COMBINING ABILTY AND HETEROSIS THROUGH LINE×TESTER ANALYSIS IN *Brassica napus* L.

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CERTIFICATE

This is to certify that the thesis entitled, "COMBINING ABILITY AND HETEROSIS THROUGH LINE×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 MASTERS OF SCIENCE IN GENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried by, ***OLIUL HASSAN, Registration No. 08-03258*** *under my supervision and my guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

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Place: Dhaka, Bangladesh

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DEDICATED TO MY

BELOVED

PARENTS

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LIST 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	=	Ctoplasmic Male Sterility
DAE	=	Days After Emergance
df	=	degree of freedom
et al	=	and others
etc	=	Etcetra
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

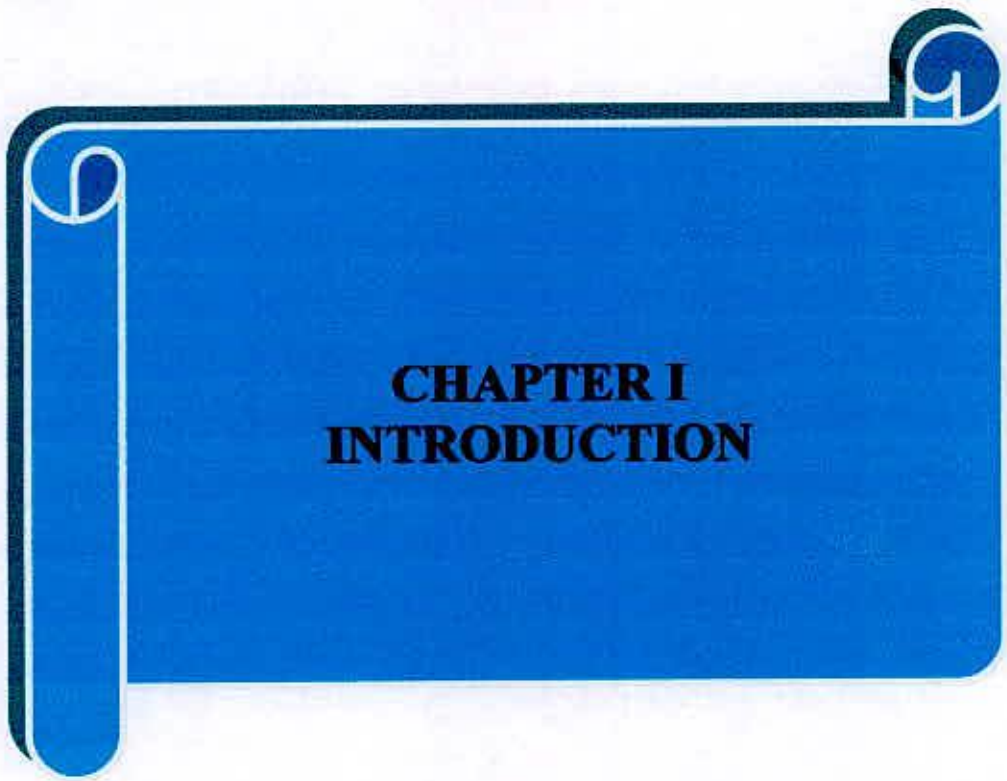
COMBINING ABILTY AND HETEROSIS THROUGH LINE×TESTER ANALYSIS IN *Brassica napus* L.

ABSTRACT

BY

OLIUL HASSAN

The study was conducted to evaluate six female parents (CMS lines) and 3 male parents (testers) in a line × tester mating design at the research field of Sher-e-Bangla Agricultural University, Dhaka, during November 2009 to March 2010 to estimate their combining and heterosis. The data recorded on 18 F_1's and their parents for their combining ability indicated that GCA effect was significant for days to fifty percent flowering, plant height, No. of siliqua per plant, seed per siliqua, primary branch & secondary branch per plant and seed yield per plant . The specific combining ability (SCA) effect was significant for all the characters. 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. Among the lines, CMS2, CMS3 and CMS5 were found as good general combiners. But seven hybrids exhibited good specific combiner among eighteen hybrids. Different types heterosis i.e. heterosis over mid parent (Hm), heterosis over better parent (Hb) and heterosis over standard check (HC) were estimated to evaluate eighteen hybrids for seed yield and yield related characters, where BARI Sharisha-7 was taken as check. The average heterosis for seed yield of eighteen hybrids over mid parent was 19.26% and that of better parent and standard check was 7.96% and 73.90%, respectively. Sixteen hybrids out of eighteen showed higher plant height than the standard check variety.



CHAPTER I
INTRODUCTION

INTRODUCTION

Rapeseed (*Brassica napus*), known as rape, oilseed rape, rapa, rappi, rapaseed . It is a bright yellow flowering member of the family Brassicaceae (The online Oxford English Dictionary relaunched in November 2010). 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).

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). The seeds of mustard and rapeseed contain 42% oil and 25% protein (Khaleque, 1985).

Recent data indicated that oil crops produces 0.16 million tons of edible oil in every year as against the total requirements of 0.5 million tons for a population of 130 million in Bangladesh (Anon., 1999 and Mondal *et al.*, 2001). The share of rapeseed and mustard was 253 640 tons, which comes to 52 percent of the total edible oil production (Anon., 2007). The yield of rapeseed and mustard is generally low in Bangladesh as compared with the world average. 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 reason 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 losses 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 F1 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, to overcome incompatibility barriers as well as plants with better agronomic characters in *Brassica.* 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. Recently, cytoplasmic-genetic male sterility has been discovered in mustard (*B.napus*) in Bangladesh. However, the maintainer for male sterility and restorer lines for mustard have not yet been identified. Extensive research efforts are being made to identify maintainer and restorer lines for the available male sterility.

Before using in hybrid seed production, these CMS lines and pollen parents need to be evaluated thoroughly for different morphological, floral and agronomic traits. In oil seed rape breeding 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 F1 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 F1 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 and synthetic 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. Varieties good in *Per se* performance may not necessarily produce desirable progenies when used in hybridization. Many workers have reported GCA and SCA effects for yield and yield components in different crops (Muraya *et al.,* 2006. Jan *et al.,* 2005; Sameena *et al.,* 2000; 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) and Diwaker and Singh (1993). Oilseed rape F_1 hybrids generated from crosses between resynthesised rape seed and elite breeding lines can exhibit high levels of yield heterosis (Seyis *et al.,* 2006). 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 2

REVIEW OF LITERATURE

REVIEW OF LITERATURE

In undertaking the present piece of research work (Line×Tester analysis) on three genotypes and six CMS line 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* avilable. These literatures are outlined here.

A study in Haryana, India, was conducted 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-significan 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, siliquae 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 *(Brassiect 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.

A line x tester experiment was conducted by Rai *et al.,* (2005) in India, on 60 F_1s of Indian mustard, derived from the crosses fifteen females and four males. The estimates of sigma 2s were higher than the sigma 2g for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, main raceme length, siliquae on main raceme, siliquae length, seeds per siliquae, 1000-seed weight, oil content and seed yield per plant. The estimates of specific combining ability (SCA) showed that approximately 43% cross combinations had significant positive SCA effects for seed yield. Only 23.07% of the crosses showed significant positive SCA effects while 76.92% of the cross combinations showed significant positive SCA effects for seed yield.

Eleven lines of Indian mustard, *Brassica juncea,* were evaluated by Patel *et al.,* (2005) for general (GCA) and specific combining ability (SCA) through line x tester cross analysis using six widely diverse testers at four locations in India. The traits studied were seed yield, number of siliquae per plant, seeds per siliqua and 1000-seed weight. The combining ability analysis revealed that non-additive type of gene effects were important for seed yield, siliquae per plant and seeds per siliqua, while additive gene effects were more important for 1000-seed weight. The combining ability for seed yield and yield attributing characters (days to flower initiation, days to maturity, plant height, number of primary branches per plant., number of secondary branches per plant, number of seeds per siliqua, 1000-seed weight and oil content) of Indian mustard were studied using a line x tester design, which involved three cytoplasmic male sterile lines and 25 testers. There were significant differences among the genotypes for all the characters indicating genetic variability. The significant differences due to parents vs. crosses indicated

the presence of heterosis in the crosses. Among lines, significant differences were observed for days to flower initiation, days to maturity, plant height and 1000-seed weight. There were significant differences among males for oil content, days to flower initiation, days to maturity, plant height and number of primary branches. The mean squares due to line x testers were highly significant for all the characters. The variances due to general combining ability (lines) were higher than those due to general combining ability (tester) for days to flower initiation and seed yield per plant indicating diversity among the females compared to the males for combining ability. A higher magnitude of variance due to testers compared to lines was observed for seed yield, per plant, plant height, primary branches, and secondary branches per plant, days to flower initiation, days to maturity and oil content.

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 F1s 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 maior characters including seed yield both additive and non additive gene action were of prime importance.

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.

