected data were subjected to statistical analysis with different options of line x testes analysis by Kempthorne (1957)

3.14.1 Analysis of Variance

Analysis of variance for general combining ability (GCA) and Specific combining ability (SCA) effects were estimated according to line x tester method (without parents).

$$S.S\,(crosses) = \frac{\Sigma\Sigma C^2\ ij}{r} - C.F(crosses)$$

Where

Cij is the observat ion for i x j th crosses

r = Number of replication

$$C.F(Crosses) = \frac{[Grand\ total\ (crosses)]^2}{Total\ Number\ of\ crosses \times Number\ of\ r}$$

$$S.S\,(Lines) = \frac{\Sigma\Sigma L^2\ ij}{r \times t} - C.F(crosses)$$

$$S.S\,(Tester) = \frac{\Sigma\Sigma T^2\ ij}{r \times l} - C.F(crosses)$$

Where,

$\sum\sum L^2\ ij$ = Sum of square of line total.

r =Number of replication

t =Number of tester

$\sum\sum T^2{}_{ij}$ =Sum of square of tester total

l= Number of line

S.S due to line x tester = S.S (Crosses)-S.S (Lines)-S.S (Testers)

3.14.2 Estimation of GCA effects

GCA effects for line and tester were calculated by the following formula

$$GCA\ for\ lines: g_i = \frac{X_{i..}}{tr} - \frac{X_{...}}{ltr}$$

$$GCA\ for\ tester: g_j = \frac{X_{.j.}}{lr} - \frac{X_{...}}{ltr}$$

3.14.3 Estimation of SCA effects

SCA effects were estimated by the following formula:

$$SCA\ of\ hybrids: S_{ij} = \frac{X_{ij.}}{r} - \frac{X_{i..}}{tr} - \frac{X_{.j.}}{lr} + \frac{X_{...}}{ltr}$$

Where,

$X_{ij.}$ = Individual cross value

$X_{i..}$=Line total

$x_{.j}$= Tester total

$x_{...}$ =Grand total(crosses)

r = Replication

l = line number

t = Tester number

3.14.4 Estimation of SE for combining ability effects

S.E of GCA for line GCA for tester and SCA effects were calculated by following Formulae

S.E. (GCA for line) = $\{\frac{Me}{r \times t}\}^{\frac{1}{2}}$

S.E. (GCA for tester) = $\{\frac{Me}{r \times l}\}^{1/2}$

S.E. (SCA effects) = $\{\frac{Me}{r}\}^{\frac{1}{2}}$

S.E. (g_i-g_j) for line= $\{\frac{2Me}{r \times t}\}^{1/2}$

S.E. (g_i-g_j) for tester= $\{\frac{2Me}{r \times l}\}^{\frac{1}{2}}$

Where,

Me = Error mean sum of square

g_i-g_j = difference of GCA for any line or tester pair

3.14.5 Estimation of Genetic Component of variation

Variance of GCA and SCA were calculated by the following formulae:

Cov. H.S. (lines) = $\frac{M_l - M_{l\times t}}{r \times t}$

Cov. H.S. (tester) = $\frac{M_t - M_{l\times t}}{r \times l}$

Cov. H.S. (average) = $\frac{1}{r(2lt - l - t)}\left[\frac{(l-1)M_l + (t-1)M_t}{(l+t) - 2} - M(l \times t)\right]$

$\sigma^2 gca =$ Cov. H.S..(average) = $\left[\frac{1+F}{4}\right]\sigma^2 A$

$\sigma^2 sca = \frac{M_{lxt} - Me}{r} = \left[\frac{1+F}{2}\right]^2 \sigma^2 D$

Where,

M_l = Mean sum of square of line

M_t = Mean sum of square of tester

$M_{l\times t}$ = Mean sum of square of LxT

Cov H.S. = Coverience of half side progress

F= Inbreeding coefficient (For self-pollinated crop,F=1)

$\sigma^2 A$ = Addetive genetic varience

$\sigma^2 D$ - Dominance genetic varience

3.14.6 Estimation of proportional contribution of line, tester and line x tester interaction to total Variance of hybrids

Contribution of lines= $\left({SS_l}/{SS_{Crosses}}\right) \times 100\%$

Contribution of tester= $\left({SS_t}/{SS_{Crosses}}\right) \times 100\%$

Contribution of $l \times t$ = $\left({SS_{l\times t}}/{SS_{Crosses}}\right) \times 100\%$

Where,

SS_l = Sum of square of lines,

SS_t = Sum of square of testers,

$SS_{l\times t}$ = Sum of square of lines x tester interaction,

SScrosses = Sum of square of crosses

3.14.7 Determination of combining ability status

We know that,t determine combining ability status over all character as studied as high (H) or low (L.).

The procedure was in brief as follows:

i. As in the heterosis, the desirable direction of improvement of each character was considered in the case of SCA also.

i i. The SCA/GCA effect was tested whether significantly different from zero on either side by two tialed t- test at 5% level of significance.

iii. 'K' is the mean value of all significant SCA/GCA effect was calculated.

iv. 'K' was used as the norm. Significant SCA/GCA effects whose Values were greater than or equal to 'K' receive a score of '+1' ;those significant effects which were less than 'K' received '-1' ;all non – significant effects receive a zero score.

v. A final SCA score was obtained for each cross by addition of the individual scores for each character. The mean across the crosses was calculated. A cross whose final score was greater than or equal to this mean was allotted a high (H) over all SCA/GCA status and one whose final score was less than this mean, got a low (L) overall SCA/GCA status.

vi. The characters like days to 50% flowering and days to maturity, negative GCA or SCA was desired to get early genotype. So during scoring significant negative GCA or SCA were scored as '+' and those of positive were ' —'.

The parents and hybrids were grouped into the class 'H' and 'L' based on their overall GCA or SCA status.

3.14.8 Estimation of heterosis

The overall mean value for each parent or hybrid in all replications for each character was taken to estimate heterosis. Heterosis was calculated as percent deviation of F_1

hybrid from the line value in question. The magnitude of heterosis was expressed as heterosis over mid parent (HM), heterosis over pollen parents (HP) and heterosis over check or economic heterosis (HC) for cloven characters. BARI sarisa -13 was taken as standard check variety to estimate economic heterosis. Heterosis was calculated by the following formula:

3.14.8.1 Estimation of heterosis over mid parent (Hm)

$$Hm\% = \frac{\overline{F_1} - \overline{MP}}{\overline{Mp}} \times 100$$

$$SE(Hm) = \frac{2ve}{r}$$

$$t\ value = \frac{(F_1 - \overline{MP})}{SE(Hm)}$$

3.14.8.2 Estimation of heterosis over better parent (Hb)

$$Hb\% = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

$$SE(Hb) = \frac{2ve}{r}$$

$$t\ value = \frac{(\overline{F_1} - \overline{BP})}{SE(Hb)}$$

3.14.8.3 Estimation of heterosis over check variety (Hc)

$$Hc\% = \frac{\overline{F_1} - \overline{CV}}{\overline{CV}} \times 100$$

$$SE(Hc) = \frac{2ve}{r}$$

$$t\ value = \frac{(\overline{F_1} - \overline{CV})}{SE(Hc)}$$

Where,

Ve =Error mean sum of square from RCBD ANOVA of parents.

R= Number of replication

$\overline{F_1}$ =Mean of F $_I$

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

$\overline{CV}$ = Mean of check variety

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

Chapter IV

Results and Discussion

CHAPTER 4

RESULTS AND DISCUSSION

An experiment was conducted with eight testers named Nap 248, Nap 179, Nap 206, Nap 2001, Nap 2057, Nap 2012, Nap 2013 and Nap 2022, five lines named Nap 94006, Nap 9908, Nap 2037, BS-7, BS-13 and forty crosses (hybrids). Data were recorded on different characters such as, days of 50% flowering, days of 50% maturity, plant height (cm), no. of silique per plant, length of sliqua (cm), seeds per siliqua, primary branches/plant, secondary branches/plant, thousand seed weight (g) and yield /plant (g) to estimate combining ability, gene action, and heterosis.

4.1 Combining ability analysis for different characters in lines, testers and crosses

To predict hybrid performance of the crosses involving five lines and eight testers, analysis of variance for Hybrid (crosses), line, tester, line X tester, combining ability and other components were estimated through line x tester method (Klempthorne 1957). The analysis of variance, proportional contribution of line, tester and line x tester interaction to the total variances of the hybrids, estimation of general combining ability effects for lines and testers, specific combining ability effects for hybrids and genotype grouping based on GCA and SCA were discussed as follows:

The analysis of variance for ten characters showed that the hybrids were significantly different at 1% level, for all characters studied (Table 3 and Table 4). Treatment mean sum of squares were further partitioned into variance due to lines (female parents), testers (male parents) and inter action (line x tester). Variance due to lines were significant for no. of primary branches/plant, no. of secondary branches/plant, day of 50% maturity and seed yield/ plant(gm) at 1%level, for plant height, number of seeds/siliqua at 5% level. Variance due to testers for days to 50% maturity was significant at 5% level and thousand seed weight (gm) at 1% level. Variance due to interaction (line X tester) was found highly significant for all the characters except no. of primary branches/plant, no. of secondary branches/plant, number of seeds/siliqua and no. of siliqua/plant. Analysis of variance showed wide range of variability for all the Characters studied. The magnitudes of SCA variance were high for all characters indicating the predominance of non-additive gene actions. The ratios of SCA and GCA variance for all characters were higher than unity suggested non-additive agene actions predominated over additive gene action for all the characters. The results of Goswami *et al.* (2005) were in agreement with the present results. This result suggests that the prevalence of non-additive gene action in these characters could be used in heterosis breeding. The proportional contribution of lines, testers and their interactions were analyzed (Table 5) and found that the contribution of lines were higher than contribution of testers to the total variances for plant height, primary branch/plant and number of siliqua/plant . These result suggested that the predominance of general combining ability for plant height, primary branches/plant and number of siliqua/plant. The contribution of line x tester (interactions) were higher than that of lines or testers for all characters. This indicated the positive indication for development heterotic hybrid. Similar results were also found by Yadav *el al.* (2005).

Table 3. Analysis of variance for combining ability for different characters in *Brassica napus* genotypes

Source of variation	Degree of Freedom	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
Treat	52	168.247	0.931	4.317	6.793	5.076	1753.164	1.044	10.830	1.510	15.586
Rep	2	270.578	14.354	3.909	1.491	7.528	27143.280	0.386	3.886	0.084	250.619
Hybrid	39	192.94**	0.752	3.62*	8.340**	5.126**	1706.895	1.010**	10.367**	1.530**	17.699**
Line(female)	4	348.71*	2.94**	12.72**	9.179	11.304**	3627.433**	0.894	25.582*	1.272	72.920**
Tester(male)	7	188.370	0.278	2.273	7.189	7.285*	1931.501	0.414	2.706	3.507**	12.962
L vs T	28	171.83**	0.558	2.656	8.508**	3.704**	1376.381	1.175*	10.109	1.072**	10.995**
Error	104	57.259	0.546	1.763	1.523	1.169	1086.410	0.159	1.891	0.052	4.802
Component of variance											
$\sigma^2 gca$		0.330	0.003	0.015	-0.003	0.022	5.162	-0.003	0.004	0.007	0.105
$\sigma^2 sca$		38.191	0.004	0.298	2.328	0.845	96.657	0.339	2.739	0.340	2.064
$\sigma^2 GCA/\sigma^2 SCA$		0.009	0.800	0.051	-0.001	0.026	0.053	-0.008	0.001	0.021	0.051
CV%		7.180	18.268	30.042	4.222	1.502	20.947	7.932	8.534	12.956	10.847

$\sigma^2 gca$: Variance of general combining ability

$\sigma^2 sca$: Variance of specific combining ability

** Significance at 1%level, * Significance at 5%level

Table 4: Analysis of variance for combining ability for different characters in *Brassica napus* hybrids and parents

Source of variation	Degree of Freedom	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
Treatment	52	168.305**	0.932	4.320*	6.798**	5.107**	1765.221	1.054**	10.830**	1.512**	15.603**
Replication	2	258.089	14.866	3.781	1.377	8.043	26768.790	0.287	3.741	0.072	258.817
Error	104	57.732	0.560	1.796	1.550	1.185	1093.844	0.168	1.971	0.052	4.839

** Significance at 1%level * Significance at 5%level

Table 5: Proportional contribution of line tester and their interactions to the total variance in *Brassica napus* hybrids

Source	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
Due to lines	18.537	40.141	36.051	11.288	22.617	21.797	9.082	25.309	8.532	42.256
Due to testers	17.523	6.634	11.272	15.472	25.505	20.311	7.366	4.684	41.156	13.145
Due to line × tester	63.940	53.225	52.676	73.239	51.878	57.893	83.553	70.007	50.313	44.599

4.2 Mean performance and combining ability effects

General combining ability (GCA) effects in respect of testers and lines (Table 6-7) and specific combining ability (SCA) effects of crosses (Table 8), maximum and minimum mean values of 40 cross combinations (Table 6), inter se mean of parents (Table 7), scoring of GCA and SCA effects (Appendix III-V), promising specific cross combination with its SCA grouping and parents GCA grouping are presented in Table 8-10. Results revealed that there was a wide range of variation in combining ability estimates and means. Forty cross combinations were categorized in two groups considering all characters. Sixteen crosses were found under high (H) SCA group and 24 crosses were under low (L) SCA group. The salient feature about the above estimates, are presented character wise as follows:

4.2.1. Plant height

a. Mean performance

The tallest plant (127.20 cm) was found from the cross Nap 9908×Nap 206 and followed by Nap 2037×Nap 2012(121.60cm) and Nap 9908×Nap2013 (116.50cm). The shortest plant (88.37cm) was found from the BS-7×Nap 2057 which was followed by Nap 94006×Nap2022 (91.83cm), Nap 2037 × Nap 206 (93.43cm) (Table 6).

b. General combining ability (GCA) effects on plant height

The general combining ability effects were significant for two lines for this trait (Table-9). GCA varied from -5.77 to 3.86 for *Brassica napus* lines and from-5.73 to 4.42 for testers. Among *Brassica napus* lines Nap 9908 exhibited the highest positive highly significant GCA effect (3.86) followed by Nap 94006 (2.91). BS-7 had the highly significant negative GCA effects (-5.77). Among *Brassica napus* testers Nap 2012 exhibited the highest positive highly significant GCA effect (4.42) followed by Nap 2013 (3.83) and Nap 206 (3.28). Nap 2057 had the highly significant negative GCA effects (-5.73). Those effects indicated that lines and testers having positive values of GCA effects possessed more positive alleles and those having negative values possessed more negative alleles for the tallness. From the above discussion, it was found that Nap 9908 (lines) and Nap 2012 (testers) were the best general combiner due to high positive GCA effects if tall type is desired. On the other hand BS-7 (lines) and Nap 2057(testers) were also found as the best general combiner due to the highest negative GCA effects if dwarf type is desired.

c. Specific combining ability (SCA) effects

Significant SCA effects was observed in 22 crosses (Table 10) out of 40 hybrids tested, of which eleven had significant positive and eleven had significant negative effect. Positive SCA effects were in favorable (positive) direction, during scoring these were scored as '1' and significant negative SCA scored as '-1' (Appendix V.) The promising hybrids with positive significant SCA effects were considered as good specific combiner for tallness. The cross Nap9908×Nap206 (15.93) showed the highest positive SCA effects and it was followed by Nap2037×Nap2012 (12.94), Nap2037×Nap2022 (7.25). Good specific combiner for tallness was evolved from low x low, high x high general combiner parents. So additive x additive gene effects were observed in good specific cross combinations. The promising hybrids with negtive significant SCA effects were considered as good specific combiner for dwarfness. The crosses Nap9908×Nap2012 (-14.11), Nap94006×Nap2022 (-13.47) and Nap9908×Nap179 (-10.69) had high negtive significant SCA effect. Sheoran el al.,(2000) observed similar result for this trait in brown sarson (*Brassica campesties* L.)

4.2.2. Number of primary branches per plant

a. Mean performance

The highest mean was observed in the cross Nap2037×Nap2022 (5.23) for number of primary branches per plant (Table 6). Another crosses closer to this value were Nap94006×Nap248 (4.83) and Nap9908xNap248 (4.83) which were higher than both of its parents (Table 6 and 7) while BS-7×Nap2057 had the lowest mean of number of primary branches per plant (2.13). It was lower than female parents and pollen parents.

b. General combining ability effects

Significant GCA effect for number of primary branches per plant was not found in three female parents. Of them one was positive and one was negative (Table 9). Nap 9908 showed highest GCA effect (0.29) and it was followed by Nap94006 (0.27). It indicated that they were good general combiners due to positive GCA effects. On the other hand, BS-7 had showed lowest GCA effect (-0.43) and it was followed by BS-13 (-0.31). So they were considered poorer general combiner due to negative GCA values. Significant GCA effect for number of primary branches per plant was not found in pollen parents (Table 8).

c. Specific combining ability effects

Twenty five cross combination showed significant SCA effects. Among them 12 were positive and 13 were negative (Table 10). The cross Nap 9908×Nap2013 showed the highest positive SCA effects (0.91)and it was followed by Nap9908×Nap2057(0.73) and BS-7×Nap179 (0.51), where as Nap2037×Nap248 (-0.67) showed the highest negative SCA effects and it was followed by Nap94006×Nap2022 (-0.53) and BS-7× Nap248 (-0.47). The former crosses were considered as good cross combinations for the trait and the latter two were considered as poor specific cross combinations. Non-Significant positive crosses were considered as above average and below average specific cross combination, respectively. The hybrid 2037×Nap2022 (0.91) was derived from high and high general combiners. It indicated that high x high general combiner parents produced good specific combination of crosses with positive SCA effects for this trait. So additive x additive type of gene action was responsible for these good specific crosses for this trait. Singh *el al.*, (2005) observed similar result for this trait in Indian mustard.

4.2.3. Number of Secondary branches per plant

a. Mean Performance

The highest mean for number of secondary branches per plant (7.27) was observed in the cross combination Nap94006×Nap2001 followed by Nap94006× Nap248 (5.83) and Nap9908×Nap248 (5.83) which were higher than both of its parents (Table 6 and 7). On the other hand the lowest mean (2.43) was found in cross combination BS-7×Nap206 and it was followed by Nap2037×Nap179 (2.47), BS-13×Nap2001(2.47) and BS-13xNap2057(2.47) which were lower than female parents and pollen parents (Table 6 and 7).

b. General combining ability effects

Out of five female parents four showed significant GCA effects, of them two were positive and two were negative. Nap 9908 had highly significant positive GCA effect (0.68) followed by Nap 94006 (0.60). On the other hand BS-7 and BS-13 had the lowest significant negative GCA value (- 0.78) (Table 9). The genotypes with significant positive GCA effects were considered as good general combiners and with significant negative GCA effects were poor general combiners. Non significant positive and negative GCA effects indicated average and below average combiners. Positive significant GCA effects was observed in pollen parent Nap 248 (0.76) and non negative GCA effects was observed in pollen parent Nap 2013 (-0.29) (Table 8).

c. Specific combining ability effects

Out of 40 crosses, 30 cross combinations showed significant SCA effects of them 16 had positive and 14 had negative GCA effects. The highest positive significant SCA effect (1.70) was found in the cross BS-7×Nap2012 and it was followed by Nap94006×Nap2001 (1.15) and Nap9908×Nap2057 (1.03). The lowest negative GCA effect (-1.43) was found in the hybrid Nap2037×Nap248 and Nap2037xNap179 followed by cross combinations Nap94006×Nap2012 (-1.24) and Nap9908×Nap2022 (-1.18) (Table 10). The best specific cross for the trait was produced by low x high combiner parents. The lowest specific combination was produced by low x high general combiner parents. These results indicated that additive x noadditive gene action governed this character. Yadav *et at.*, (2005) found additive and non additive types of gene action in the expression of this trait.

Table 6.Per se performance (mean) of forty crosses in *Brassica napus* L.

Cross	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length (cm)	Number of seeds/ siliqua	1000 seed weight (gm)	Seed yield/plant (gm)
Nap 94006 x Nap 248	105.10	4.83	5.83	37.00	87.00	121.10	7.40	23.83	2.33	11.47
Nap 94006 x Nap 179	112.40	3.20	5.10	35.00	86.00	146.60	8.50	22.80	4.33	9.10
Nap 94006 x Nap 206	110.90	3.00	3.58	35.00	86.00	115.70	7.60	23.43	3.17	9.47
Nap 94006 x Nap 2001	108.20	3.70	7.27	36.33	88.30	161.20	8.20	24.60	2.10	9.27
Nap 94006 x Nap 2057	106.70	2.83	3.40	35.33	89.00	111.90	6.40	24.57	4.13	7.40
Nap 94006 x Nap 2012	109.20	3.37	3.03	37.00	88.00	123.90	7.90	23.33	2.53	8.87
Nap 94006 x Nap 2013	111.60	3.13	5.10	37.00	87.70	146.60	7.50	22.67	4.00	11.50
Nap 94006 x Nap 2022	91.83	2.87	3.80	37.67	86.00	87.20	8.30	25.80	3.10	10.27
Nap 9908 x Nap 248	105.10	4.83	5.83	37.00	87.00	121.10	7.40	23.83	2.33	11.47
Nap 9908 x Nap 179	95.83	3.10	5.00	38.00	86.70	98.80	6.80	20.27	2.17	9.13
Nap 9908 x Nap 206	127.20	3.37	5.10	37.33	89.00	175.40	7.50	23.53	2.33	10.83
Nap 9908 x Nap 2001	108.50	2.97	4.80	36.00	88.00	123.30	7.10	22.47	3.03	16.87
Nap 9908 x Nap 2057	100.00	3.83	5.40	35.00	87.70	129.80	7.10	20.33	4.10	14.73
Nap 9908 x Nap 2012	118.50	2.63	3.37	34.00	85.00	143.70	7.30	21.10	3.00	14.83
Nap 9908 x Nap 2013	116.50	3.33	3.90	35.00	88.30	105.70	7.90	22.50	3.06	15.07

Table 6 Continued

Cross	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length (cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
Nap 9908 x Nap 2022	98.33	3.00	3.23	33.00	84.70	100.10	6.80	24.43	2.13	8.43
Nap 2037 x Nap 248	100.50	2.67	3.50	36.00	87.00	71.73	6.90	19.57	3.80	10.73
Nap 2037 x Nap 179	99.30	2.67	2.47	36.33	86.30	90.51	8.00	23.40	3.13	12.13
Nap 2037 x Nap 206	93.43	3.37	5.07	32.67	84.70	120.90	7.10	20.73	3.17	8.10
Nap 2037 x Nap 2001	104.50	3.73	5.40	35.33	86.30	116.90	7.90	23.83	2.10	9.40
Nap 2037 x Nap 2057	99.98	2.87	4.47	35.67	86.70	79.53	7.70	21.13	4.33	7.47
Nap 2037 x Nap 2012	121.60	2.80	4.40	32.00	83.30	139.60	7.60	20.47	3.33	10.93
Nap 2037 x Nap 2013	105.00	2.97	3.47	37.00	87.70	126.00	5.90	18.23	2.17	10.07
Nap 2037 x Nap 2022	109.80	5.23	4.60	36.00	86.30	128.80	7.80	20.70	3.10	8.33
BARI Sarisha-7 x Nap 248	97.40	2.23	3.47	35.00	85.70	82.67	7.40	23.20	3.10	6.07
BARI Sarisha-7 x Nap 179	98.07	2.97	2.97	36.67	87.00	87.27	7.30	23.83	4.10	8.17
BARI Sarisha-7 x Nap 206	94.20	2.30	2.43	35.33	87.00	87.83	8.10	23.20	3.10	6.37
BARI Sarisha-7 x Nap 2001	101.60	2.37	2.97	36.67	87.30	107.30	6.70	20.33	3.17	9.17
BARI Sarisha-7 x Nap 2057	88.37	2.13	2.67	35.00	87.70	75.73	7.50	21.90	4.10	7.90
BARI Sarisha-7 x Nap 2012	102.30	2.60	4.60	37.67	86.00	142.30	8.10	24.10	4.03	11.00

Table 6 Continued

Cross	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length (cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
BARI Sarisha-7 x Nap 2013	103.30	2.57	2.43	37.00	88.30	113.00	7.03	20.37	2.33	8.73
BARI Sarisha-7 x Nap 2022	101.30	3.07	3.73	33.33	86.00	113.40	6.90	19.63	3.03	8.73
BARI Sarisha-13 x Nap 248	101.10	3.17	4.63	32.00	83.70	99.70	6.60	20.30	3.20	9.27
BARI Sarisha-13 xNap 179	107.70	2.50	2.97	35.00	86.00	96.70	7.23	21.27	4.13	8.86
BARI Sarisha-13 xNap 206	111.10	3.03	2.93	37.00	87.00	99.93	7.10	20.50	3.17	10.30
BARI Sarisha-13 xNap 2001	95.37	2.53	2.47	34.67	86.30	79.45	6.40	19.10	2.10	8.50
BARI Sarisha-13 xNap 2057	96.73	2.40	2.47	34.00	84.30	100.30	7.70	23.27	4.10	10.37
BARI Sarisha-13 xNap 2012	97.20	2.63	3.00	31.67	82.70	104.80	7.00	23.27	2.53	10.33
BARI Sarisha-13 xNap 2013	103.20	2.27	3.10	37.33	85.70	125.70	8.00	24.00	3.97	8.23
BARI Sarisha-13 xNap 2022	110.70	2.47	3.33	36.00	87.00	116.80	7.80	24.83	3.10	8.70
Mean	104.20	2.96	3.90	35.53	86.58	112.97	7.39	22.27	3.15	9.91
Maximum	127.20	5.23	7.27	38.00	89.00	175.40	8.50	25.80	4.33	16.87
Minimum	88.37	2.13	2.43	31.67	83.67	71.73	5.90	18.23	2.10	6.07

Table 7: Inter se (estimated) mean of thirteen *Brassica napus* L. genotypes

Parents	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
Nap 94006	105.80	4.10	6.00	36.00	85.00	89.30	7.20	19.40	3.20	8.10
Nap 9908	106.80	3.53	2.56	36.00	89.00	113.10	6.80	18.70	3.00	7.06
Nap 2037	106.30	3.87	6.10	36.33	87.00	160.40	8.30	24.10	4.00	10.40
BARI Sarisha-7	111.40	3.73	3.20	35.33	87.00	118.70	6.87	21.87	4.00	7.33
BARI Sarisha-13	103.30	2.93	3.73	35.33	87.30	130.00	7.90	22.20	3.10	9.43
Nap 248	104.60	2.73	2.77	36.33	87.00	105.20	8.10	23.67	4.30	11.03
Nap 179	98.90	3.63	5.13	35.67	85.00	101.40	7.40	20.33	3.20	11.50
Nap 206	109.90	2.93	3.07	36.00	84.70	120.70	8.10	23.23	4.20	8.13
Nap 2001	99.63	2.50	3.00	37.00	86.30	122.20	7.60	22.17	2.90	11.00
Nap 2057	109.20	3.33	4.83	36.67	86.30	153.50	6.70	21.57	4.33	10.43
Nap 2012	101.10	2.88	3.63	35.33	87.70	138.10	8.20	22.83	3.40	12.40
Nap 2013	113.40	3.13	5.93	36.00	86.70	156.30	7.50	22.50	3.80	12.00
Nap 2022	92.53	2.63	4.77	35.00	87.00	99.90	8.50	24.20	2.20	11.23
Mean	104.80	3.30	4.30	35.92	86.62	124.29	7.63	22.26	3.51	10.00
Maximum	113.40	3.87	6.10	37.00	89.00	160.40	8.50	24.20	4.33	12.40
Minimum	92.53	2.50	2.56	35.00	84.67	89.30	6.70	18.70	2.20	7.06

Table-8. GCA effects of testers for different Characters in *Brassica napus* L.