Liu *et al.*, (2001) conducted an experiment between four double-low male sterile lines of rapeseed with glucosinolate lower than 30μmol/g and erucic acid lower than 1% were crossed with four good restorer lines based on North Carolina 11 design and the cornbining, ability and heritability of eight main agronomic characters of the crosses were estimated. The sterile line 121A, known as the sterile line of Shanyou 6, was shown to be most outstanding, with high general combining ability for many yield contributing characters, thus having relatively high yield potential. Of the fertility restorers studied, 116C, known as the restorer line of Shanyou 6, performed the best.

Combining ability and heritability was estimated by *Liu et al.*, (2001) of eight main agronomic characters of the crosses obtained by crossing four double-low male sterile lines of rapeseed with 4 good restorer lines based on North Carolina II desing. They observed high general combining ability for many yield-contributing characters, thus having relatively high yield potential.

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.

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.

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 ($5S_3$ and $4S_4$), their pollinator (tester) Taplidor and 9 F_1 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 perdominated in control of number of primary branches, seed yield/plant, plant height and silliqua 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 (1987). 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 vigour 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 India 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.

An observation on the inter subgenomic heterosis for seed yield among hybrids between natural Brassica napus (AnAnCnCn) and a new type of B. napus with introgressions of genomic components of Brassica rapa (ArAr) was made by Qian *et al.*, (2005). This B. napus was selected from the progeny of B. napus x B. rapa and (B. napus x B. rapa) x B. rapa based on extensive phenotypic and cytological observation. Among the 129 studied partial intersubgenomic hybrids, which were obtained by randomly crossing 13 lines of the new type of B. napus in F3 or BC1F3 to 27 cultivars of B. napus from different regions as tester lines, about 90% of combinations exceeded the yield of their respective tester lines, whereas about 75% and 25% of combinations surpassed two elite Chinese cultivars, respectively. This strong heterosis was further confirmed by reevaluating 2 out of the 129 combinations in a successive year and by surveying hybrids between 20 lines of the new type of B. napus in BC1F5 and its parental B. napus in two locations. Some DNA segments from B. rapa were identified with significant effects on seed yield and yield components of the new type of B. napus in BC1F5 and intersubgenomic hybrids in positive or negative direction. It seems that the genomic components introgressed from B. rapa contributed to improvement of seed yield of rapeseed.

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, siliquae 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.

The nature and magnitude of combining ability and heterosis on yield and its components were studied by Kumar *et al.,* (2004) in Indian mustard genotypes CS-52, CSTR 338-1, CZM-2, Kranti, NDR-9501, RH-39, SAL-2 and SAL-3 following an 8x8 diallel analysis on normal (ECe 1.8 ds/m) and saline (ECe 106 dS/m) soils. There were significant differences in the general (GCA) and specific combining ability (SCA) components for days to flowering, days to maturity, number of pods per plant, 1000-seed weight and seed yield on normal soil, whereas on saline soil, the differences were significant for days to flowering for GCA and pods per plant for SCA only. Among the parents, CS-52 showed significant positive GCA on both soils for pods per plant, whereas on saline soil, SAL-3 showed significant positive GCA for seed yield. CS-52 was also a good general combiner for early flowering on normal soil.

The crosses NDR-9501 x RH-30 and Kranti x NDR-9501 showed the highest significant SCA effects for yield on normal soil, whereas, CSTR 338-1 x CZM-2 was characterized with the highest significant SCA for this trait on saline soil. CSTR 338-1 x CZM-2 (33.61%) and CSTR 338-1 x SAL-2 (5.2%) showed the highest heterotic effects for seed yield on saline soil. However, on normal soil, Kranti x NDR 9501 (29.8%) and NDR 9501 x RH-30 (23.2%) showed the highest heterotic effects for seed yield. There was no cross showing significant positive heterosis for seed yield on both soils.

Heterosis for yield and yield components was in 30 crosses of Indian mustard was estimated by Goswami *et al.,* (2004) in an experiment conducted in 1999-2000 (E1) and 2000-01 (E2) in Haryana, India. Results showed that the cross RH9404 x RH30 had the maximum heterosis for seed yield per plant (92.88 and 106.23%) during E1 and E2, respectively. This cross also showed high heterosis for 1000-seed weight. The crosses RH9617 x RWH1 and RH9621 x RWH1 were selected because of high heterosis for all the parameters tested.

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). These hybrids can be grown for 2 or 3 generations.

Mahak *et al.,* (2003) studied heterosis for days to flowering, plant height, number of primary and secondary branches, length of main raceme, days to maturity, thousand seed weight, harvest index, oil content, protein content, and seed yield in 10 Indian mustard cultivars and 45 F_1 and F_2 hybrids. High heterosis for seed yield was observed.

An investingation was conducted by Pourdad *el al.,* (2003) to study heterosis in rapeseed *(B. napus, B. napus* var. *oleiferal)* 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 F1s 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. napes* 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_1s 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_1sand 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 (Girke *et al, 2000).*

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.

Hu (1999) investigated the F_1 progeny of five breeding lines of *B. juncea* and showed hybrid vigour, giving good disease resistance, vigorous growth and high yields. However the large-SCAle production of hybrid seed by manual pollination is hampered by the small size and large numbers of flowers, the small number of seeds per pod (10-20), the high costs of manual pollination and the inability to guarantee seed purity. Other subspecies of *B. juncea* produce very high yields of pure-bred seed when naturally self crossed and it is suggested that use of cytoplasmically male sterile (CMS) lines is ideal for breeding tuber mustard under these circumstances. Dozens of hybrids have been produced from CMS and inbred lines, and yields are up to 36% higher than in normal selfed cultivars.

A 22 line x 3 tester analysis of Brassica juncea was studied by Rakesh *et al.*, (1999) and they reported heterosis on seed yield and oil content in. Data are tabulated with respect to parent GCA classes (high x high, high x low and low x low).

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%.

Starmer 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. Hybrids and 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 DB_1 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 *Br assica,* and future strategies.

CHAPTER 3
MATERIALS AND METHODS

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 2008 to March 2009 and November 2009 to March 2010. The experiment field is located at $90^0$33′ E longitude and $23^0$77′ latitudeat 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 10.5-11.0hours 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

Three tester such as 130,94006, 9906 and Six line i.e CMS line such as CMS1 , CMS2, CMS3 CMS4, CMS5, CMS6 were collected from the department of Genetics and Plant Breeding Sher-e-Bangla Agricultural University, Dhaka-1207 . These nine parent were grown in the experimental farm of Sher-e-Bangla Agricultural University during the winter season of 2008 to 2009 to obtain F_1 test cross progenies for estimation of combinig ability and heterosis (Table 3.1.). In winter season 2009 to 2010 the parents and F_1 test cross progenies were also grown in the same farm.

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

Three genotypes of *B.napus* were grown in different row in the experimental field on 11 November, 2008. Each CMS line was also grown in each alternate row with *B. napus* genotypes. The row spacing was 30 cm having plant spacing of 15 cm within the row. The seedlings emerged out within four days after sowing.

Plate 1. A field view of the experimental site at SAU farm (Rabi 2009)

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.

3.9. Crossing among the selected genotypes of rape seed

Six cytoplasmic-genetic male sterile (CMS) line were crossed with three genotypes of *B.napus* as tester in one direction during December 2008 to January 2009. 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 pollinationwas 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 18 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.

3.10 Growing test cross (F_1s) and their parental population

Evaluation of test cross progenies were carried out during November 2009 to March 2010 in the experimental field. Dept. of Genetics and Plant Breeding, SAU.

3.10.1 Plant material used

The seeds of nine parents (Six CMS line and 3 *B. napuss* genotypes as tester) and their 18 F_1s obtained from previous year and BS-7 (CV)were used as plant materials.

3.10.2 Land Preparation

The land was prepared thoroughly by3-4 times ploughing and cross ploughing following by laddering to attain a good tilth. During land preparation. Weed and stubble of the previous crops were collected and removed from the field.

3.10.3 Layout and design

The seeds of 18F_1s (hybrids) and 9 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.

3.10.4 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.

Table 1.List of the seed parent ,pollen parent, standard check and their F1 hybrids for combining ability and heterosis estimation

Seed parents	Standard check vriety	pollen parents	F_1hybrids		
CMS1	BARI Sharisa-7	nap130	CMS1×nap130	CMS1×nap94006	CMS1×nap9906
CMS2		Nap94006	CMS2×nap130	CMS2×nap94006	CMS2×nap9906
CMS3		nap9906	CMS3×nap130	CMS3×nap94006	CMS3×nap9906
CMS4			CMS4×nap130	CMS4×nap94006	CMS4×nap9906
CMS5			CMS5×nap130	CMS5×nap94006	CMS5×nap9906
CMS6			CMS6×nap130	CMS6×nap94006	CMS6×nap9906

3.10.5 Sowing of seeds

Seeds of 18 F_1s were grown in separate line in the experimental field on 12November, 2009. 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.

3.10.6 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 when necessary. For suppression of aphid population Malathion 57 EC was applied three times as spray at an interval of 10-15 days after seedling emergence.

3.11 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 nine characters:

3.11.1 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.