Parents	Plant height	Number of primary branches/plant	Number of secondary branches/ plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)	GCA Group
Nap 248	-2.24	0.17	0.76**	-0.12	-0.34	-13.27*	-0.23**	-0.12	-0.19**	-0.16	L
Nap 179	-1.42	-0.08	-0.26	0.67*	-0.20	-8.55	0.18*	0.05	0.39**	-0.48	L
Nap 206	3.28*	0.04	-0.07	-0.05	0.25	7.38	0.05	0.01	-0.17**	-0.95*	H
Nap 2001	-0.45	0.09	0.45	0.27	0.65**	5.12	-0.11	-0.20	-0.65**	0.68	H
Nap 2057	-5.73**	-0.15	-0.21	-0.52*	0.45*	-13.06*	-0.10	-0.03	0.97**	-0.39	L
Nap 2012	4.42**	-0.16	-0.21	-1.05**	-1.14**	18.36**	0.18*	0.19	-0.06	1.59**	H
Nap 2013	3.83*	-0.07	-0.29	1.14**	0.92**	7.28	-0.12	0.81 **	0.04	0.78	H
Nap 2022	-1.69	0.15	-0.15	-0.32	-0.60**	-3.26	0.14	-0.71*	-0.25**	-1.07*	L
SE (±)	1.95	0.19	0.34	0.31	0.27	8.51	0.10	0.35	0.05	0.56	
SE(gi-gj)T	2.76	0.26	0.48	0.45	0.39	12.03	0.14	0.50	0.08	0.80	
MAX	4.42	0.17	0.76	1.14	0.92	18.36	0.18	0.81	0.97	1.59	
MIN	-5.73	-0.16	-0.29	-1.05	-1.14	-13.27	-0.23	-0.71	-0.65	-1.07	

* Significance at 5%level, ** Significance at 1%level, SE: Standard error , SE(gi-gj): Standard error difference between GCA effect of two tester, H: GCA group-High , L: GCA group- low.

Table-9. GCA effects along with their combining ability status for different Characters in five line of *Brassica napus* L.

Parents	Plant Height	No. of primary branches/plant	No. of secondary branches/ plant	Days to 50% flowering	Days to 50% maturity	No. of siliqua/plant	siliqua length(cm)	No. of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)	GCA Group
Nap 94006	2.91	0.27	0.60*	0.76**	0.64**	14.25*	0.32**	1.61**	0.04	-0.30	H
Nap 9908	3.86*	0.29	0.68*	0.14	0.43*	12.22	-0.14	0.04	-0.38**	2.95**	H
Nap 2037	0.18	0.19	0.27	-0.40	-0.44*	-5.52	-0.01	-1.26**	-0.03	-0.32	L
BARI Sarisha-7	-5.77**	-0.43**	-0.78**	0.30	0.35	-11.37	-0.01	-0.20	0.22**	-1.70**	L
BARI Sarisha-13	-1.20	-0.31*	-0.78**	-0.81**	-0.98**	-9.59	-0.14	-0.20	0.14**	-0.64	L
SE(±)	1.54	0.15	0.27	0.25	0.22	6.72	0.08	0.28	0.04	0.44	
SE(gi-gj)L	**2.18**	**0.21**	**0.38**	**0.35**	**0.31**	**9.51**	**0.11**	**0.39**	**0.06**	**0.63**	
MAX	3.86	0.29	0.68	0.76	0.64	14.25	0.32	1.61	0.22	2.95	
MIN	-5.77	-0.43	-0.78	-0.81	-0.98	-11.37	-0.14	-1.26	-0.38	-1.7	

* Significance at 5%level, ** Significance at 1%level, SE: Standard error, SE(gi-gj): Standard error difference between GCA effect of two line, H: GCA group-High, L: GCA group- low.

Table-10. SCA effects along with their combining ability status of *B. napus* hybrids (cross) for different Characters

Hybrids (cross)	Plant height	Number of primary branches/ plant	Number of secondary branches/plant	Days to 50% flowerig	Days to 50% maturity	Number of siliqua/ Plant	siliqua length (cm)	Number of seeds/ siliqua	1000 seed weight (gm)	Seed yield/plant (gm)	SCA group
Nap 94006 x Nap 248	0.34	0.41**	0.57**	0.83**	0.09	7.56	-0.07	0.07	-0.66**	1.96**	H
Nap 94006 x Nap 179	6.82**	0.04	0.87**	-1.96**	-1.04**	28.34**	0.57**	-1.13**	0.56**	-0.08	H
Nap 94006 x Nap 206	0.65	-0.28*	-0.83**	-1.23**	-1.50**	-18.42**	-0.19**	-0.46*	0.15**	0.75*	L
Nap 94006 x Nap 2001	1.68	0.36**	1.15**	-0.23	0.42*	29.29**	0.58**	0.92**	-0.44**	-1.08**	H
Nap 94006 x Nap 2057	5.43**	-0.25*	-0.88**	-0.43*	1.29**	-1.78	-1.23**	0.71**	-0.02	-1.88**	L
Nap 94006 x Nap 2012	-2.24	0.28*	-1.24**	1.76**	1.89**	-21.23**	-0.03	-0.73**	-0.60**	-2.39**	L
Nap 94006 x Nap 2013	0.77	-0.03	0.89**	-0.43*	-0.50**	12.57*	-0.11	-0.50*	0.85**	1.06**	H
Nap 94006 x Nap 2022	-13.47**	-0.53**	-0.54*	1.70**	-0.64**	-36.31**	0.48**	1.11**	0.17**	1.67**	L
Nap 9908 x Nap 248	-0.60	0.39**	0.49*	1.45**	0.30	9.59	0.47**	1.65**	-0.25**	-1.28**	H
Nap 9908 x Nap 179	-10.69**	-0.07	0.69**	1.65**	-0.16	-17.39**	-0.59**	-2.09**	-0.99**	-3.29**	L
Nap 9908 x Nap 206	15.93**	0.06	0.56**	1.72**	1.70**	18.11**	0.07	1.21**	-0.27**	-1.13**	H
Nap 9908 x Nap 2001	1.00	-0.38**	-0.22	0.05	0.30	-6.57	0.01	0.36	0.91**	3.28**	L
Nap 9908 x Nap 2057	-2.21	0.73**	1.03**	-0.14	0.16	43.30**	-0.03	-1.95	0.36**	2.21**	H
Nap 9908 x Nap 2012	-14.11**	-0.46**	-0.99**	-0.60**	-0.90**	0.62	-0.09	-1.40**	0.29**	2.13**	L
Nap 9908 x Nap 2013	4.69**	0.91**	-0.38	-1.80**	0.36*	-26.32**	0.90**	3.02**	0.33**	1.48**	H
Nap 9908 x Nap 2022	-7.92**	-0.41**	-1.18**	-2.34**	-1.75**	-21.35**	-0.62**	1.31**	-0.39**	-3.41**	L

Table-10 continued

Hybrids (cross)	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowerig	Days to 50%maturity	Number of siliqua/ Plant	siliqua length (cm)	Number of seeds/ siliqua	1000 seed weight (gm)	Seed yield/plant (gm)	SCA group
Nap 2037 x Nap 248	-1.55	-0.67**	-1.43**	1.00**	1.17**	-21.98**	-0.22**	-1.32**	0.88**	1.25**	L
Nap 2037 x Nap 179	-3.54**	-0.41**	-1.43**	0.53**	0.37*	-7.94	0.45**	2.35**	-0.37**	2.97**	L
Nap 2037 x Nap 206	-0.19	0.15	0.97**	-2.40**	-1.75**	6.52	-0.35**	-0.29	0.22**	-0.60	L
Nap 2037 x Nap 2001	0.64	0.47**	0.77**	-0.06	-0.49**	4.81	0.69**	0.90**	-0.37**	-0.92**	L
Nap 2037 x Nap 2057	1.42	-0.14	0.50*	1.06**	0.04	-14.40**	0.45**	0.15	0.05	-1.79**	L
Nap 2037 x Nap 2012	12.94**	-0.20	0.44*	-2.58**	-0.69**	14.24**	0.02	-0.73**	0.28**	-0.30	H
Nap 2037 x Nap 2013	-3.06*	-0.12	-0.41*	0.73**	0.57**	-6.27	-1.37**	-2.06**	-0.91**	-0.36	L
Nap 2037 x Nap 2022	7.25**	0.15	0.58**	1.20**	0.77**	25.03**	0.33**	-1.12**	0.24**	-0.24	H
BARI Sarisha-7 x Nap 248	1.32	-0.47**	-0.40*	-0.70**	-0.95**	-5.21	0.25**	1.25**	-0.07*	-2.04**	L
BARI Sarisha-7 x Nap 179	1.17	0.51**	-0.24	0.15	0.25	-5.33	-0.25**	1.72**	0.35**	0.38	L
BARI Sarisha-7 x Nap 206	-7.40**	-0.27*	-0.60**	-0.44*	0.45**	-21.03**	0.65**	1.12**	-0.13**	-0.95**	L
BARI Sarisha-7 x Nap 2001	3.73**	-0.25*	-0.59**	0.55**	-0.28	1.05	-0.57**	-1.54**	0.45**	0.22	L
BARI Sarisha-7 x Nap 2057	-4.22**	-0.24*	-0.23	-0.30	0.25	-12.35*	0.21**	-0.14	-0.23**	0.02	L
BARI Sarisha-7 x Nap 2012	-0.40	0.23*	1.70**	2.89**	0.18	22.82**	0.52**	1.84**	0.73**	1.14**	H
BARI Sarisha-7 x Nap 2013	1.15	0.11	-0.38	0.02	0.45**	4.57	-0.20**	-0.99**	-0.99**	-0.31	L
BARI Sarisha-7 x Nap 2022	4.63**	0.37**	0.77**	-2.17**	-0.35*	15.47**	-0.61**	-3.25**	-0.08*	1.54**	H

Table-10 continued

Hybrids (cross)	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowerig	Days to 50%maturity	Number of siliqua/ Plant	siliqua length (cm)	Number of seeds/ siliqua	1000 seed weight (gm)	Seed yield/plant (gm)	SCA group
BARI Sarisha-13 x Nap 248	0.48	0.33**	0.76**	-2.58**	-1.76**	10.04*	-0.43**	-1.65**	0.11**	0.11	H
BARI Sarisha-13 x Nap 179	6.23**	-0.06	0.12	-0.38*	0.58**	2.32	-0.19**	-0.85**	0.46**	0.03	H
BARI Sarisha-13 x Nap 206	4.92**	0.33**	-0.10	2.35**	1.11**	-10.37*	-0.19**	-1.58**	0.05	1.93**	L
BARI Sarisha-13 x Nap 2001	-7.07**	-0.20	-1.09**	-0.31	0.05	-28.58**	-0.71**	-2.77**	-0.54**	-1.50**	L
BARI Sarisha-13 x Nap 2057	-0.42	-0.09	-0.43*	-0.18	-0.61**	10.43*	0.61**	1.23**	-0.15**	1.43**	H
BARI Sarisha-13 x Nap 2012	-10.10**	0.14	0.10	-1.98**	-0.48**	-16.45**	-0.42**	1.01**	-0.70**	-0.58	L
BARI Sarisha-13 x Nap 2013	-3.55**	-0.10	0.28	1.48**	-0.88**	15.45**	0.79**	2.65**	0.72**	-1.87**	H
BARI Sarisha-13 x Nap 2022	9.50**	-0.34**	0.37	1.61**	1.98**	17.16**	0.42**	1.95**	0.07	0.45	H
SE(±)	1.19	0.11	0.20	0.19	0.17	5.21	0.06	0.21	0.03	0.34	
SE(sij-kl)	6.18	0.60	1.08	1.00	0.88	26.91	0.32	1.12	0.18	1.78	
Max	15.93	0.91	1.70	2.89	1.98	43.30	0.90	3.02	0.91	3.28	
Min	-14.11	-0.67	-1.43	-2.58	-1.76	-36.31	-1.37	-3.25	-0.99	-3.41	

* Significance at 5%level, ** Significance at 1%level, SE: Standard error SE(sij-kl):Standard error of difference between for any two SCAeffect of hybrids

H: SCA group-High L: SCA group- low

4.2.4. Days to -50 percent flowering

a. Mean performance

The earliest (flowering) three hybrids were BS-13 x Nap 2012 (31.67days), BS-13× Nap 248(32 days) and Nap 2037× Nap 2012 (32 days). All these crosses were earlier than both of their estimated parental mean. The three crosses Nap 9908 × Nap 179 (38 days), BS-7 × Nap2012 (37.67days) and Nap 94006 × Nap 2022 (37.67 days) were take highest time to 50% flowering. All these crosses were take higher time to 50% flowering than their parental mean (Table 6 - 7).

b. General combining ability effects

General combining ability effects were desired for days to flowering. The general combining ability effects ranged from 0.76 to -0.81 for *B. napus* line and -1.05 to 1.14 for testers (Table 8-9). Among five (5) *B. napus* lines, two (2) showed significant GCA effect for days to 50% flowering, among them one was negative and one was positive. Parents with negative GCA effect were good general combiner earliness. BS-13 showed the lowest (-0.81) and Nap 94006 showed the highest GCA effects (0.76) (Table 9). In case of eight testers four showed significant GCA effect for days to 50% flowering, among them two were positive and two were negative, those are Nap 179 (0.67), Nap 2057 (-0.52), Nap 2012 (-1.05), Nap 2013 (1.14) (Table 8). It indicated that the genotype Nap 2012 designated as good general combiner contained more negative alleles for the trait than the poorer. Tak and Khan (2000) found significant combining ability effect for earliness.

c. Specific combining ability effects

Out of 40 genotypes, 31 hybrids showed significant SCA effects of which sixteen were positive and fifteen were negative. The cross BS-13 × Nap 248, Nap 2037 x Nap 2012 (-2.58) showed the highest (-2.58) negative SCA effect whereas, BS-7 x Nap 2012 (2.89), showed the highest positive SCA value (Table 10). It indicated that the first two combination was the best for earliness. The best specific combination evolved from low x low general combiners. It indicated that additive x additive gene action existed in this specific cross. Similar result was found by Singh *et al.*, (2005). Low x low general combiner parents normally produce good specific cross combination.