3.11.2 Plant height at maturity(cm)

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

3.11.3 Number of primary branches per plant

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

3.11.4 Number of secondary branches per plant

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

3.11.5 Number of siliqua per plant

The total number of siliqua of five plants were counted and average number of siliqua per plant were rcorded.

3.11.6 Length of siliqua(cm)

Length taken from the base to the tip of the siliqua. Length of siliqua of (five siliqua perplant) five plants was taken and avereged.

3.11.7 No. of seeds per siliqua

All siliqua front the sample plant were collected and10 siliqua were randomly selected. Seeds obtained from them were counted and recorded. average number ofseeds per ssiliqua. 1000-seed weight: From each sample plant 1000 dry seeds were CoUnted and weighted by electronic balance in gram.

3.11.8 Seed yield per plant (g)

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

3.11.9 Thousand seed weight (g)

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

3.12 Statistical Analysis

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

3.12.1 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).

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

Where

Cij is the observat ion for i x j th crosses

r = Number of replication

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

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

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

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)

3.12.2 Estimation of GCA effects

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

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

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

3.12.3 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

3.12.4 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) = $\{\frac{Me}{r\times t}\}^{½}$

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

S.E. (SCA effects) = $\{\frac{Me}{r}\}^{½}$

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

S.E. (g_i-g_j) for tester= $\{\frac{2Me}{r\times l}\}^{½}$

Where,

Me = Error mean sum of square

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

3.12.5 Estimation of Genetic Component of variation

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

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

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

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) $=\left[\frac{1+F}{4}\right]\sigma^2 A$

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

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

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

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

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

3.12.7 Determination of combining ability status

The procedure described by Aranachalam and Rabdopadliva (1979) was followed 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 overallGCA or SCA status.

3.12.8 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 -8 was taken as standard check variety to estimate economic heterosis. Heterosis was calculated by the following formula:

3.12.8.1 Estimation of heterosis over mid parent (Hm)

$$Hm\% = \frac{\bar{F}_1 - \overline{MP}}{\overline{Mp}} \times 100$$

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

$$t\ value = \frac{(\bar{F}_1 - \overline{MP})}{SE(Hm)}$$

3.12.8.2 Estimation of heterosis over better parent (Hb)

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

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

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

3.12.8.3 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 4
RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

An experiment was conducted with three testers named Nap 130, Nap 94006 and Nap 9906, six CMS lines (line) and eighteen crosses (hybrids) and the data were recorded on different characters such as, days of 50% flowering, plant height (cm), no. of silique per plant, length of sliqua (cm), seeds per siliqua, primary branch/plant, secondary branch/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 six CMS (cytoplasmic male sterile) test genotypes(line)and three genotypes (testers), analysis of variance for Hybrid (crosses),line, tester, line X tester, combining ability and other components were analyzed 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 for lines and testers, specific combining ability for hybrids and genotype grouping based on GCA and SCA were discussed as follows:

The analysis of variance for nine characters showed that the hybrids were significantly different at 1% level, for all characters studied except thousand seed weight (Table 2 and Table 3). 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 days of 50% flowering and plant height (cm) at 1% level, for primary branches per plant at 5% level. Variance due to testers for days to 50% flowering and primary branch/plant were significant at 5% level. Variance due to interaction

(line X tester) was found highly significant for all the characters except plant height (cm), siliqua length and thousand seed weight. Analysis of variance showed wide range of variability was present in 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 except no. of silique per plant 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 4) and found that the contribution of lines were higher than contribution of line X tester (interactions) or contribution of testers to the total variances for days to 50% flowering, plant height and primary branch/plant. These result suggested that the predominance of general combining ability for days to 50% flowering, plant height and primary branch/plant. The contribution of line x tester (interactions) were higher than that of lines or testers for all characters except days to 50% flowering, plant height and primary branch/plant; this indicated the positive direction for development heterotic hybrid. Similar results were also found by Yadav *el al.* (2005).

Table 2. Analysis of variance for combining ability for different characters in *Brassica napus* genotypes

Source of variation	Degree of freedom	Days to 50%flowering	Plant height(cm)	No. of silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant(g)	Yield /plant(g)
Replication	2	6.78	11.58	3365.59	0.62	23.46	0.11	48.05*	0.02	6.07
Hybrids	17	26.19**	354.49**	14163.67**	0.83*	23.43**	2.47**	95.17**	0.19	49.84**
Line(females)	5	41.26*	747.13**	15576.37	0.78	35.45	3.82*	117.14	0.19	53.75
Tester(male)	2	58.02*	190.59	6622.91	1.13	6.13	4.67*	78.24	0.24	42.13
Line×Tester	10	12.29**	190.94	14965.46**	0.79	20.89**	1.36**	87.57**	0.19	49.43**
Errors	52	2.57	123.71	1257.58	0.40	7.39	0.48	14.04	0.18	3.34**
Component of variance										
$\sigma^2 gca$		0.417	4.904	1.733	0.001	0.076	0.033	0.228	0.000	0.012
$\sigma^2 A$		0.83	9.81	3.47	0.00	0.15	0.07	0.46	0.0004	0.02
$\sigma^2 sca$ or $\sigma^2 D$		3.24	22.41	4690.12	0.13	4.50	0.30	24.51	0.002	15.37
$\sigma^2 GCA/\sigma^2 SCA$		0.129	0.219	0.000	0.009	0.017	0.115	0.009	0.092	0.001
CV%		11.043	9.04	17.06	6.77	11.31	13.90	24.24	6.80	6.18

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

$\sigma^2 sca$: Variance of specific combining ability $\sigma^2 D$: Dominance genetic variance

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

Table 3: Analysis of variance for combining ability for different characters in *Brassica napus* hybrids and parents

Source of variation	Degree of freedom	Days to 50%flowering	Plant height(cm)	No. of silique per plant	Length of sliqua (cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant (g)	Yield /plant (g)
Replication	2	6.78	11.58	3365.59	0.62	23.46	0.11	48.05*	0.02	6.07
Entries	27	32.18**	347.06**	12107.18**	0.68	21.26**	2.57**	112.78**	0.21	39.37**
Error	52	2.57	123.71	1257.58	0.40	7.39	0.48	14.04	0.18	3.34**
CV%		11.043	9.04	17.06	6.77	11.31	13.90	24.24	6.80	6.18

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

Table 4: Proportional contribution of line tester and their interactions to the total variance in *Brassica napus* hybrids

Source	Days to 50%flowering	Plant height(cm)	No. of Silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primary Branch/plant	Secondary Branch/plant	Thousand seeds weight/plant(g)	Yield /plant
Due to lines	46.34	61.99	34.73	27.95	44.50	45.50	36.20	28.87	31.72
Due to testers	26.06	6.33	6.68	16.06	3.08	22.22	9.67	14.43	9.94
Due to line×tesers	27.59	31.68	58.60	55.99	52.43	32.28	54.13	56.70	58.34

4.2 Mean performance and combining ability effects

General combining ability (GCA) effects in respect of testers and lines (Table 7-8) and specific combining ability (SCA) effects of crosses (Table 9), maximum and minimum mean values of 18 cross combinations (Table 2), inter se mean of parents (Table 3), scoring of GCA and SCA effects (Appendix III-V), promising specific cross combination with its SCA grouping and parents GCA grouping (Table 7 -9) are presented. Results revealed that there was a wide range of variation in combining ability estimates and means. Eighteen cross combinations were categorized in two groups considering all characters (Arunachalam and Bandhopdhya 1979). Seven crosses were found under high (H) SCA group and eleven crosses were under low (L) SCA group. The salient feature about the above estimates, are presented character wise as follows:

4.2.1 Days to -50 percent flowering

a) Mean performance

The earliest (flowering) three hybrids were CMS4 x nap 94006(21days) CMS1× nap94006 (26.33 days) and CMS5× nap94006 (27 days). All these crosses were earlier than both of their estimated parental mean. The three crosses CMS6× nap9906 (35 days), CMS6×nap130 (33.67days) and CMS1×nap9906 (31.33 day) were take highest time to 50%flowering. All these crosses were took higher time to 50% flowering than their parental mean (Table 5 - 6).

b) General combining ability effects

Negative general combining ability effects were desired for days to flowering. The general combining ability effects ranged from -2.09 to 4.13 for *B. napus* CMS line and -1.9 to 1.52 for testers (Table 7-8). Among six (6) *B. napus* CMS lines, three (3)

showed significant GCA effect for days to 50% flowering, among them two were negative and one was positive. Parents with negative GCA effect were good general combiner earliness. CMS4 showed the lowest (-2.01) and it was followed by CMS2 (-.98). CMS6 showed the highest GCA effects (4.13) (Table 8). In case of three testers two showed significant GCA effect, those were Nap 94006 (-1.98) and Nap9906 (1.52) (Table 7). It indicated that the genotype Nap 94006 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 18 genotypes, ten hybrids showed significant SCA effects of which five were positive and five were negative. The cross CMS4×nap94006 showed the highest (-3.69) negative SCA effect whereas, CMS3×nap94006 (2.20), CMS2×nap94006 (2.20) and CMS4×nap130 (1.87) showed positive SCA value (Table 9). It indicated that the first combination was the best for earliness and rest crosses were poor in terms of 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.