4.2.5. Days to -50 percent Maturity

a. Mean performance

The earliest (flowering) three hybrids were BS-13 x Nap 2012 (82.70 days), Nap 2037× Nap 2012 (83.30 days) and BS-13xNap248(83.70 days). All these crosses were earlier than both of their estimated parental mean. The crosses Nap94006xNap2057(89days),Nap9908xNap206(89days),Nap94006xNap2001 (88.30 days) and Nap9908xNap2013 (88.30 days) were take highest time to 50% maturity. All these crosses were take higher time to 50% maturity than their parental mean except female parent Nap 9908 (Table 6 - 7).

b.General combining ability effects

General combining ability effects were desired for days to maturity. The general combining ability effects ranged from 0.64 to -0.98 for lines and 0.65 to -0.60 for testers (Table 8-9). Among five (5) lines, four (4) showed significant GCA effect for days to 50% maturity, among them two were negative and two were positive. Parents with negative GCA effect were good general combiner for earliness. BS-13 showed the lowest (-0.98) and Nap 94006 showed the highest GCA effects (0.64) (Table 9). In case of eight testers, five(5) showed significant GCA effect for days to 50% maturity, among them three were positive and two were negative, those are Nap 2001 (0.65), Nap 2057 (0.45), Nap 2012 (-1.14), Nap 2013(0.92) and Nap 2022 (-0.60) (Table 8). It indicated that the genotype Nap 2012 and Nap 2022 designated as good general combiner for the trait than the poorer. Tak and Khan (2000) found significant general combining ability effect for earliness.

c. Specific combining ability effects

Out of 40 hybrids, 29 showed significant SCA effects of which 14 were positive and 15 were negative. The cross BS-13 × Nap 2022 (1.98) showed the highest positive SCA effect whereas, BS-13 x Nap 248 (-1.76), showed the highest negative SCA value (Table 10). It indicated that the second combination was the best for earliness. The best specific combination evolved from low x low general combiners. It indicated that additive x additive gene action existed in this specific cross. Similar result was found by Singh *et al.,* (2005). Low x low general combiner parents normally produce good specific cross combination.

4.2.6. Number of Siliqua per plant

a. Mean performance

The highest three cross combinations for number of siliqua per plant were Nap 9908 × Nap 206 (175), Nap 94006 × Nap 2001(161.20) and Nap 94006 × Nap 179 (146.60) (Table 5); all of which exceeded their estimated parental means (Table 6). The lowest three cross combinations were Nap2037×Nap248 (71.73), BS-7×Nap2057 (75.73) and BS-13×Nap2001 (79.45). These values were lower than their inter se (estimated) pollinator means.

b. General combining ability effects

General combining ability of eight testers ranged 18.36 to -13.27 . GCA effect of 3 testers out of 8 were significant of them one is positive and two was negative. Nap2012 had highest positive GCA effects (18.36). Nap 248, showed negative GCA effect viz. -13.27 (Table-8). In case of five lines, one had positive significant GCA effect.Nap94006 showed highest positive GCA effects (14.25)(Table-9).These facts indicated that among the tester Nap2012 with significant positive GCA value are good general combiner for the trait and possessed more positive alleles for the trait. These materials could be utilized for evolving more siliqua per plant. On the other hand, the genotype showing negative GCA effect considered as poor general combiner and possessed more negative alleles for the trait. Singh et al., (2005) and Shweta *et al.,* (2005) found good general combiners in their experiments in Indian mustard and cited similar interpretation.

c. Specific combining ability effects

Twenty six combinations showed significant SCA effects (Table 10) in 40 cross combinations. Among significant values 13 were positive and 13 were negative. The cross combination Nap9908×Nap2057 (43.30) followed by Nap94006× Nap2001 (29.29) and Nap94006×Nap179 (28.34) showed highest value. The above said hybrids were considered as he best specific combiners for the trait number of siliqua per plant in *Brassica napus.* The best specific combination was evolved from low x low general combiners for the trait. It revealed that additive x additive type of' gene action governed this trait. Chaudhary *et al.,* (1997) suggested that both additive and non additive type of gene action were present in the expression of the trait.

4.2.7. Length of Siliqua

a. Mean performance

The highest mean siliqua length was found in the hybrid Nap94006×Nap179 (8.50 cm) and the lowest mean siliqua length was found in the cross combination Nap2037 × Nap2013 (5.90cm) (Table 6). The highest inter se mean was found in the genotype Nap2022 (8.50cm) and the lowest inter se mean was found in the genotype Nap2057 (6.70) (Table 7)

b. General combining ability effects

Out of five lines one showed positive significant GCA effects. Out of eight pollen parents three showed significant GCA effects, of them two were positive and one was negative (Table 8-9). Positive significant GCA effect was found in the genotype Nap94006 (0.32) in lines and Nap2012 (0.18) followed by Nap179 (0.18) in testers. It indicated that Nap94006 and Nap2012 was good general combiner for siliqua length. The negative significant GCA effects were found in the genotypes Nap248 (- 0.23). Positive significant GCA effect was considered as good general combiner and negative significant GCA effects were considered poor general combiner. Non significant positive and negative GCA effects considered as average and below average general combiners.

c. Specific combining ability effects:

Thirty two(32) out of 40 combinations showed significant SCA effects (Table 10). Among them 16 were positive and 16 were negative. The highest positive SCA effect was found in the hybrid Nap9908 × Nap2013 (0.90) followed by Nap BS-13 ×Nap2013 (0.79) (Table 10). The lowest negative SCA effect (-1.37) was found in the cross combination Nap 2037×Nap2013 and it was followed by Nap94006 × Nap2057 (-1.23). The Good cross combination evolved from high x high general combiners. This result revealed that additive x additive gene action involved in this trait. Chaudhray *el al.*, (1997) suggested that both additive and non additive type of gene action were present in the expression of the trait.

4.2.8. Number of seeds per siliqua

a. Mean performance

The highest mean for no. of seeds per siliqua (25.80) was observed in the cross Nap94006×Nap2022 and it was followed by BS-13×Nap2022 (24.83), Nap94006× Nap2001 (24.60) where the range was 18.70 to 25.80 (Table 6 and 7). So the cross combinations produced higher number of seeds per siliqua than both of the respective parents.

b. General combining ability effects

Among the CMS lines, two (2) showed significant GCA effects. Of them one (1) showed positive and one showed negative GCA effects. Nap94006 was the best combiner due to highest significant positive GCA value (1.61) for no. of seeds / siliqua. On the other hand, Nap2037 had lowest significant GCA value (-1.26) hence, it was a poor general combiner (Table 9). Among eight (8) pollen parents, two (2) showed significant GCA effect. Of them one (1) showed positive and one showednegative GCA effects. Nap2013 had significant positive GCA value (0.81) and Nap2022 (-0.71) had significant negative GCA value (Table 8). It indicated that good general combiners possessed more positive alleles but poor general combiners possessed less positive alleles. Ghosh *et al.*, (2002) agreed with these finding.

d. Specific combining ability effects

Among the hybrids, 34 cross combinations showed significant SCA effect. Among them 17 were positive and 17 were negative. The cross combination Nap9908× Nap2013 showed the highest SCA effect (3.02). It was the good specific cross combination for the trait (Table 10). Other two cross combinations closer to this value were BS-13× Nap2013 (2.65) and Nap2037×Nap179 (2.35). On the other hand, the cross BS-7× Nap2022 showed the lowest SCA effect (-3.25) for number of seeds per siliqua. It was the poorest specific cross combination. Two other specific crosses nearer to this value were BS-13×Nap2001 (-2.77) and Nap9908 × Nap179 (-2.09). In this experiment high x low and high x high general combiner parents produced best specific combination of crosses with positive SCA effects for this character. It indicated that additive x dominance and additive x additive type of gene action is exhibited here. Yadav et al., (2004) and Singh et al., (2005) observed the best specific cross combination from high x low, low x low and high x high general combiner parents and they proposed that both additive and non additive type of gene action were predominant for the trait.

4.2.9. Thousand (1000) seed weight

a. Mean performance

The highest mean for 1000-seed weight (4.33) was observed in the cross combination Nap94006×Nap179 and Nap2037xNap2057 which was higher than both of the parents inter se mean (Table 6-7). Contrary the lowest mean (2.10) was found in cross combination Nap94006xNap2001. However, mean value of forty cross combinations were higher than their both parents, *inter se* means except pollen parent Nap2057 (Table 6-7).

b. General combining ability effects

Among five female parents three showed significant GCA effect, of them two were positive and one was negative for 1000 seed weight (Table 9). BS-13 had highly significant positive GCA effect (0.22) followed by BS-7 (0.14). On the other hand Nap9908 had the lowest significant negative GCA value (- 0.38) (Table 9). The genotypes with significant positive GCA effects were considered as good general combiners and with significant negative GCA effects were poor general combiners. Non significant positive and negative GCA effects indicated average and below average combiners. Among the eight (8) Testers six parents exhibited significant GCA effects, of them two were positive and four were negative. Highest Positive significant GCA effects was observed in pollen parent Nap 2057 (0.97) and highest negative significant GCA effects was observed in pollen parent Nap 2001(-0.65) (Table 8)

c. Specific combining ability effects

Among the cross combinations s 36 crosses exhibited significant SCA effects for 1000 seeds weight. 18 cross combinations were found with positive and 18 with negative SCA effects (Table 10). The cross combination Nap9908×Nap2001 showed the highest (0.91) positive SCA effects, followed by Nap2037×Nap248 (0.88) and Nap94006×Nap2013 (0.85). The lowest SCA value was found in the cross Nap9908×Nap179 (-0.99) and BS-7xNap2013 (-0.99). It was the poorest cross for the trait. The cross Nap2037× Nap2013 (-0.91) and BS-13×Nap2012 (-0.70) were with SCA values Closer to the lowest (Table 10).

Best specific cross combination Nap9908×Nap2001 was evolved from the parents having negative GCA effects (-0.65 and -0.38 respectively) (Table 8-9). However, the cross combinations Nap2037×Nap248 (0.88) and Nap94006×Nap2013 (0.85) showed high SCA effects. The two hybrids were evolved from the parents with low and low (-0.03 and -0.06) and high and high (0.04 and 0.14) GCA effects (Table 8-9). It revealed that good specific combination could be obtained from low x low, low x high or high x low general combiner parents. It indicated additive x additive, dominant x additive and dominant x dominant gene interaction acted upon the character 1000 seeds weight. Similar' result was reported by Yadav *el al.*, (2005) in Indian mustard.

4.2.10. Seed yield per plant

a. Mean performance

The highest mean seed yield per plant (16.87 gm) was observed in the hybrid Nap9908×Nap2001 and it was followed by Nap9908×Nap2013 (15.07) and Nap9908×Nap2012 (14.83). The seed yields per plant of the above crosses were higher than both of their parents (Table 6-7). Seed yield per plant (6.07gm) was produced by the cross BS-7× Nap248 which was lower than both female and male.

b. General combining ability effects

Among the five female parents two were with significant GCA effects, of them one was positive and one was negative. Nap 9908 had highly significant highest positive GCA effect (2.95). On the contrary BS-7 had the lowest (highly significant negative) GCA value (-1.70) (Table 9). The genotypes with significant positive GCA effects were considered as good general combiner and with significant negative GCA effect were poor general combiners. Goswami *et al.*, (2005) and Sheoran *et al.*, (2000) reported good and well general combiner parents in rape seed for yield. Both significant positive and negative GCA effects were observed in pollen parents. The positive GCA effect was observed in Nap 2012 (1.59) and the negative GCA effect was observed in Nap2022 (-1.07) followed by Nap 206 (-0.95) (Table 8).

c. Specific combining ability effects

Among 40 crosses, 27 cross combinations showed significant SCA effects, of them 14 had positive and 13 had negative effects (Table 10). The cross combination, Nap9908×Nap2001 had the highest SCA value (3.28) and two of its closest values were 2.97 and 2.13 for cross combination Nap2037×Nap179 and Nap9908×Nap2012 respectively. The cross combinations with positive significant SCA value were good specific cross for the trait and it was produced by poor x good, good x good and good x poor general combiner parents. The lowest SCA value (-3.41) was observed in the cross combination Nap9908×Nap2022 and it was followed by Nap9908×Nap179 (-3.29) and Nap94006×Nap2012 (-2.39). The poorest specific combination was produced by good x good general combiners. It indicated that dominant x dominant and dominant x additive gene action was responsible to produce good hybrid for seed yield per plant in *Brassica napus*. This result was supported by many researchers. Ghosh *et al.* (2002) and Sood *et al.* (2000) supported this finding in their reports.