4.2.2 Plant height

a. Mean performance

The tallest plant (139.83 cm) was found from the cross CMS5×nap9906 and followed by CMS1×nap94006 (127.67 cm) and CMS2×nap94006 (126.9cm). The shortest plant (93cm) was found from the CMS4× nap94006 which was followed by CMS3×nap130 (103.1cm), CMS4 × nap9906 (105.27cm) (Table 5).

Table 5. Per se performance (mean) of eighteen crosses in *Brassica napus* L.

Cross	Days to 50%flowering	Plant height (cm)	No. of silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primery branch/plant	Secondary branch/plant	Thousand seeds weight/plant(g)	Yield /plant(g)
CMS1×nap130	28.33	119.73	217.33	6.25	21	3.67	11.33	4.08	12.16
CMS2×nap130	28	117.97	213	6.65	20	4.67	22	3.57	8.1
CMS3×nap130	28	103.1	163.33	7.41	28	4.67	8.67	3.84	9.37
CMS4×nap130	29	111.13	333.67	6.65	21.67	5.33	20	3.98	20.46
CMS5×nap130	28.33	123.93	206	7.06	26	4.33	17	3.56	7.12
CMS6×nap130	33.67	110.75	131.67	6.49	22.33	3.33	8.67	3.82	8.52
CMS1×nap94006	26.33	127.67	204.67	6.8	25.33	4.33	13	3.6	11.97
CMS2×nap94006	28	126.9	378	8.47	28.33	6.67	25.33	4.3	20.13
CMS3×nap94006	28.33	123.4	322.33	6.43	25	6.33	19.33	3.73	18.46
CMS4×nap94006	21	93	153	6.7	20	4.67	10	4.15	12.27
CMS5×nap94006	27	123.33	226.67	7.6	27.33	4.33	16	4	12.4
CMS6×nap94006	30	120.93	242.67	7.43	20	3.67	17.33	4.24	8.75
CMS1×nap9906	31.33	125.17	198.67	6.9	24.33	3.33	9	4.07	10.66
CMS2×nap9906	27.33	116.4	303.33	7.3	23	4.33	11	4.18	12.64
CMS3×nap9906	28	111.87	306.67	7.37	23	4.33	17	3.53	17.46
CMS4×nap9906	30	105.27	196.33	6.94	21	3.67	8	4.23	11.3
CMS5×nap9906	30	139.83	253	6.87	26	4.33	22.67	4.08	10.25
CMS6×nap9906	35	125.4	134.67	7.23	25	4	8.33	3.98	10.86
Mean	28.76	118.10	232.50	7.03	23.74	4.44	14.70	3.94	12.38
Maximum	35	139.83	378	8.47	28.33	6.67	25.33	4.3	20.46
Minimum	21	93	131.67	6.25	20	3.33	8	3.53	7.12

Table6: Inter se (estimated) mean of nine *Brassica napus* L. genotypes

Parents	Days to 50%flowering	Plant height(cm)	No. of silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant(g)	Yield /plant(g)
nap130	25.67	102.6	132	6.8	22	3.33	4.67	3.46	8.32
Nap94006	28.33	114.6	197.33	7.26	23	4.33	6	3.59	12.41
nap9906	32.67	109.67	135.33	7.03	22	3	4	3.77	10.47
CMS1	31	126.13	183	7.4	25	5.67	22	4.33	11.21
CMS2	30	132.47	186.67	7.1	25	5	20.33	3.71	8.32
CMS3	22	111	173.67	7.62	24	4.33	15	3.61	11.98
CMS4	23.67	118.67	201	6.24	18	5	22	3.82	7.49
CMS5	29	124.37	191.67	7.07	26.67	5.67	16.33	3.9	14.51
CMS6	34	136	228	6.93	22.67	5.67	17.33	3.65	11.97
Mean	28.48	119.50	180.96	7.05	23.15	4.67	14.18	3.76	10.74
Maximum	34	136	228	7.62	26.67	5.67	22	4.33	14.51
Minimu	22	102.6	132	6.24	18	3	4	3.46	7.49

Table-7. GCA effects for different characters in *Brassica napus* L.(Tester)

Parents	Days to 50%flowering	Plant height(cm)	No. of silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant(g)	Yield /plant(g)	GCA Group
Nap130	0.46	-3.66	-21.67**	-0.28	-0.57	-0.11	-0.09	-0.13	-1.43**	L
Nap94006	-1.98**	1.11	22.06**	0.21	0.59	0.56**	2.13*	0.06	1.61**	H
Nap9906	1.52**	2.56	-0.39	0.07	-0.02	-0.44**	-2.04*	0.07	-0.19	L
(±)	.38	2.62	7.58	.15	.64	.16	.88	.10	.43	
SE(gi-gj)T	0.61	3.71	10.73	0.21	0.91	0.23	1.25	0.14	0.61	
MAX	1.52	2.56	22.06	.21	.59	.56	2.13	.07	1.61	
MIN	-1.98	-3.66	-21.67	-.28	-.58	-.44	-2.04	-.13	-1.43	

* 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-8. GCA effects for characters in six male sterile line of *Brassica napus* L.

Parents	Days to 50%flowering	Plant height(cm)	No. of silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primary branch/plan	Secondary branch/plant	Thousand seeds weight/plant(g)	Yield /plant(g)	GCA Group
CMS1	-0.09	6.09*	-25.61**	-0.38*	-0.19	-0.67**	-3.59**	-0.03	-0.79	L
CMS2	-0.98*	2.32	65.61**	0.44**	0.04	0.78**	4.74**	0.08	1.24**	H
CMS3	-0.65	-5.31	31.61**	0.04	1.59	0.67**	0.30	-0.24	2.71**	H
CMS4	-2.09**	-14.97**	-4.83	-0.27	-2.85**	0.11	-2.04	0.18	2.29**	L
CMS5	-0.31	10.93**	-3.94	0.15	2.70**	-0.11	3.85**	-0.06	-2.46**	H
CMS6	4.13**	0.93	-62.83**	0.02	-1.30	-0.78**	-3.26*	0.07	-3.01**	L
SE(±)	.53	3.70	10.73	.21	.90	.23	1.25	.14	.60	
SE(gi-gj)L	**0.86**	**5.24**	**15.18**	**0.30**	**1.28**	**0.33**	**1.77**	**0.20**	**0.86**	
MAX	4.13	10.93	65.61	0.44	2.7	0.78	4.74	0.18	2.71	
MIN	-2.09	-14.97	-62.82	-.38	-2.85	-.78	-3.59	-.24	-3.01	

* 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-9. SCA effects of *B. napus* hybrids (cross)for different Characters

Hybrids (cross)	Days to 50%flowering	Plant height(cm)	No. of silique per plant	Length of sliqua(cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant (g)	Yield /plant(g)	SCA group
CMS1×nap130	-0.80*	-0.79	32.11**	-0.12	-1.98**	0.00	0.31	0.30**	1.99**	H
CMS2×nap130	-0.24	1.21	-63.44**	-0.54**	-3.20**	-0.44**	2.65**	-0.31**	-4.10**	L
CMS3×nap130	-0.57	-6.03*	-79.11**	0.62**	3.24**	-0.33*	-6.24**	0.27**	-4.30**	L
CMS4×nap130	1.87**	11.66**	127.67**	0.16	1.35*	0.89**	7.43**	-0.01	7.21**	H
CMS5×nap130	-0.57	-1.44	-0.89	0.16	0.13	0.11	-1.46	-0.19	-1.37**	L
CMS6×nap130	0.31	-4.61	-16.33*	-0.28	0.46	-0.22	-2.69**	-0.06	0.57	L
CMS1×nap94006	-0.35	2.37	-24.28**	-0.06	1.19	0.00	-0.24	-0.38**	-1.24**	L
CMS2×nap94006	2.20**	5.37*	57.83**	0.79**	3.96**	0.89**	3.76**	0.22*	4.89**	H
CMS3×nap94006	2.20**	9.50**	36.17**	-0.85**	-0.93	0.67**	2.20*	-0.03	1.75**	H
CMS4×nap94006	-3.69**	-11.24**	-96.72**	-0.27	-1.48*	-0.44**	-4.80*	-0.03	-4.02**	L
CMS5×nap94006	0.54	-6.81*	-23.94**	0.22	0.30	-0.56**	-4.69**	0.06	0.86	L
CMS6×nap94006	-0.91*	0.80	50.94**	0.17	-3.04**	-0.56**	3.76**	0.16	-2.24**	L
CMS1×nap9906	1.15**	-1.58	-7.83	0.18	0.80	0.00	-0.07	0.08	-0.75	H
CMS2×nap9906	-1.96**	-6.58*	5.61	-0.24	-0.76	-0.44**	-6.41**	0.09	-0.79	L
CMS3×nap9906	-1.63**	-3.48	42.94**	0.23	-2.31**	-0.33*	4.04**	-0.24*	2.55**	L
CMS4×nap9906	1.81**	-0.42	-30.94**	0.11	0.13	-0.44**	-2.63**	0.04	-3.19**	L
CMS5×nap9906	0.04	8.24**	24.83**	-0.38*	-0.43	0.44**	6.15**	0.13	0.51	H
CMS6×nap9906	0.59	3.82	-34.61**	0.11	2.57**	0.78**	-1.07	-0.11	1.67**	H
SE(±)	0.38	2.62	7.59	0.15	0.64	0.16	0.88	0.10	0.43	
SE(sij-kl)	**1.49**	**9.08**	**26.29**	**0.52**	**2.22**	**0.57**	**3.06**	**0.35**	**1.49**	
Max	2.20	11.66	127.67	0.79	3.96	0.89	7.43	0.30	7.21	
Min	-3.69	-11.24	-96.72	-0.85	-3.20	-0.56	-6.41	-0.38	-4.30	

* Significance at 5%level, ** Significance at 1%level, SE: Standard error SE(sij-kl):Standard error of difference between for any two SCA effect of hybrids H: SCA group-High L: SCA group- low

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

The general combining ability effects (Table 7-8) were significant for three CMS lines for the trait. GCA varied from -14.97 to 10.93 for *Brassica napus* lines and from-3.66 to 2.56 for testers. Among *Brassica napus* lines CMS5 exhibited the highest positive highly significant GCA effect (10.93) followed by CMS1 (6.09). There was no significant GCA effect found for the testers. CMS4 had the highly significant negative GCA effects(-14.97). Those effects indicated that the lines 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 CMS5 was the best general combiner due to high positive GCA effects if tall type is desired. On the other hand CMS4 was also found as the best general combiner due to the highest negative GCA effects if dwarf type is desire. From the testers Nap9906 was the average general combiner and for the trait.

c.Specific combining ability (SCA) effects

Significant SCA effects observed in eight crosses (Table 9) out of 18 hybrids tested, of which four had significant positive and four 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 possitive significant SCA effects were considered as good specific combiner for tallness. First three of them were CMS4×nap130 (11.66), CMS3×nap94006 (9.50) and CMS5× nap9906 (8.24). 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 CMS4×nap94006 (-11.24), CMS5×nap94006 (-6.81) and CMS2× nap9906 (-6.58) had high negtive significant SCA effect.

4.2.3 Number of Siliqua per plant

a. Mean performance

The highest three cross combinations for number of siliqua per plant were CMS2× nap94006 (378), CMS4×nap130 (333.67) and CMS3× nap94006 (322.33) (Table 5); all of which exceeded their estimated parental means (Table 6). The lowest three cross combinations were CMS6×nap130 (131.67), CMS6 ×nap9906 (134.67) and CMS4×nap94006 (153). These values were lower than their inter se (estimated) pollinator means.

b. General combining ability effects

General combining ability of three testers ranged from-21.67 to 22.06 and -62.82 to 65.61 for six CMS lines. GCA effect of 2 testers out of 3 was significant of them one is positive and one is negative. Nap94006 is showing highest positive GCA effects (22.06). Nap 130, showing negative GCA effect viz. -21.6. (Table-7) In case of six CMS lines, 4 was significant in GCA effect of them two were positive and two were negative. CMS2 showed highest positive GCA effects (65.61) followed by CMS3 (31.61). GCA effect of CMS6 was highest significant negative (-62.82). (Table-8) These facts indicated that among the tester Nap94006 with significant positive GCA value are good general combiner for the trait and possessed more possitive 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. Patel *et al.*, (2005) and Rai *et al.*, (2005) found good general combiners in their experiments in Indian mustard and cited similar interpretation.

c. Specific combining ability effects

Fifteen combinations showed significant SCA effects (Table 9) in 18 cross combinations. Among significant values seven were positive and eight were negative. The cross combination CMS4×nap130 (127.67) followed by CMS2×nap94006 (57.43) and CMS6×nap94006 (50.94) 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.

4.2.4 Length of Siliqua

a. Mean performance

Present, study revealed that siliqua length ranged from 6.25 to 8.47 cm in hybrids and 6.8 to 7.26 cm in pollen parents. The highest mean siliqua length was found in the hybrid CMS2×nap94006 (8.47 cm) and the lowest mean siliqua length was found in the cross combination CMS1× nap130 (6.25crn) (Table 5). The highest *inter se* mean was found in the genotype nap94006 (7.26cm) and the lowest *inter se* mean was found in the genotype nap130(Table 6).

b. General combining ability effects

Out of six CMS lines two showed significant GCA effects, of them one had positive and one had negative GCA effects and pollen parents showed not significant GCA effect.

(Table 7-8). Positive significant GCA effect was found in the genotype CMS2 (0.44). It indicated that CMS2 was a good general combiner for siliqua length. The negative significant GCA effects were found in the genotypes CMS1 (- 0.38). 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:

Five cross combinations showed significant SCA effects. Among them two were positive and three were negative.The highest positive SCA effect (0.35) was found in the hybrid CMS2×nap94006 (.79) followed by CMS3× nap130 (0.62) (Table 9). The lowest negative SCA effect (-0.85) was found in the cross combination CMS3×nap94006 and it was followed by CMS2×nap130 (-0.54) and CMS5×nap9906 (-0.38). The Good cross combination evolved from high x high general combiners. This result revealed that additive x additive gene action involved in this trait.

4.2.5 Number of seeds per siliqua

a. Mean performance

The highest mean for no. of seeds per siliqua (28.33) was observed in the cross CMS2× nap94006 and it was followed by CMS3×nap130 (28), CMS5×nap94006 (27.33) where the range was 18 to 28.33(Table 5 and 6). 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. CMS5 was the best combiner due to highest significant positive GCA value (2.70) for no. of seeds siliqua. On the other hand, CMS4 had lowest significant GCA value (-2.85) hence, it was a poor general combiner (Table 8). Among three (3) pollen parents, there was no significant GCA effect. nap94006 had positive GCA value (0.59). Hence, this genotype was average general combiner. However, nap130 (-.57) and nap9906 (-.02) had negative GCA value and these were poor general combiner for the trait (Table 7). It indicated that good general combiners possessed more positive alleles but poor general combiners possessed less positive alleles. Ghosh *et al.,* (2002) and Shcoran *et al.,* (2000) agreed with these finding.

c) Specific combining ability effects

Among the hybrids, nine cross combination showed significant SCA effect. Among them four (4) were positive and five were negative. The cross combination CMS2× nap94006showed the highest SCA effect (3.96). It was the good specific cross combination for the trait (Table 9). Other two cross combinations closer to this value were CMS3×nap130 (3.24) and CMS6×nap9906 (2.57). On the other hand, the cross CMS2× nap130 showed the lowest SCA effect (-3.20) for number of seeds per siliqua. It was the poorest specific cross combination. Two other specific crosses nearer to this value were CMS6× nap94006 (-3.04) and CMS3×nap9906 (-2.31). 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.

4.2.6. Number of primary branches per plant

a. Mean performance

The highest mean was observed in the cross CMS2×nap94006 (6.67) for number of primary branches per plant (Table 5). Other cross closer to this value is CMS3×nap94006 (6.33) which were higher than both of its parents (Table 5 and 6) while CMS1× nap9906 and CMS6×nap130 had the lowest mean of number of primary branches per plant (3.33). It was lower than female parents but higher than pollen parent.

b. General combining ability effects

Significant GCA effect for number of primary branches per plant was not found in four female parents. Of them two were positive and two were negative (Table 8).CMS2 showed highest GCA effect (.78) and it was followed by CMS3 (.67). It indicated that they were good general combiners due to positive GCA effects. On the other hand, CMS6 had showed lowest GCA effect (-.78) and it was followed by CMS1 (-.67). So they were considered poorer general combiner due to negative GCA values. Among pollen parent two showed significant GCA effect, one was positive another one was negative (Table 7)

c. Specific combining ability effects

Thirteen cross combination showed significant SCA effects. Among them five were positive and eight were negative (Table 9). The cross CMS2× nap94006 and CMS4× nap130 showed the highest positive SCA effects (0.89)and they were followed by CMS6×nap9906 (0.78) and CMS3×nap94006 (0.67), where as CMS5×nap94006 and CMS6×nap94006 showed the highest negative SCA effects and they were followed by CMS4×nap94006 (-0.44) and CMS2×nap130 (-0.44). The former crosses were considered as good cross combinations for the trait and the latter two were considered as poor specific cross combinations. Non-Significance positive crosses were considered as above average and below average specific cross combination, respectively. The hybrid CMS2×nap94006 (.89) was derived from high and high general combiners. It indicated 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.