4.3 Heterosis Analysis

4.3.1 Analysis of variance

Analysis of variance is presented in Table 4. It revealed highly significant differences for all characters except Number of primary branches/plant and Number of siliqua/plant among the hybrids and parents. Heterosis study or average performance of the hybrids (F_1s) as percent increases or decreases over the mid parent (Hm), over better parents (Hb) and over standard check variety (Hc) are presented in Table 11. The heterosis of F_1 (Hybrid) over pollen parent and line are shown in Plate 3-11. The nature and magnitude of heterosis are presented character wise as follows:

4.3.2 Heterosis for different characters

a) Plant height

28 hybrids exhibited significant heterosis over mid (Hm) parent (Table 11). The range of the heterosis was -19.89% to 17.38% with a mean of-1.00%. It indicated that some hybrids were smaller and some were taller (plant height) than their mid parental value about -0.41% to 17.38%. For this character the estimated values of heterosis over better parent were significant for 26 hybrids. The hybrids Nap9908xNap206 (15.75%) had the highest significant estimate over better (Hb) parent and it was followed by Nap2037×Nap2012(14.39%). The hybrid BS-7×Nap2057 showed significant negative estimate. It indicated that this hybrid was shorter than its better parent. In case of heterosis over check variety (Hc) Bari Sharisha-13, 50% hybrids exhibited significant positive heterosis and 50% hybrids negative. The hybrid Nap9908×Nap206 possessed the highest estimate (23.14%) and the hybrid BS-7×Nap2057 had the lowest (-14.43%). It indicated the hybrid Nap9908×Nap206 was the tallest among the hybrids and the hybrid BS-7×Nap2057 was the shortest one and it was a dwarf hybrid in respect of standard check variety. Saurabh *et al.*, (2005) observed positive heterosis for plant height over parents in *Brassica juncea* they mentioned that heterosis for plant height did not change the plant type as in their experiment both parents had semi dwarf gene. In this experiment most of the hybrid expressed positive heterosis for plant height and were taller than their parents. This might be due to presence of positive alleles with dominant gene action in their parents.

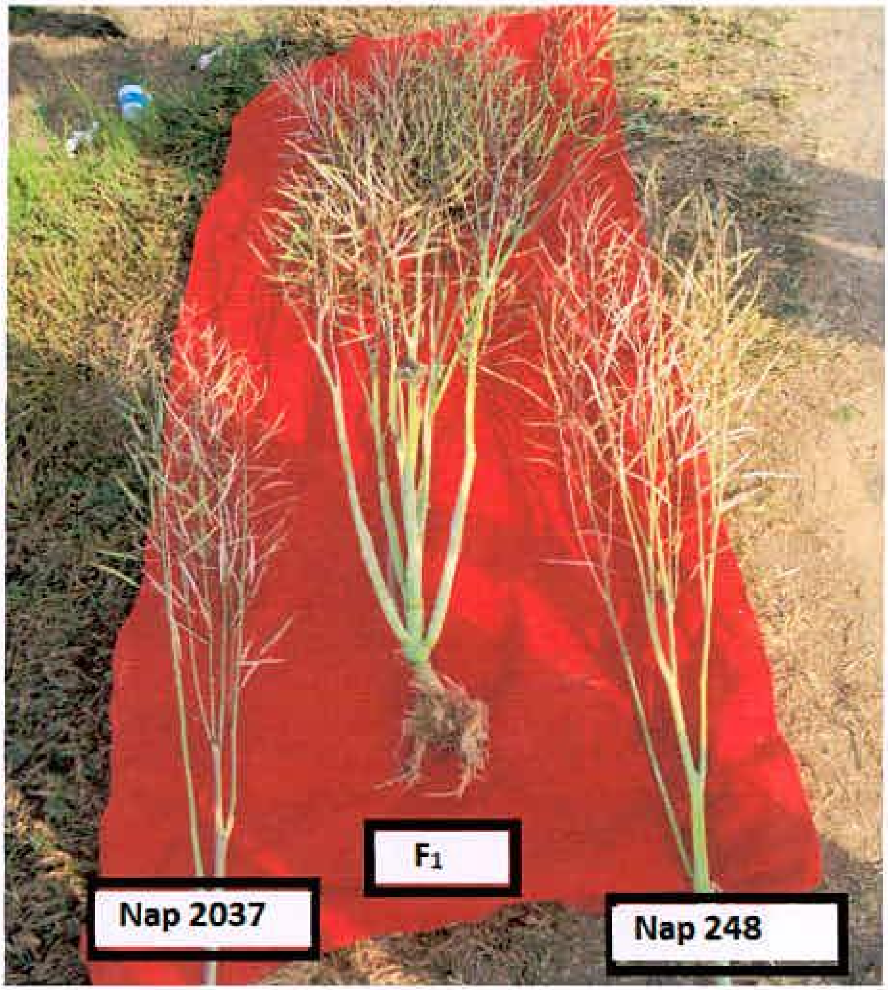

Plate 4: Photograph showing Nap 2037 (Line), Nap 248 (Tester) and their hybrid (F_1).

b) No. of primary branches per plant

Two hybrids out of forty exhibited significant positive and negative mid parent heterosis for number of primary branches per plant. Maximum estimate was obtained from Nap9908×Nap248 (22.34%). The range was -39.62% to 22.34%. One hybrids had significant negative value and one had zero heterosis, others had non significant positive and negative velues. In case of better parent heterosis, one hybrid showed positive and one negative significant values with a range of -45.21% to 15.85%. Maximum estimate was obtained by BS-13×Nap248 (15.85%). The hybrids Nap2037×Nap248 and

Nap2037xNap179 showed the highest significant negative better parent heterosis (-45.21%).

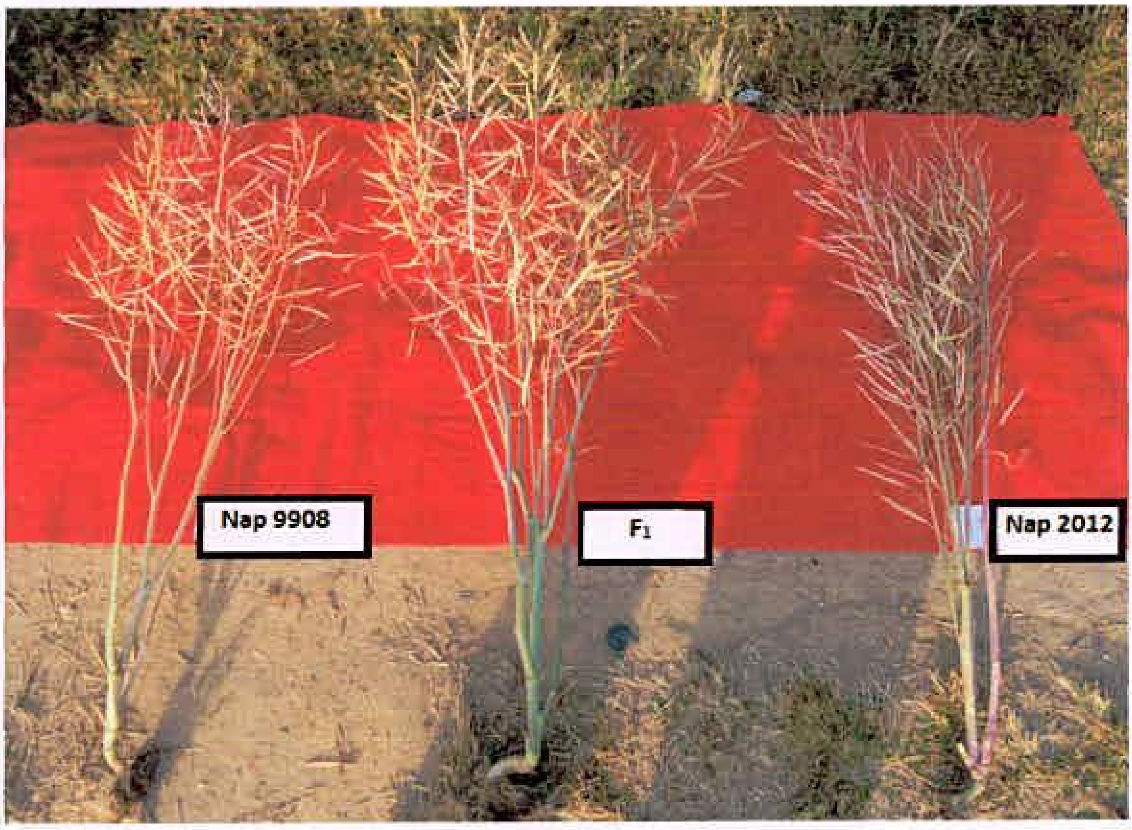

Plate 5: Photograph showing branches of Nap 9908 (Line), Nap 2012 (Tester) and their hybrid (F_1).

On the other hand, when the heterosis was measured against standard check variety, six hybrids showed significant positive and one negative heterosis. Others were non-significant negative and positive values. Nap2037×Nap2022 showed the highest significant positive standard heterosis (44.32%). The range of rendered heterosis was -27.27% to 44.32% with a mean of 1.19% where as mean of mid parent heterosis and better parent heterosis were -12.02% and -15.57% respectively (Table 11). Result revealed that. there was significant positive heterosis for number of primary branches per plant (higher number of pods). Saurabh *et al.,* (2005) observed both positive and negative heterosis for the trait in Indian mustard (*Braissica juncea* L).

Table 11: Estimation of heterosis over mid parents , better parents, and standard check for different characters in *Brassica napus*

Hybrids	Plant height			Number of primary branches/plant			Number of secondary branches/plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 94006 x Nap 248	-0.41	-1.28	1.78	12.75	-5.74	30.68***	32.93***	-2.94	56.25***
Nap 94006 x Nap 179	9.52***	5.57*	8.84	-16.88	-21.31	9.09	-8.47	-15.14	36.61***
Nap 94006 x Nap 206	2.56	0.97	7.42	-14.29	2.27	2.27	-21.19	-40.49	-4.20
Nap 94006 x Nap 2001	5.03*	1.66	4.81	12.69	-9.02	26.14***	35.41***	1.50	63.39***
Nap 94006 x Nap 2057	-1.04	-2.26	3.32	-23.42	-15.00	-3.41	-37.29	-43.43	-8.93
Nap 94006 x Nap 2012	5.20*	2.54	5.71	-3.02	-17.21	14.77	-37.09	-49.53	-18.75
Nap 94006 x Nap 2013	1.50	-1.62	8.07	-12.96	0.00	6.82	-14.60	-15.14	36.61
Nap 94006 x Nap 2022	-7.71***	-13.74***	-11.07	-14.43	-29.51	-2.27	-29.48	-36.77	1.79
Nap 9908 x Nap 248	-0.57	-1.59	1.78	22.34***	8.49	30.68***	118.75***	110.84***	56.25***
Nap 9908 x Nap 179	-6.78**	-10.27***	-7.20	-13.49	-12.26	5.68	29.87***	-2.60	33.93***
Nap 9908 x Nap 206	17.38***	15.75***	23.14***	4.12	-4.72	14.77	79.88***	65.22***	35.71***
Nap 9908 x Nap 2001	5.12*	1.59	5.07	-1.66	-16.04	1.14	72.46***	60.00***	28.57***
Nap 9908 x Nap 2057	-7.39***	-8.40***	-3.16	11.65	8.49	30.68***	45.95***	11.72***	44.64***
Nap 9908 x Nap 2012	7.92***	5.02*	8.62	-17.84	-25.47	-10.23	8.60	-7.34	-9.82
Nap 9908 x Nap 2013	5.77**	2.67	12.78*	0.00	5.66	13.64	-8.24	-34.27	4.46
Nap 9908 x Nap 2022	-1.34	-7.93***	-4.78	-2.70	-15.09	2.27	-11.82	-32.17	-13.39
Nap 2037 x Nap 248	-4.74*	-5.52*	-2.71	-29.82	-45.21***	-9.09	-30.23	-51.83	-6.25
Nap 2037 x Nap 179	-3.18	-6.61**	-3.84	-37.25	-45.21	-9.09	-60.22***	-66.06***	-33.93
Nap 2037 x Nap 206	-13.57***	-14.96***	-9.52	-13.68	-30.82	14.77	-1.94	-30.28***	35.71***
Nap 2037 x Nap 2001	1.44	-1.76	1.16	1.36	-23.29	27.27***	5.19	-25.69	44.64***
Nap 2037 x Nap 2057	-7.22***	-8.43***	-3.20	-30.08	-41.10	-2.27	-26.17	-38.53	19.64
Nap 2037 x Nap 2012	17.29***	14.39***	17.79**	-27.68	-42.47	-4.55	-19.27	-39.45	17.86
Nap 2037 x Nap 2013	-4.41*	-7.41***	1.71	-25.83	-39.04	1.14	-47.47	-52.29	-7.14

Table 11: Continued

Hybrids	Plant height			Number of primary branches/plant			Number of secondary branches/plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 2037 x Nap 2022	10.46***	3.29	6.36	12.89	-13.01	44.32***	-23.55	-36.70	23.21***
BARI Sarisha-7 x Nap 248	-9.83***	-12.59***	-5.68	-30.93	-40.18	-23.86	16.20***	8.33	-7.14
BARI Sarisha-7 x Nap 179	-6.71**	-12.00***	-5.04	-19.46	-20.54	1.14	-37.60	-49.35	-30.36
BARI Sarisha-7 x Nap 206	-14.87***	-15.47***	-8.78	-31.00	-38.39	-21.59	-22.34	-23.96	-34.82***
BARI Sarisha-7 x Nap 2001	-3.73	-8.82***	-1.61	-24.06	-36.61	-19.32	-4.30	-7.29	-20.54
BARI Sarisha-7 x Nap 2057	-19.89***	-20.70***	-14.43*	-39.62***	-42.86	-27.27***	-33.61	-44.83	-28.57
BARI Sarisha-7 x Nap 2012	-3.69	-8.17***	-0.90	-21.33	-30.36	-11.36	34.63***	26.61	23.21***
BARI Sarisha-7 x Nap 2013	-8.12***	-8.93***	0.03	-25.24	-31.25	-12.50	-46.72	-58.99	-34.82***
BARI Sarisha-7 x Nap 2022	-0.70	-9.12***	-1.94	-3.66	-17.86	4.55	-6.28	-21.68	0.00
BARI Sarisha-13 x Nap 248	-2.69	-3.31	-2.07	11.76	15.85***	7.95	42.56***	24.11	24.11***
BARI Sarisha-13 x Nap 179	6.60**	4.29	4.29	-23.86	-31.19	-14.77	-33.08	-42.21	-20.54
BARI Sarisha-13 x Nap 206	4.25*	1.12	7.59	3.41	3.41	3.41	-13.73	-21.43	-21.43
BARI Sarisha-13 x Nap 2001	-6.00**	-7.65**	-7.65	-6.75	-13.64	-13.64	-26.73	-33.93	-33.93
BARI Sarisha-13 x Nap 2057	-8.93***	-11.39***	-6.33	-23.40	-28.00	-18.18	-42.41	-48.97	-33.93
BARI Sarisha-13 x Nap 2012	-4.86*	-5.87*	-5.87	-9.35	-10.23	-10.23	-18.55	-19.64	-19.64
BARI Sarisha-13 x Nap 2013	-4.78*	-9.05***	-0.10	-18.68	-21.28	-15.91	-35.86	-47.75	-16.96
BARI Sarisha-13 x Nap 2022	13.07***	7.20**	7.20	-11.38	-15.91	-15.91	-21.57	-30.07	-10.71
Mean	-1.00	-3.97	0.79	-12.02	-19.92	1.19	-4.93	-19.06	4.27
Maximum	17.38	15.75	23.14	22.34	15.85	44.32	118.75	110.84	63.39
Minimum	-19.89	-20.70	-14.43	-39.62	-45.21	-27.27	-60.22	-66.06	-34.82

* Significance at 5%level, ** Significance at 1%level, ***Significance at 0.1%level

H(m): Heterosis over mid parent,H(b): Heterosis over better parent,H(c):Heterosis over standard check variety

Table 11: Continued

Hybrids	Days to 50% flowering			Days to 50% maturity			Number of siliqua/Plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 94006 x Nap 248	2.30	2.78	4.72	1.36	2.35	-0.38	24.47***	35.57***	-6.87
Nap 94006 x Nap 179	-2.33	-2.78	-0.94	0.98	1.18	-1.53	53.74***	64.13***	12.74**
Nap 94006 x Nap 206	-2.78	-2.78	-0.94	1.78	2.38	-1.53	10.20***	-4.14*	-10.97*
Nap 94006 x Nap 2001	-1.80	0.93	2.83	3.52	3.92	1.15	52.46***	80.52***	34.95***
Nap 94006 x Nap 2057	-2.75	-3.64	0.00	3.89	3.09	1.91	-7.79***	-27.06***	-13.90**
Nap 94006 x Nap 2012	3.74	2.78	4.72	1.73	3.53	0.76	8.96***	38.75***	-4.69
Nap 94006 x Nap 2013	2.78	2.78	4.72	2.53	1.94	0.38	19.41***	-6.18***	12.79**
Nap 94006 x Nap 2022	6.10	4.63	6.60	-0.19	1.18	-1.53	-7.84***	-2.35	-32.92***
Nap 9908 x Nap 248	2.30	2.78	4.72	-0.95	-2.25	-0.38	10.90***	7.04**	-6.87
Nap 9908 x Nap 179	6.05	5.56	7.55	-0.57	-2.62	-0.76	-7.86***	-12.64***	-24.00***
Nap 9908 x Nap 206	3.70	3.70	5.66	2.89	5.95	1.91	50.05***	45.31***	24.00***
Nap 9908 x Nap 2001	-2.70	0.00	1.89	0.76	-1.12	0.76	4.82**	9.02***	-5.15
Nap 9908 x Nap 2057	-3.67	-4.55	-0.94	0.00	1.54	0.38	-2.61	-15.42***	-0.15
Nap 9908 x Nap 2012	-4.67	-5.56	-3.77	-3.95	-4.49	-2.67	14.42***	27.09***	10.56*
Nap 9908 x Nap 2013	-2.78	-2.78	-0.94	0.95	2.71	1.15	-21.53***	-32.37***	-18.69***
Nap 9908 x Nap 2022	-7.04	-8.33	-6.60	-3.97	-4.87	-3.05	-5.99**	-11.46***	-22.97***
Nap 2037 x Nap 248	-0.92	-0.92	1.89	0.19	0.00	-0.38	-47.38***	-57.15***	-44.82***
Nap 2037 x Nap 179	0.93	0.00	2.83	0.19	-0.77	-1.15	-32.66***	-45.94***	-30.38***
Nap 2037 x Nap 206	-9.68	-9.26	-7.55	-0.97	0.79	-3.05	-16.08***	0.14	-7.00
Nap 2037 x Nap 2001	-4.93	-2.75	0.00	0.00	-0.77	-1.15	-19.24***	-30.15***	-10.05*
Nap 2037 x Nap 2057	-2.28	-2.73	0.94	0.00	0.39	-0.76	-50.43***	-48.18***	-38.82***
Nap 2037 x Nap 2012	-10.70	-11.93	-9.43	-3.62	-3.07	-3.44	-8.62***	-16.61***	7.38
Nap 2037 x Nap 2013	2.30	1.83	4.72	1.35	0.77	0.38	-33.27	-35.48	-16.92

Table 11: Continued

Hybrids	Days to 50% flowering			Days to 50% maturity			Number of siliqua/Plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 2037 x Nap 2022	0.93	-0.92	1.89	-0.96	-1.15	-1.15	-3.67*	-23.08***	-0.95
BARI Sarisha-7 x Nap 248	-2.33	-3.67	-0.94	-1.34	-1.53	-1.91	-26.16***	-30.34***	-36.41***
BARI Sarisha-7 x Nap 179	3.29	2.80	3.77	0.97	0.00	-0.38	-20.68***	-26.46***	-32.87***
BARI Sarisha-7 x Nap 206	-0.93	-1.85	0.00	2.53	0.77	0.38	-26.90***	-27.53***	-32.69***
BARI Sarisha-7 x Nap 2001	0.00	-3.51	3.77	1.16	0.38	0.00	-10.87***	-12.14***	-17.44***
BARI Sarisha-7 x Nap 2057	-2.78	-4.55	-0.94	1.15	0.77	0.38	-44.34***	-50.65***	-41.74***
BARI Sarisha-7 x Nap 2012	6.60	6.60	6.60	-1.71	-2.27	-1.53	10.85***	3.04	9.49*
BARI Sarisha-7 x Nap 2013	3.74	2.78	4.72	2.12	1.53	1.15	-17.81***	-27.70***	-13.08**
BARI Sarisha-7 x Nap 2022	-5.21	-5.66	-5.66	-1.34	-1.53	-1.53	3.72	-4.47*	-12.79**
BARI Sarisha-13 x Nap 248	-10.70	-11.93	-9.43	-2.68	-3.05	-3.05	-15.23***	-23.31**	-23.31***
BARI Sarisha-13 x Nap 179	-1.41	-1.87	-0.94	-0.39	-1.53	-1.53	-16.41***	-25.62***	-25.62***
BARI Sarisha-13 x Nap 206	3.74	2.78	4.72	1.56	-0.38	-0.38	-20.29***	-23.13***	-23.13***
BARI Sarisha-13 x Nap 2001	-5.45	-8.77	-1.89	-0.19	-1.15	-1.15	-36.97***	-38.87***	-38.87***
BARI Sarisha-13 x Nap 2057	-5.56	-7.27	-3.77	-2.88	-3.44	-3.44	-29.23***	-34.64***	-22.85***
BARI Sarisha-13 x Nap 2012	-10.38	-10.38	-10.38	-4.18	-4.55	-3.82	-21.81***	-24.11***	-19.36***
BARI Sarisha-13 x Nap 2013	4.67	3.70	5.66	-1.15	-1.91	-1.91	-12.21***	-19.60***	-3.33
BARI Sarisha-13 x Nap 2022	2.37	1.89	1.89	-0.38	-0.38	-0.38	1.62	-10.13***	-10.13*
Mean	-1.21	-2.08	0.54	0.00	-0.90	-0.83	-7.46	-16.19	-13.45
Maximum	6.60	6.60	7.55	3.89	3.11	1.91	53.74	45.31	34.95
Minimum	-10.70	-11.93	-10.38	-4.18	-4.87	-3.82	-50.43	-57.15	-44.82

* Significance at 5%level, ** Significance at 1%level, *** Significance at 0 .1%level

H(m): Heterosis over mid parent, H(b): Heterosis over better parent, H(c): Heterosis over standard check

Table 11: Continued

Hybrids	siliqua length(cm)			Number of seeds/siliqua		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 94006 x Nap 248	-3.27	8.64	-5.93	10.77	0.70	7.36
Nap 94006 x Nap 179	15.98	14.41	7.63	14.86	12.13	2.70
Nap 94006 x Nap 206	-1.09	-6.58	-3.81	10.02	0.86	5.56
Nap 94006 x Nap 2001	10.36	13.43	3.81	18.46	10.98	10.81
Nap 94006 x Nap 2057	-8.39	-11.57	-19.07	20.03	13.91	10.66
Nap 94006 x Nap 2012	2.39	3.67	0.00	10.58	2.19	5.11
Nap 94006 x Nap 2013	1.59	-0.44	-5.08	8.37	0.89	2.10
Nap 94006 x Nap 2022	6.16	-1.96	5.93	11.77	-3.73	16.22***
Nap 9908 x Nap 248	0.45	-7.82	-5.08	12.60	0.70	7.36
Nap 9908 x Nap 179	-3.53	-7.66	-13.14	3.93	-0.33	-8.71
Nap 9908 x Nap 206	-0.90	-9.05	-6.36	12.33	1.29	6.01
Nap 9908 x Nap 2001	-0.70	-6.14	-9.32	10.04	1.35	1.20
Nap 9908 x Nap 2057	5.45	4.93	-9.75	1.08	-5.72	-8.41
Nap 9908 x Nap 2012	-1.79	-10.20	-6.78	1.69	-7.59	-4.95
Nap 9908 x Nap 2013	10.75	5.33	0.42	9.40	0.15	1.35
Nap 9908 x Nap 2022	-11.35	-20.39	-13.98	7.48	-8.83	10.06
Nap 2037 x Nap 248	-15.68	-16.53	-12.29	-18.07*	-18.81	-11.86
Nap 2037 x Nap 179	2.13	-3.23	1.69	5.33	-2.90	5.41
Nap 2037 x Nap 206	-13.65	-14.52	-10.17	-12.39	-13.97	-6.61
Nap 2037 x Nap 2001	0.00	-4.03	0.85	3.03	-1.11	7.36
Nap 2037 x Nap 2057	2.90	-6.85	-2.12	-7.45	-12.31	-4.80
Nap 2037 x Nap 2012	-7.91	-8.47	-3.81	-12.78	-15.08	-7.81

Table 11: Continued

Hybrids	siliqua length(cm)			Number of seeds/siliqua		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 2037 x Nap 2013	-25.58	-29.03	-25.42	-21.69*	-24.34*	-17.87*
Nap 2037 x Nap 2022	-6.56	-7.84	-0.42	-18.66*	-22.76*	-6.76
BARI Sarisha-7 x Nap 248	-1.56	-9.05	-6.36	1.90	-1.97	4.50
BARI Sarisha-7 x Nap 179	2.34	-1.35	-7.20	12.95	8.99	7.36
BARI Sarisha-7 x Nap 206	7.80	-0.41	2.54	2.88	-0.14	4.50
BARI Sarisha-7 x Nap 2001	-7.83	-12.28	-15.25	-7.65	-8.27	-8.41
BARI Sarisha-7 x Nap 2057	10.07	8.74	-5.08	0.84	0.15	-1.35
BARI Sarisha-7 x Nap 2012	7.32	-1.22	2.54	7.83	5.55	8.56
BARI Sarisha-7 x Nap 2013	-2.09	-6.22	-10.59	-8.12	-9.35	-8.26
BARI Sarisha-7 x Nap 2022	-10.20	-18.82	-12.29	-19.32*	-26.74**	-11.56
BARI Sarisha-13 x Nap 248	-17.75	-18.93	-16.53	-11.48	-14.23	-8.56
BARI Sarisha-13 x Nap 179	-5.24	-8.05	-8.05	0.00	-4.20	-4.20
BARI Sarisha-13 x Nap 206	-11.06	-12.35	-9.75	-9.76	-11.76	-7.66
BARI Sarisha-13 x Nap 2001	-17.24	-18.64	-18.64	-13.90	-13.96	-13.96
BARI Sarisha-13 x Nap 2057	6.18	-1.69	-1.69	6.32	4.80	4.80
BARI Sarisha-13 x Nap 2012	-12.68	-14.29	-11.02	3.33	1.90	4.80
BARI Sarisha-13 x Nap 2013	4.12	1.69	1.69	7.46	6.82	8.11
BARI Sarisha-13 x Nap 2022	-4.68	-8.24	-0.85	1.36	-7.34	11.86
Mean	-2.37	-6.69	-6.22	1.38	-4.05	0.30
Maximum	15.98	14.41	7.63	20.03	13.91	16.22
Minimum	-25.58	-29.03	-25.42	-21.69	-26.74	-17.87

* Significance at 5%level, ** Significance at 1%level, ***Significance at 0.1%level

H(m): Heterosis over mid parent,H(b): Heterosis over better parent,H(c):Heterosis over standard check variety