4.2.7. Number of Secondary branches per plant

a. Mean Performance

The highest mean for number of secondary branches per plant (25.33) was observed in the cross combination nap94006×CMS2 followed by nap9906×CMS5 (22.67) and nap130×CMS2 (22). On the other hand the lowest mean (8) was found in cross combination nap9906×CMS4 and it was followed by nap130×CMS3 (8.67) and nap130×CMS6 (8.67) (Table 5) The mean performance of all crosses for the number of secondary branches per plant (14.18) was higher than that of (mean) of all pollen parents(Table 6)

b. General combining ability effects

Out of six female parents four showed significant GCA effects, of them two were positive and two were negative. CMS2 had highly significant positive GCA effect (4.74) followed by CMS5 (3.85). On the other hand CMS1had the lowest significant negative GCA value (- 3.59), it was followed by CMS6 (-3.26), (Table 8). 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 nap94006 (2.13).and nap9906 showed negative significant GCA effect.

c. Specific combining ability effects

Out of eighteen crosses, thirteen cross combinations showed significant SCA effects of them seven had positive and six had negative GCA effects. The highest positive significant SCA effect (7.43) was found in the cross CMS3×nap130 and it was followed by CMS5×nap9906 (6.15) and CMS3×nap9906 (4.04). The lowest negative GCA effect (-6.41) was found in the hybrid CMS2×nap9906 followed by cross combinations nap130×CMS3 (-6.24) and CMS5×nap94006 (-4.69) (Table 9). 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.

4.2.8 Thousand (1000) seed weight

a. Mean performance

The highest mean for 1000-seed weight (4.33) was observed in the cross combination CMS2×nap94006 which was higher than both of the parents inter se mean (Table 2-3). Contrary the lowest mean (3.53) was found in cross combination nap9906×CMS3. However, mean value of forty cross combinations were higher than their both parents, *inter se* means except female parent CMS1 (Table 5-6).

b. General combining ability effects

Among the parents non showed significant GCA effect for 1000 seed weight (Table 7-8).Among them female parents CMS2, CMS4, CMS6 and pollen parent nap940006and nap 9906 had showed positive GCA value and other showed negative value. It indicated that three pollen parents and one female parent with positive GCA value were above general combiners for the trait. In the same way one pollen parents and three female parent with negative GCA values were below general combiner for the trait.

c. Specific combining ability effects

Among the cross combinations six (6) crosses exhibited significant SCA effects for 1000 seeds weight. Three cross combinations were found with positive and three with negative SCA effects (Table 9). The cross combination CMS1×nap130 showed the highest (0.30) positive SCA effects, followed by CMS3×nap130 (0.27) and CMS2×nap94006 (0.22). The lowest SCA value was found in the cross CMS1× nap94006 (-0.38). It was the poorest cross for the trait. The cross CMS2×nap130 (-0.31) and CMS3×nap9906 (-0.24) were with SCA values Closer to the lowest

(Table 7). Best specific cross combination CMS1× nap130was evolved from the parents having negative GCA effects (-0.13 and -0.03 respectively). However, the cross combinations CMS3×nap130 (0.27) and CMS2× nap94006 (0.22) showed high SCA effects. The two hybrids were evolved from the parents with low and low (-0.13 and .0.24) and high and high (0.07 and -.08) GCA effects. 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 Patel *el at.*,(2005) and Yadav *el al.*, (2005) in Indian mustard.

4.2.9 Seed yield per plant

a. Mean performance

The highest mean seed yield per plant (20.46 g) was observed in the hybrid CMS4×nap130 and it was followed by CMS2×nap94006 (20.13), CMS3nap×94006 (18.46) and CMS3×nap9906 (17.46). The seed yields per plant of the above crosses were higher than both of their parents (Table 2-3). Seed yield per plant (7.12g) was produced by the cross nap94006×CMS5 which was lower than both female and male.

b.General combining ability effects

Among the six female parents five were with significant GCA effects, of them three were positive and two were negative. CMS3 had highly significant highest positive GCA effect (2.71), two of its followers were CMS4 (2.29) and CMS2 (1.24). On the contrary CMS6 had the lowest (highly significant negative) GCA value (-3.26) (Table 6). 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), Liu *et al.*, (2001) 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 nap94006 (1.61) and the negative GCA effect was observed in nap130 (-1.43) (Table 7).

c.Specific combining ability effects

Among eighteen crosses, thirteen cross combinations showed significant SCA effects, of them six had positive and seven had negative effects (Table 9). The cross combination, CMS4×nap130 had the highest SCA value (7.21) and two of its closest values were 4.89 and 2.555 for cross combination CMS2×nap94006 and CMS3×nap9906, respectively. The cross combinations with positive significantSCA 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 (-4.30) was observed in the cross combination CMS3×nap130 and it was followed by CMS2×nap130 (-4.10) and CMS4×nap94006 (-4.02). 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 yieldper plant in *Brassica napus.* This result was supported by many researchers. Ghosh *et al.* (2002), Patel *et al.* (2005), Rai *et al.* (2005) 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 thousand seed weight 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 10. The heterosis of F_1 (Hybrid) over pollen parent and CMS are shown in Plate 2-10. The nature and magnitude of heterosis are presented character wise as follows:

4.3.2 Heterosis for different characters

i) Days to 50 percent flowering

Ten hybrids exhibited significant negative values for heterosis over mid parent (Hm). Such types of heterosis are desirable due to indication of earliness (Table 10). Mid parent heterosis ranged from -19.23% to 17.57% with a mean of .98% and for standard check the range was -34.38% to 9.38 with a mean of -10.13%. The hybrid CMS4×nap94006 had the highest negative heterosis over standard check (-34.38%). Results with negative heterosis indicated that the hybrids were early compared to their parents.

ii) Plant height

Thirteen hybrids exhibited significant heterosis over mid (Hm) parent (Table 10). The range of the heterosis was -20.27% to 19.5% with a mean of 1.07%. It indicated that all hybrids were about 0.37% to 19.5% taller (plant height) than their mid parental value. For

this character the estimated values of heterosis over better parent were significant for thirteen hybrids. The hybrids CMS5×nap9906 (12.44%) had the highest significant estimate over better (Hb) parent and it was followed by CMS3×nap94006 (7.68%). The hybrid CMS4 ×nap94006 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-7, all hybrids exhibited significant positive heterosis except hybrids CMS3×nap130 and CMS4×nap94006. The hybrid CMS5×nap9906 possessed the highest estimate (44.19%) and the hybrid CMS4×nap94006 had the lowest (-10.74%). It indicated the hybrid CMS5×nap9906 was the longest among the hybrids and the hybrid CMS4×nap94006 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 2: Photograph showing nap 94006, CMS line and their hybrid (F_1)

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iii) Number of siliqua per plant

Six hybrids showed significant heterosis over mid (Hm) parent for no. of siliqua per plant (Table 10). Nine had positive but non significant value. The hybrid CMS4×nap130 had the highest value of heterosis over and mid parent (100.40%) and it was followed by the hybrid CMS39×nap9906 (98.49). The hybrid CMS2×nap94006 had the highest value over the better parent. On the other hand when compared the heterosis with standard check fourteen hybrids exhibited significant positive heterosis, The hybrid CMS2× nap94006 had the highest (182.09%) estimate but CMS4× nap9906 exhibited the lowest (46.51%) significant estimate. It indicated that the hybrid nap94006×CMS2 1produced the highest number of siliqua per plant and the hybrid nap9906×CMS4 produced the lowest. Shen *et al.*, (2005) and Saurabh *et al.*, (2005) also observed positive heterosis for the number of siliqua per plant.

Table 10: Estimation of heterosis over mid parents , better parents, and standard check for different characters in *Brassica napus*

Hybhrids	Days to 50% flowering			Plant height(cm)			No. of silique per plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
CMS1×nap130	0.00	-8.60***	-11.47***	4.69	-5.07***	14.9***	37.99	18.76***	62.18***
CMS2×nap130	0.60	-6.67***	-12.5***	0.37	-10.95***	13.21***	33.68	14.11***	58.96***
CMS3×nap130	17.48***	9.09***	-12.5***	-3.46	-7.12***	-1	6.87	-5.95**	21.89
CMS4×nap130	17.57***	12.99***	-9.38***	0.45	-6.35***	6.65***	100.40***	66.00***	149***
CMS5×nap130	3.66	-2.30	-11.47***	9.21	-0.35	18.93***	27.29	7.48***	53.73***
CMS6×nap130	12.85***	-0.98	5.22***	-7.17	-18.57***	6.29***	-26.85	-42.25***	-1.74
CMS1×nap94006	-11.24***	-15.05***	-17.72***	6.06	1.22	22.52***	7.62	3.72	52.74***
CMS2×nap94006	-4.00	-6.67***	-12.5***	2.73	-4.20**	21.79***	96.88***	91.55***	182.09***
CMS3×nap94006	12.58***	0.00	-11.47***	9.40	7.68***	18.42***	73.76***	63.34***	140.54***
CMS4×nap94006	-19.23***	-25.88***	-34.38***	-20.26***	-21.63***	-10.74***	-23.18	-23.88***	14.18
CMS5×nap94006	-5.81***	-6.90***	-15.63***	3.22	-0.83	18.35***	16.54	14.86***	69.16***
CMS6×nap94006	-3.74	-11.76***	-6.25***	-3.48	-11.08***	16.06***	14.11	6.43***	81.1***
CMS1×nap9906	-1.57	-4.08***	-2.1	6.16	-0.77	20.12***	24.82	8.56***	48.26**
CMS2×nap9906	-12.77***	-16.33***	-14.59***	-3.85	-12.13***	11.71***	88.41***	62.50***	126.37***
CMS3×nap9906	2.44	-14.29***	-12.5***	1.39	0.78	7.36***	98.49***	76.58***	128.86***
CMS4×nap9906	6.51***	-8.16***	-6.25***	-7.80	-11.29***	1.03***	16.75	-2.32	46.51***
CMS5×nap9906	-2.70	-8.16***	-6.25***	19.50***	12.44***	34.19***	54.74***	32.00***	88.81***
CMS6×nap9906	5.00**	2.94*	9.38***	2.09	-7.79***	20.35***	-25.87	-40.94***	0.5
Mean	0.98	-6.16	-10.13	1.07	-5.33	13.34	34.58	19.47	73.51
Maximum	17.57	12.99	9.38	19.5	12.44	34.19	100.4	91.55	182.09
Minimum	-19.23	-25.88	-34.38	-20.26	-21.63	-10.74	-26.85	-42.25	-1.74