Table 11: Continued

Hybrids	1000 seed weight(gm)			Seed yield/plant (gm)		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 94006 x Nap 248	-37.78	-45.74	-23.91	18.01	0.88	21.55
Nap 94006 x Nap 179	29.84	29.17	34.78	-6.98	-20.87	-3.53
Nap 94006 x Nap 206	-14.03	-24.00	3.26	16.87	16.39	0.35
Nap 94006 x Nap 2001	-30.77	-34.38	-31.52	-2.80	-15.76	-1.77
Nap 94006 x Nap 2057	9.73	-4.62	34.78	-20.00	-29.07	-21.55
Nap 94006 x Nap 2012	-22.84	-24.75	-17.39	-13.21	-28.30	-6.01
Nap 94006 x Nap 2013	14.83	6.19	30.43	14.62	-4.17	21.91
Nap 94006 x Nap 2022	14.81	-3.13	1.09	6.39	-8.61	8.83
Nap 9908 x Nap 248	-36.07	-45.74	-23.91	24.64	0.88	21.55
Nap 9908 x Nap 179	-29.73	-31.58	-29.35	-1.44	-20.58	-3.18
Nap 9908 x Nap 206	-34.88	-44.00	-23.91	42.86	33.20	14.84
Nap 9908 x Nap 2001	3.41	1.11	-1.09	87.06***	53.33*	78.80**
Nap 9908 x Nap 2057	11.82	-5.38	33.70	68.70**	41.21	56.18
Nap 9908 x Nap 2012	-5.76	-10.89	-2.17	71.48**	34.50	76.33**
Nap 9908 x Nap 2013	-9.36	-18.58	0.00	59.37**	26.39	60.78**
Nap 9908 x Nap 2022	-17.95	-28.89	-30.43	-7.66	-24.93	-10.60
Nap 2037 x Nap 248	-8.43	-11.63	23.91	-1.38	-5.57	13.78
Nap 2037 x Nap 179	-12.56	-21.67	2.17	10.81	5.51	28.62
Nap 2037 x Nap 206	-22.45	-24.00	3.26	-12.59	-22.12	-14.13
Nap 2037 x Nap 2001	-38.83	-47.50	-31.52	-12.15	-14.55	-0.35
Nap 2037 x Nap 2057	-0.80	-4.62	34.78	-28.32	-28.43	-20.85
Nap 2037 x Nap 2012	-9.50	-16.67	8.70	-3.95	-11.59	15.90

Table 11: Continued

Hybrids	1000 seed weight(gm)			Seed yield/plant (gm)		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
Nap 2037 x Nap 2013	-44.21	-45.83	-29.35	-10.12	-16.11	6.71
Nap 2037 x Nap 2022	0.00	-22.50	1.09	-22.96	-25.82	-11.66
BARI Sarisha-7 x Nap 248	-25.30	-27.91	1.09	-35.12	-46.63	-35.69
BARI Sarisha-7 x Nap 179	14.42	2.50	33.70	-13.27	28.99	-13.43
BARI Sarisha-7 x Nap 206	-24.90	-23.33	0.00	-17.67	-21.72	-32.51
BARI Sarisha-7 x Nap 2001	-7.77	-20.83	3.26	0.00	-16.67	-2.83
BARI Sarisha-7 x Nap 2057	-1.60	-5.38	33.70	-11.07	-24.28	-16.25
BARI Sarisha-7 x Nap 2012	9.50	0.83	31.52	11.68	-11.05	16.61
BARI Sarisha-7 x Nap 2013	-39.91	-38.05	-23.91	-9.66	-27.22	-7.42
BARI Sarisha-7 x Nap 2022	-2.15	-24.17	-1.09	-5.92	-22.26	-7.42
BARI Sarisha-13 x Nap 248	-13.12	-25.58	4.35	-10.90	-18.48	-1.77
BARI Sarisha-13 x Nap 179	32.62	30.53	34.78	-15.29	-22.90	-6.01
BARI Sarisha-13 x Nap 206	-12.44	-24.00	3.26	17.27	9.19	9.19
BARI Sarisha-13 x Nap 2001	-29.21	-31.52	-31.52	-16.80	-22.73	-9.89
BARI Sarisha-13 x Nap 2057	10.81	-5.38	33.70	4.36	-0.64	9.89
BARI Sarisha-13 x Nap 2012	-21.24	-24.75	-17.39	-5.20	-16.44	9.54
BARI Sarisha-13 x Nap 2013	16.10	5.31	29.35	-23.17	-31.39	-12.72
BARI Sarisha-13 x Nap 2022	17.72	1.09	1.09	-15.81	-22.55	-7.77
Mean	-9.20	-17.26	2.58	3.27	-9.72	5.60
Maximum	32.62	30.53	34.78	87.06	53.33	78.80
Minimum	-44.21	-47.50	-31.52	-35.12	-46.63	-35.69

* Significance at 5%level, ** Significance at 1%level, ***Significance at 0.1%level

H(m): Heterosis over mid parent,H(b): Heterosis over better parent,H(c):Heterosis over standard check variety

c) Number of secondary branches per plant

Out of forty hybrids ten showed significant positive and one significant negative mid parent heterosis for number of secondary branches per plant and the rest showed non significant positive and negative estimates. The hybrid Nap9908×Nap248 exhibited the highest significant positive (118.75%) mid parent heterosis for number of secondary branches per plant. In case of better parent heterosis Nap9908×Nap248 showed the highest (127.27%) significant heterosis. The hybrid Nap2037×Nap179 showed the lowest (-66.06) significant negetive heterosis are presented in (Table 11). During the estimation of standard heterosis thirteen of forty hybrids exhibited significant positive and two were significant negative heterosis for number of secondary branches per plant. However the range of standard heterosis was -34.82% to 63.39% with a mean of 4.27%. The hybrid Nap94006 x Nap 2001 showed the highest (63.39 %) significant positive and the hybrid BS-7xNap2013 (-34.82) showed the highest significant negative standard heterosis for the trait. Saurabh *et al.,* (2005) also observed both positive and negative heterosis for number of secondary branches per plant in Indian mustard *(Brassica juncea* L.*)*

d) Days to 50 percent flowering

Hybrids exhibited positive and negative values for heterosis over mid parent (Hm). Such types of heterosis are desirable due to indication of earliness (Table 11). Mid parent heterosis ranged from -10.70% to 6.60% with a mean of -1.21% and for standard cheek the range was -10.38% to 7.55% with a mean of -0.54%. The hybrid Nap2037×Nap2012 and BS-13xNap248 had the highest negative heterosis over standard check (-10.38%). Results with negative heterosis indicated that the hybrids were early compared to their parents. Priti Gupta *et al.,* (2011) found heterosis for 50% days to flowering in Indian Mustard (*Brassica juncea* L.)

e) Days to 50 percent maturity

Hybrids exhibited positive and negative values for heterosis over mid parent (Hm). Such types of heterosis are desirable due to indication of earliness (Table 11). Mid parent heterosis ranged from -4.18% to 3.89% with a mean of 0.00%

and for standard cheek the range was -3.82% to 1.91% with a mean of -0.83%. The hybrid BS-13×Nap2012 had the highest negative heterosis over standard check (-3.82%). Results with negative heterosis indicated that the hybrids were early compared to their parents. Priti Gupta *et al.,* (2011) found heterosis for days to maturity in Indian Mustard (*Brassica juncea* L.)

f) Number of siliqua per plant

37 hybrids showed significant heterosis over mid (Hm) parent for no. of siliqua per plant (Table 11). 11 had positive significant value. The hybrid Nap94006×Nap179 had the highest value of heterosis over mid parent (53.74%) and it was followed by the hybrid Nap94006×Nap2001 (52.46%). The hybrid Nap9908×Nap206 (45.31%) had the highest value over the better parent. On the other hand when compared the heterosis with standard check six hybrids exhibited significant positive heterosis. The hybrid Nap94006×Nap2001 had the highest (34.95%) estimate but BS-7×Nap2012 exhibited the lowest (9.49%) significant estimate. It indicated that the hybrid Nap94006×Nap2001 produced the highest number of siliqua per plant and the hybrid BS-7xNap2012 produced the lowest. Shen *et al.,* (2005) and Saurabh *et al.,* (2005) also observed positive heterosis for the number of siliqua per plant.

g) Length of siliqua

Heterosis over mid parent for siliqua length ranged frond -25.98% to 15.98% with a mean of-2.37% while heterosis over better parent ranged from -29.03% to 14.41% a mean value of -6.69% (Table 11). Hybrids were not showed significant +ve and -ve heterosis over mid parent for siliqua length. Highest positive heterosis (15.98%) was estimated in the cross Nap94006×Nap179 which was desirable for high yield. In case of better parent 19 hybrids showed non significant -ve heterosis. This result indicated that hybrids produced shorter siliqua than better parent. Standard heterosis ranged from -25.42% to 7.63% with a mean of -6.22% for siliqua length. The hybrids Nap94006×Nap179 showed the highest positive heterosis (7.63%) for the trait which was desirable for high yield. Saurabh *et al.*, (2005) found +ve heterosis for siliqua length.

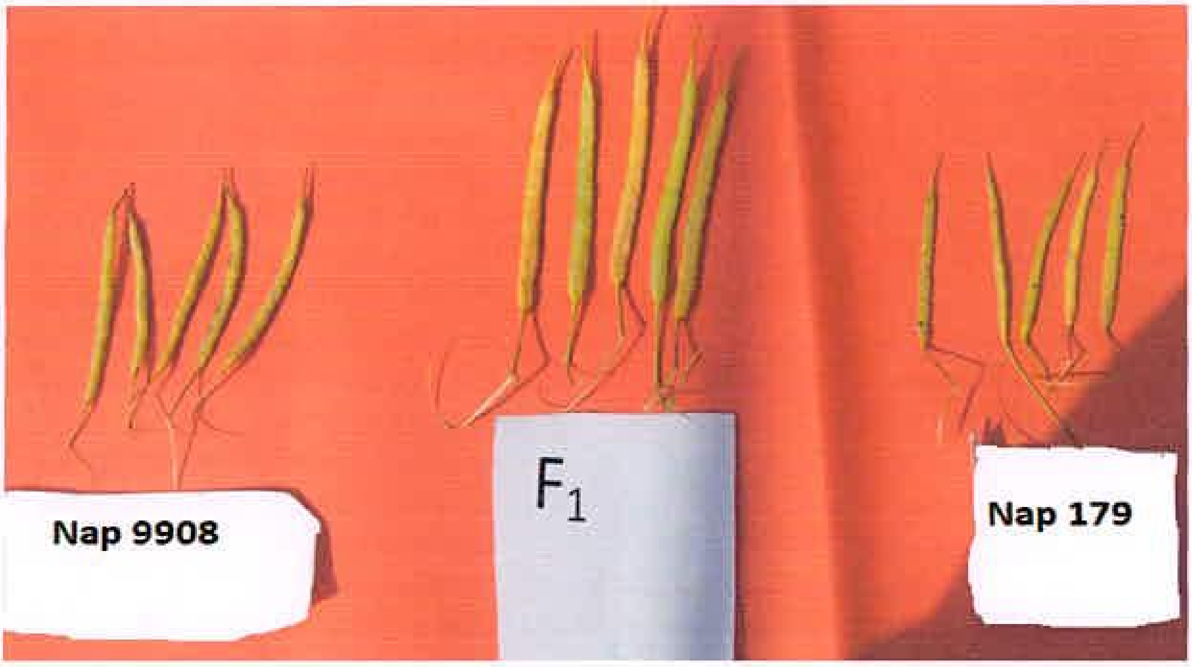

Plate 6: Photograph showing siliqua of Nap 9908 (Line), Nap179 (Tester), and their hybrid (F_1)

h) Number of seeds per siliqua

Three hybrids showed significant +ve and one -ve over mid parent heterosis for seeds per siliqua (Table 11). The hybrids showed mid parent heterosis with the range -21.69% to 20.03% and mean 1.38%. In case of better parent heterosis the hybrid Nap94006×Nap2057 also showed maximum significant +ve heterosis (13.91%) which was folloowed by Nap94006×Nap179(12.13%), and Nap94006×Nap2001 (10.98%). The range of better parent heterosis was -26.74% to 13.91% with a mean of -4.05%. On the other hand- one hybrids exhibited significant positive and one significant negative standard heterosis for the trait. The rests were non significant positive and negative. The hybrid Nap94006×Nap2022 exibited the highest (16.22%) standard heterosis which was followed by BS-13×Nap2022 (11.86%), Nap94006×Nap2001(10.81%) The range of standard heterosis was -17.87% to 16.22% with a mean 0.30%. The result revealed that most of the hybrids exhibited significant positive heterosis for the trait. Saurabh et *al.*, (2005) found heterosis for seeds per siliqua.

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 2022)

Pollen parents
(Nap 2022)

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 179)

Pollen parents
(Nap 179)

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 2013)

Pollen parents
(Nap 2013)

Plate 7: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 2057)

Pollen parents
(Nap 2057)

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 2001)

Pollen parents
(Nap 2001)

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 2012)

Pollen parents
(Nap 2012)

Plate 8: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(Nap 94006)

Hybrids
(Nap 94006 X Nap 206)

Pollen parents
(Nap 206)

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 206)

Pollen parents
(Nap206)

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 2012)

Pollen parents
(Nap 2012)

Plate 9: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 2057)

Pollen parents
(Nap 2057)

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 2001)

Pollen parents
(Nap 2001)

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 248)

Pollen parents
(Nap 248)

Plate 10: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 2022)

Pollen parents
(Nap 2022)

Female parents
(Nap 9908)

Hybrids
(Nap 9908 X Nap 2013)

Pollen parents
(Nap 2013)

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap 2012)

Pollen parents
(Nap 2012)

Plate 11: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap2001)

Pollen parents
(Nap 2001)

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap 2022)

Pollen parents
(Nap 2022)

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap 248)

Pollen parents
(Nap 248)

Plate 12: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap 2013)

Pollen parents
(Nap 2013)

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap 179)

Pollen parents
(Nap 179)

Female parents
(Nap 2037)

Hybrids
(Nap 2037 X Nap 2057)

Pollen parents
(Nap 2057)

Plate 13: Photograph showing variation in morphology among female parent, hybrid and pollen parent

Female parents
(BS-7)

Hybrids
(BS-7 X Nap 206)

Pollen parents
(Nap 206)

Female parents
(BS- 7)

Hybrids
(BS-7 X Nap 2001)

Pollen parents
(Nap 2001)

Female parents
(BS-7)

Hybrids
(BS-7 X Nap 2013)

Pollen parents
(Nap 2013)

Plate 14: Photograph showing variation in morphology among female parent, hybrid and pollen parent

i) Thousand (1000)seed weight

Out of forty hybrids twelve showed non significant positive mid parent, nine showed positive better parent and 23 positive standard heterosis for 1000-seed weight. Mid parent heterosis ranged from -44.21% to 32.62% with a mean of -9.20 % (Table 11). Better parent heterosis ranged from -47.50% to 30.53% with a mean of -17.26% and standard heterosis ranged from -31.52 % to 34.78% with a mean of 2.58% for the trait. The hybrid BS-13×Nap179 showed the highest estimate (32.62%) mid parent and the hybrid BS-13×Nap179 showed the highest estimate (30.53%) better parent heterosis. The hybrid BS-13×Nap179 showed the highest estimate (34.78%) for standard heterosis. Many researchers observed heterosis in 1000-seed weight. Such as Shen *et al.*, (2005) and Saurabh *et al.*, (2005) observed similar result in their research findings and supported this result.

j) Seed yield per plant

Out of forty hybrids four exhibited significant positive mid parent heterosis for seed yield per plant. One exhibited significant zero heterosis and others are non significant negative. The range of mid parent heterosis was -35.12% to 87.06% with a mean of 3.27 %. The hybrid Nap9908×Nap2001 had the highest (87.06%) estimate. In case of better parent heterosis, two hybrids exhibited significant positive values with a range of -46.63% to 53.33%, where mean heterosis was -9.72%. The hybrid Nap9908×Nap2001 showed the highest (53.33 %) better parent heterosis for seed yield per plant and it was followed by Nap9908×Nap2057 (41.21%) and Nap9908×Nap2012 (34.50%). On the other hand in case of standard heterosis three hybrids had significant positive estimates. The hybrid Nap9908×Nap2001 showed the highest (78.80%) significant positive standard heterosis for the trait and it was followed by Nap9908×Nap2012 (76.33%) and Nap9908×Nap2013 (60.78%) in (Table 11). The mean of standard heterosis was 5.60% with a range of -35.69% to 78.80% for seed yield per plant. Saurabh *et al.*, (2005) observed similar heterosis in Indian mustard hybrids for this trait. They observed 63.19% - 104.40% better parent heterosis. In India Katiyar et al.,

(2004) observed standard heterosis of 43.38% and best parent heterosis of 150.33% for yield yellow sarson (*Brassica campestris*). In India Chander and Verma (2004) found hetersis over both better parent and mid parent for seed yield/ plant in cabbage. Kishor et al., (2006), Shen et al.,(2005), Sood et al.,(2000) and Katiyar et al.,(2000) found heterosis for seed yield per plant. In the present study most of the hybrids showed positive heterosis for seed yield/plant. It might be due to selection of good specific cross combinations for yield and yield related characters as promising hybrids.

Keeping in view the importance of early emergence, flowering and maturity and shorter plant height, emphasis was focused on negative heterosis for these characteristics. Cross showing significant negative values (in certain crosses) for these traits, suggested that these crosses could be used to develop new early maturing and shorter lines.

No. of siliqua per plant, seed per siliqua, primary branch & secondary branch per plant and seed yield per plant are the yield contributing traits hence more no. of silique per plant, seed per siliqua, primary branch &secondary branch per plant and seed yield per plant are desirable therefore positive values were preferred.

The presence of significantly positive heterosis for no. of silique per plant, seed per siliqua, primary branch &secondary branch per plant and seed yield per plant in our certain crosses indicate the potential of their use for developing high yielding genotypes.

Chapter V

Summary and Conclusion

CHAPTER 5

SUMMARY AND CONCLUSION

Five female parents (lines) were crossed with eight male parents (testers) in a line × tester mating design. Then forty hybrids (F_1) and parents were evaluated for estimating combining ability effect and magnitude of heterosis over mid parent, better parent and standard check variety.

Analysis of combining ability showed that GCA effect was significant for plant height, primary and secondary branches per plant, days to fifty percent flowering, fifty percent maturity, Number of siliqua per plant, length of siliqua, seeds per siliqua, thousand seed weight and seed yield per plant and the specific combining ability (SCA) effect was significant for all the characters.

Estimates of GCA effect for different characters suggested that among lines Nap9908 was best general combiner for, no. of primary branches per plant, no. secondary branch per plant and seed yield per plant respectively. BS-7 was best for plant height, thousand seed weight. Line BS-13 was best general combiner for days to 50% flowering and days to 50% maturity. Line Nap94006 was best general combiner for no. of silique per plant, no. of seed per siliqua and length of siliqua. Among testers Nap2057 was general combiner for plant height, thousand seed weight. Tester Nap2012 was best general combiner for days to 50% flowering, days to 50% maturity, no. of siliqua per plant, length of siliqua and seed yield per plant. Tester Nap2013 was best general combiner for no. of seeds per siliqua. Tester Nap248 was best general combiner for no. of secondary branches/plant.

High ratio of SCA and GCA variance was observed, indicating preponderance of non additive gene effects in the inheritance of the yield and yield relating characters under study.

Estimates of SCA effect for different characters revealed that the cross Nap9908×Nap2012 was best specific combiner for plant height. Cross Nap9908xNap2001 was best specific combiner for thousand seed weight and seed yield per plant. Cross Nap9908×Nap2013 was best for no. of primary branches per plant, length of siliqua, no. of seeds per siliqua. Cross Nap9908×Nap2057 showed best SCA effect for no. of siliqua per plant. The cross BS-7×Nap2012 was best specific combiner for no. of secondary branch per plant and BS-13×Nap248 was best specific combiner for days to 50% flowering and days to 50% maturity.

Different types of heterosis i.e. heterosis over mid parent (Hm), heterosis over better parent (Hb) and heterosis over standard check (Hc) were estimated to evaluate forty hybrids for seed yield and yield contributing characters; where BARI Sharisha-13 was taken as check. The average heterosis for seed yield of forty hybrids over mid parent was 3.27% and that of better parent and standard check was -9.72% and 5.60% respectively.

From the findings of the present study, the following recommendation could be made:

1. The crosses Nap9908×Nap2001, Nap9908×2057, Nap9908×Nap2012 and Nap9908×Nap2013 could be used for development of hybrid variety in mustard.

Chapter VI

References

CHAPTER 6

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Chapter VII

Appendices

CHAPTER 7

APPENDICES

Appendix I. Physical and chemical properties of soil (0-15 cm) of the experimental field

A. Physical properties of soil	
% sand (0.2-.02 mm)	21.75
% silt (0.02-.002 mm)	66.60
% clay (< 0.002 mm)	11.65
Textural class	Silty loam
Consistency	Granular
B. Chemical properties of soil	
Soil pH	6.4
Organic carbon (%)	1.30
Organic matter (%)	1.28
Total nitrogen (%)	0.11
Available phosphorus (ppm)	27
Exchangeable potassium (me/100 g soil)	0.12
Available sulphur (ppm)	9.00

Source: Soil Science Department, SAU, Dhaka-1207

Appendix II: Inter se (estimated) mean of BARI Sharisa-13

Parents	Plant height	Number of primary branches/plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)
BARI Sharisa-13	103.30	2.93	3.73	35.33	87.30	130.00	7.90	22.20	3.10	9.43

Appendix III: Scoring of GCA effects of three tester for different Characters in *Brassica napus* L..

Parents	Plant height	Number of primary branches/ plant	Number of secondary branches/plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)	
Nap 248	0	0	1	0	0	-1	-1	0	-1	0	-2L
Nap 179	0	0	0	1	0	0	1	0	1	0	3H
Nap 206	1	0	0	0	0	0	0	0	-1	-1	-1L
Nap 2001	0	0	0	0	1	0	0	0	-1	1	1H
Nap 2057	-1	0	0	-1	1	-1	0	0	1	0	-1L
Nap 2012	1	0	0	-1	-1	1	1	0	0	1	2H
Nap 2013	1	0	0	1	1	0	0	-1	0	0	2H
Nap 2022	0	0	0	0	-1	0	0	1	-1	-1	-2L
Total Significance	**4**	**0**	**1**	**4**	**5**	**3**	**3**	**2**	**6**	**3**	**Average**
											0.25
High Score	**2**	**0**	**1**	**2**	**3**	**1**	**2**	**1**	**2**	**1**	
Low score	**2**	**0**	**0**	**2**	**2**	**2**	**1**	**1**	**4**	**2**	

Appendix IV: Scoring of GCA effects of six line (Male sterile) for different Characters in *Brassica napus* L..

Parents	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)	GCA Group
Nap 94006	0	0	1	1	1	1	1	1	0	0	6H
Nap 9908	1	0	1	0	1	0	0	0	-1	1	3H
Nap 2037	0	0	0	0	-1	0	0	-1	0	0	-2L
BARI Sarisha 7	-1	-1	-1	0	0	0	0	0	1	-1	-3L
BARI Sarisha 13	0	-1	-1	-1	-1	0	0	0	1	0	-3L
Total significance	**2**	**2**	**4**	**2**	**4**	**1**	**1**	**2**	**3**	**2**	**Average** **0.20**
High score	**1**	**1**	**2**	**1**	**2**	**1**	**1**	**1**	**2**	**1**	
Low score	**1**	**1**	**2**	**1**	**2**	**0**	**0**	**1**	**1**	**1**	

Appendix V: Scoring of SCA effects of Hybrids (cross) for different Characters in *Brassica napus* L..

Parents	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)	SCA Group
Nap 94006 x Nap 248	0	1	1	1	0	0	0	0	-1	1	3H
Nap 94006 x Nap 179	1	0	1	-1	-1	1	1	-1	1	0	2H
Nap 94006 x Nap 206	0	-1	-1	-1	-1	-1	-1	-1	1	1	-5L
Nap 94006 x Nap 2001	0	1	1	0	1	1	1	1	-1	-1	4H
Nap 94006 x Nap 2057	1	-1	-1	-1	1	0	-1	1	0	-1	-2L
Nap 94006 x Nap 2012	0	1	-1	1	1	-1	0	-1	-1	-1	-2L
Nap 94006 x Nap 2013	0	0	1	-1	-1	1	0	-1	1	1	1H
Nap 94006 x Nap 2022	-1	-1	-1	1	-1	-1	1	1	1	1	0
Nap 9908 x Nap 248	0	1	1	1	0	0	1	1	-1	-1	3H
Nap 9908 x Nap 179	-1	0	1	1	0	-1	-1	-1	-1	-1	-4L
Nap 9908 x Nap 206	1	0	1	1	1	1	0	1	-1	-1	4H
Nap 9908 x Nap 2001	0	-1	0	0	0	0	0	0	1	1	1H
Nap 9908 x Nap 2057	0	1	1	0	0	1	0	0	1	1	5H
Nap 9908 x Nap 2012	0	-1	-1	-1	-1	0	0	-1	1	1	-3L
Nap 9908 x Nap 2013	1	0	0	-1	1	-1	1	1	1	1	4H
Nap 9908 x Nap 2022	-1	-1	-1	-1	-1	-1	-1	1	-1	-1	-8L
Nap 2037 x Nap 248	0	-1	-1	1	1	-1	-1	-1	1	1	-1L
Nap 2037 x Nap 179	-1	-1	-1	1	1	0	1	1	-1	1	1H
Nap 2037 x Nap 206	-1	0	1	-1	-1	0	-1	0	1	0	-2L
Nap 2037 x Nap 2001	0	1	1	1	-1	0	1	1	-1	-1	2H
Nap 2037 x Nap 2057	0	0	1	1	0	-1	1	0	0	-1	1H
Nap 2037 x Nap 2012	1	0	1	-1	-1	1	0	-1	1	0	1H
Nap 2037 x Nap 2013	-1	0	-1	1	1	0	-1	-1	-1	0	-3L
Nap 2037 x Nap 2022	1	1	1	1	1	1	1	-1	1	0	7H
BARI Sarisha-7 x Nap 248	0	-1	-1	-1	-1	0	1	1	-1	-1	-4L

Appendix V Continued

Parents	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Days to 50% flowering	Days to 50% maturity	Number of siliqua/plant	siliqua length(cm)	Number of seeds/siliqua	1000 seed weight(gm)	Seed yield/plant (gm)	SCA Group
BARI Sarisha-7 x Nap 179	0	1	0	0	0	0	-1	1	1	0	2H
BARI Sarisha-7 x Nap 206	-1	-1	-1	-1	1	-1	1	1	-1	-1	-4L
BARI Sarisha-7 x Nap 2001	1	-1	-1	1	0	0	-1	-1	1	0	-1L
BARI Sarisha-7 x Nap 2057	-1	-1	0	0	0	-1	1	0	-1	0	-3L
BARI Sarisha-7 x Nap 2012	0	1	1	1	0	1	1	1	1	1	8H
BARI Sarisha-7 x Nap 2013	0	0	0	0	1	0	-1	-1	-1	0	-2L
BARI Sarisha-7 x Nap 2022	1	1	1	-1	-1	1	-1	-1	-1	1	0
BARI Sarisha-13 x Nap 248	0	1	1	-1	-1	1	-1	-1	1	0	0
BARI Sarisha-13 x Nap 179	1	0	0	-1	1	0	-1	-1	1	0	0
BARI Sarisha-13 x Nap 206	1	1	0	1	1	-1	-1	-1	0	1	2H
BARI Sarisha-13 x Nap 2001	-1	0	-1	0	0	-1	-1	-1	-1	-1	-7L
BARI Sarisha-13 x Nap 2057	0	0	-1	0	-1	1	1	1	-1	1	1H
BARI Sarisha-13 x Nap 2012	-1	0	0	-1	-1	-1	-1	1	-1	0	-5L
BARI Sarisha-13 x Nap 2013	-1	0	0	1	-1	1	1	1	1	-1	2H
BARI Sarisha-13 x Nap 2022	1	-1	0	1	1	1	1	1	0	0	5L
Total Significance	22	25	30	31	29	26	32	34	36	27	Average
High Score	11	12	16	16	14	13	16	17	18	14	0.075
Low Score	11	13	14	15	15	13	16	17	18	13	