Table 10: Continued

Hybhrids	Length of sliqua(cm)			Seeds per siliqua			Primary branch/plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
CMS1×nap130	-11.92***	-15.50***	-4.62	-10.64***	-16.00***	5***	-18.52***	-35.29***	10.1***
CMS2×nap130	-4.27	-6.29***	1.47	-14.89***	-20.00***	0	12.00***	-6.67***	40.1***
CMS3×nap130	2.82**	9.02***	13.07***	21.74***	16.67***	40***	21.74***	7.69***	40.1***
CMS4×nap130	1.97	-2.21	1.47	8.33**	-1.52	8.35***	28.00***	6.67***	59.9***
CMS5×nap130	1.83	-0.09	7.73***	6.85**	-2.50	30***	-3.70	-23.53***	29.9***
CMS6×nap130	-5.49***	-6.39***	-0.96	0.00	-1.47	11.65***	-25.93***	-41.18***	-0.09
CMS1×nap94006	-7.25***	-8.11***	3.76***	5.56**	1.33	26.65***	-13.33***	-23.53***	29.9***
CMS2×nap94006	17.89***	19.25***	29.24***	18.06***	13.33***	41.65***	42.86***	33.33***	100.1***
CMS3×nap94006	-13.55***	-11.43***	-1.88	6.38**	4.17**	25***	46.15***	46.15***	89.9***
CMS4×nap94006	-0.79	-7.76***	2.23*	-2.44	-13.04***	0	0.00	-6.67***	40.1***
CMS5×nap94006	6.07***	4.64**	15.97***	10.07**	2.50*	36.65***	-13.33***	-23.53***	29.9***
CMS6×nap94006	4.72***	7.21***	13.37***	-12.41***	-13.04***	0	-26.67***	-35.29***	10.1***
CMS1×nap9906	-4.39	-1.85	5.29***	3.55**	-2.67	21.65***	-23.08***	-41.18***	-0.09
CMS2×nap9906	3.35**	2.82**	11.39***	-2.13	-8.00***	15***	8.33	-13.33***	29.9***
CMS3×nap9906	0.59	-3.32	12.46***	0.00	-4.17	15***	18.18***	0.00	29.9***
CMS4×nap9906	4.60**	-1.23	5.9***	5.00**	-4.55	5***	-8.33***	-26.67***	10.1***
CMS5×nap9906	-2.51	-2.78	4.83***	6.85**	-2.50	30***	0.00	-23.53***	29.9***
CMS6×nap9906	3.63**	2.94**	10.32***	11.94***	10.29***	25***	-7.69***	-29.41***	20***
Mean	-0.15	-1.17	7.28	3.4	-2.287	18.7	2.04	-13.1	33.32
Maximum	17.89	19.25	29.24	21.74	16.67	41.65	46.15	46.15	100.1
Minimum	-13.55	-15.5	-4.62	-14.89	-20	0	-26.67	-41.18	-0.09

Table 10: Continued

Hybhrids	Secondary branch/plant			Thousand seeds weight/plant(g)			Yield /plant(g)		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
CMS1×nap130	-15.00	-48.48***	161.48***	4.79	-5.77***	7.37***	24.55***	8.51***	70.78***
CMS2×nap130	76.00***	8.20***	407.73***	-0.23	-3.60	-6.05***	-2.62	-2.61	13.76***
CMS3×nap130	-11.86	-42.22***	100.09***	8.58***	6.28***	1.05**	-7.70	-21.79***	31.6***
CMS4×nap130	50.00***	-9.09***	361.57***	9.25***	4.01**	4.74***	158.73***	145.87***	187.36***
CMS5×nap130	61.90***	4.08**	292.33***	-3.22	-8.72***	-6.32***	-37.61***	-50.92***	0
CMS6×nap130	-21.21***	-50.00***	100.09***	7.65***	4.84**	0.53	-16.06***	-28.87***	19.66***
CMS1×nap94006	-7.14	-40.91***	200.02***	-9.09***	-16.86***	-5.26***	1.36	-3.55	68.12***
CMS2×nap94006	92.41***	24.59***	484.58***	17.95***	16.10***	13.16***	94.27***	62.25***	182.72***
CMS3×nap94006	84.13***	28.89***	346.11***	3.70***	3.42**	-1.84	51.41***	48.79***	159.27***
CMS4×nap94006	-28.57***	-54.55***	130.78***	11.96***	8.54***	9.21***	23.32***	-1.10	72.33***
CMS5×nap94006	43.28***	-2.04	269.26***	6.90***	2.65*	5.26***	-7.88*	-14.56***	74.16***
CMS6×nap94006	48.57***	0.00	299.95***	17.09***	16.18***	11.58***	-28.19***	-29.45***	22.89***
CMS1×nap9906	-30.77***	-59.09***	107.71***	0.41	-6.08***	7.11***	-1.63	-4.85*	49.71***
CMS2×nap9906	-9.59	-45.90***	153.87***	11.90***	10.96***	10***	34.58***	20.72***	77.53***
CMS3×nap9906	78.95***	13.33***	292.34***	-4.43***	-6.45***	-7.11***	55.55***	45.78***	145.22***
CMS4×nap9906	-38.46***	-63.64***	84.63***	11.50***	10.72***	11.32***	25.79***	7.89***	58.71***
CMS5×nap9906	122.95***	38.78***	423.19***	6.39***	4.62**	7.37***	-17.98***	-29.40***	43.96***
CMS6×nap9906	-21.88***	-51.92***	92.25***	7.24***	5.48***	4.74***	-3.24	-9.30***	52.53***
Mean	26.31	-19.44	239.33	6.018	2.57	3.71	19.26	7.96	73.90
Maximum	122.95	38.78	484.58	17.95	16.18	13.16	158.73	145.87	187.36
Minimum	-38.46	-63.64	84.63	-9.09	-16.86	-7.11	-37.61	-50.92	0

* 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.

iv) Length of siliqua

Hterosis over mid parent for siliqua length ranged frond -13.55% to 17.89% with a mean of-.15% while heterosis over better parent ranged from -15.5% to 19.25.% a mean value of -1.17% (Table 10). Four hybrids showed significant negative heterosis over mid parent for siliqua length. Highest positive heterosis (17.89%) was estimated in the cross CMS2×nap94006 which was desirable for high yield. In case of better parent Six hybrids showed significant negative hetcrosis. This result indicated that hybrids produced shorter siliqua than better parent. Standard heterosis ranged from -4.62% to 29.24% with a mean of 7.28% for siliqua length. The hybrids CMS2× nap94006showed the highest positive heterosis (29.24%) and it was followed by nap94006×CMS5 (15.97%) and CMS6×nap94006 (13.37 %) for the trait which were desirable for high yield. Saurabh *et al.*, (2005) found +ve heterosis for siliqua length.

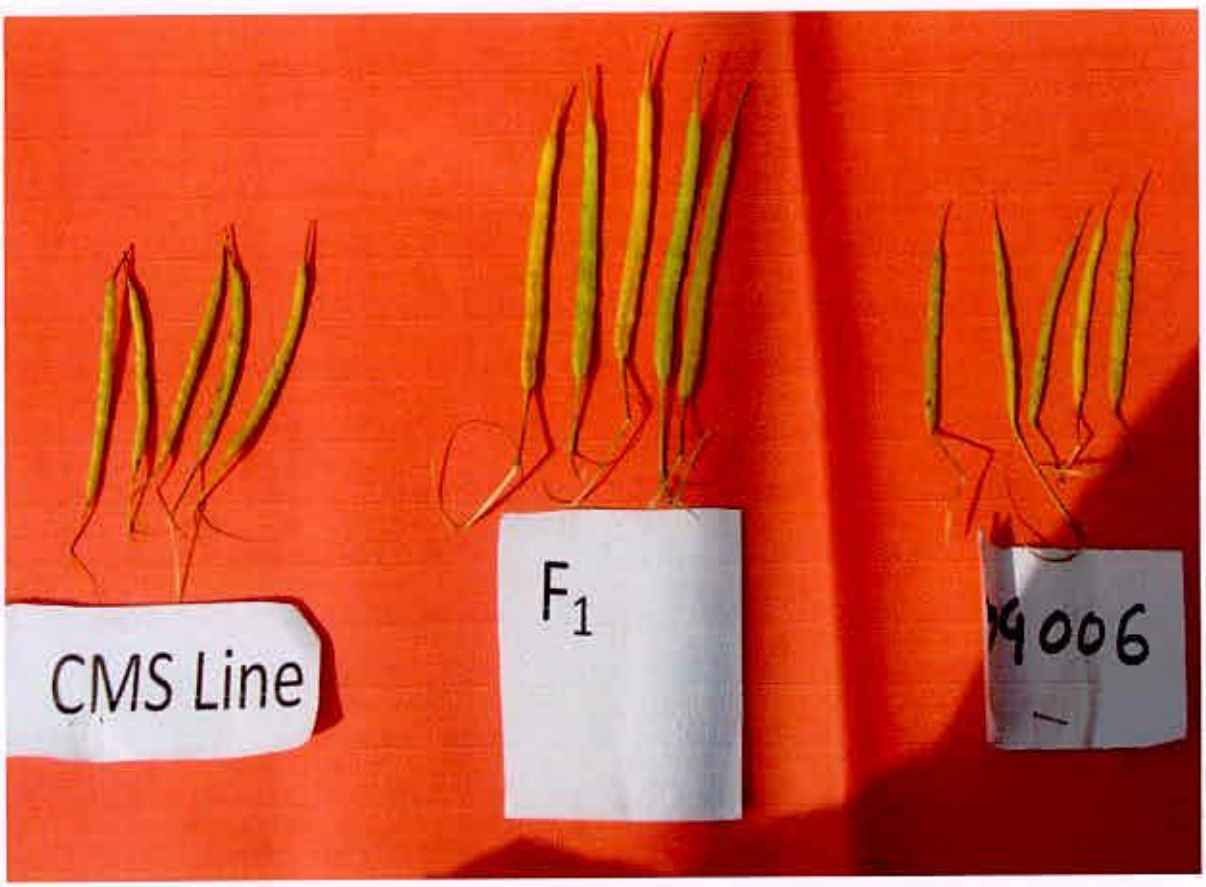

Plate 3: Photograph showing siliqua of nap 94006, CMS line and their hybrid (F_1)

v) Number of seeds per siliqua

Fourteen hybrids showed significant over mid parent heterosis for seeds per siliqua (Table 10), of which three were negative.The hybrids showed mid parent heterosis with the range -14.89% to 21.74% and mean 3.4%. In case of better parent heterosis the hybrid CMS3×nap130 also showed maximum heterosis (16.67%) which was folloowed by CMS2×nap94006 (13.33%), and CMS6× nap9906 (10.29%). The range of better parent heterosis was -20% to 16.67%) with a mean of -2.29%. On the other hand- three hybrids exhibited zero standard heterosis for the trait. The rests were positive significant. The hybrid CMS2×nap94006 exibited the highest (41.67%) standard hcterosis which was followed by CMS3×nap130 (40%), CMS5×nap94006 (36.65%) The range of standard heterosis was 0% to 41.67% with a mean 18.7%. 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.

vi) No. of primary branches per plant

Six hybrids out of eighteen exhibited significant positive mid parent heterosis for number of primary branches per plant. Maximum estimate was obtained from CMS3×nap94006 (46.15%) and it was followed by CMS2×nap94006 (42.86%) and CMS3×nap130 (28%). The range was -26.67% to 46.15%. Eight hybrids had significant negative value and two had zero heterosis. In case of better parent heterosis, four hybrids showed positive significant values with a. range of -41.18% to 46.15%. Maximum estimate was obtained by CMS3× nap94006 (46.15%). The hybrid CMS1×nap9906 showed the highest significant negative better parent heterosis (-41.18%).

Plate 4: Photograph showing branches of nap 94006, CMS line and their hybrid (F_1)

On the other hand, when the heterosis was measured against standard check variety, sixteen hybrids showed significant positive heterosis. Others were non-significant and CMS2×nap94006 was with the highest positive standard heterosis (100.1%). The range of rendered heterosis was -09% to 100.1% with a mean of 33.32% where as mean of mid parent heterosis and better parent heterosis were 46.15% and 46.15% respectively (Table 8). 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 *(Brtissicajuncea L).*

vii) Number of secondary branches per plant

Out of eighteen hybrids nine showed positive mid parent heterosis for number of secondary branches per plant, four showed negative and the rest showed non significant estimates. The hybrid CMS5× nap9906 exhibited the highest significant positive (122.95%) mid parent heterosis for number of secondary branches per plant and it was followed by CMS2×nap94006 (92.41%) and CMS3×nap94006 (84.13%). In case of better parent heterosis CMS5×nap9906 showed the highest (38.78%) significantheterosis. The hybrid CMS4×nap9906 showed the lowest (-63.64) significant negetive heterosis are presented in (Table 10). The two hybrids showed non-significant pollen parent heterosis. During the estimation of standard heterosis all of eighteen hybrids exhibited significant positive heterosis for number of secondary branches per plant. However the range of standard heterosis was 84.63% to 484.58 % with a mean of 239.33%. The hybrid CMS2 x Nap 9904 showed the highest (484.58 % significant positive standard for the trait. Saurabh *et al.*, (2005) also observed both positive and negative heterosis for number of secondary branches per plant in Indian mustard *(Brassico juncea L.)*

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Plate 5: Photograph showing variation in morphology among pollen parent, hybrid and female parent

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Plate 6: Photograph showing variation in morphology among pollen parent, hybrid and female parent

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parent

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

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

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

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

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

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

Pollen parents

Hybrids

Female parents

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

viii) Thousand (1000)seed weight

Out of eighteen hybrids twelve showed significant positive mid parent, twelve showed positive better parent and twelve positive standard heterosis for 1000-seed weight. Mid parent heterosis ranged from -9.09% to 17.95% with a mean of 6.01% (Table 10). Better parent heterosis ranged from -16.86% to 16.18% with a mean of 2.57% and standard heterosis ranged from -7.11% to 13.16% with a mean of 3.17% for the trait. The hybrid CMS2×nap94006 showed the highest estimate (17.95%) mid parent and the hybrid CMS6×nap94006 showed the highest estimate (16.18%) better parent heterosis. The hybrid CMS2×nap94006 showed the highest estimate (13.16%) for standard heterosis. Many researchers observed heterosis in 1000-seed weight. Such as Shen *et al.*, (2005), Wo iciechowski *et al.*, (2002) and Saurabh *et al.*, (2005) observed similar result in their research findings and supported this result.

ix) Seed yield per plant

Out of eighteen hybrids eight exhibited significant positive mid parent heterosis for seed yield per plant. Five exhibited significant negative heterosis others are non significant. The range of mid parent heterosis was -37.61% to 158.73% with a mean of 19.26%, The hybrid CMS4×nap130the highest (158.73%) estimate. In case of better parent heterosis, fourteen hybrids exhibited significant of them seven were positive and seven were negative values with a range of -50,92% to 145.87%, where mean heterosis was 7.96%. The hybrid CMS4×nap130 showed the highest (145.87%) better parent heterosis for seed yield per plant and it was followed by CMS2×nap94006 (62.26%) and CMS3×nap94006 (48.79%). One the other hand in case of standard hcterosis sixteen hybrids had significant positive estimates. The hybrid CMS4×nap130 showed the highest (187.36%) significant positive standard heterosis

for the trait and it was followed by CMS2×nap94006 (182.72%) and CMS3×nap94006 (159.27%) are presented in Table 10. The mean of standard heterosis was 73.90% with a range of 0% to 147.36% 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% beter parent heterosis. In India Katiyar *et al.*, (2004) observed stanndard 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), Hu (1999), Rakesh *et al.*, (1999), 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 preferd.

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 5
SUMMARY AND CONCLUSION

SUMMARY AND CONCLUSION

Six female parents (CMS lines) were crossed with three male parents (testers) in a line × tester mating design. Then eighteen 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.

Analsyis of combining ability showed that GCA effect was significant for days to fifty percent flowering, plant height, No. of siliqua per plant, seed per siliqua, primary branch &secondary branch per plant and seed yield per plant but the specific combining ability (SCA) effect was significant for all the characters except thousand seed weight.

Estimates of GCA effect for different characters suggested that among lines CMS4 was the best general combiner for days to 50% and plant height, CMS2 was the best for no. of silique per plant, length of siliqua, no. of primary branch per plant and no. secondary branch per plant. Line CMS5 and CMS3 was the best general combiner for no. of seed per siliqua and seed yield per plant, respectively. Among testers Nap94006 was general combiner for days to 50% flowering, no. of silique per plant, no. of seed per siliqua, no. secondary branch per plant and seed yield per plant tester Nap130 was the best for plant height.

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 studying.

Estimates of SCA effect for different characters revealed that the cross CMS4× nap94006 was the best specific combiner for days to 50% flowering, plant height and length of siliqua, cross CMS4×nap130 was the best for no. of silique per plant. Cross CMS2×nap94006 showed the best SCA effect for no. of seed per siliqu and for no. of

primary branch per plant. Combination CMS3×nap130, CMS1×nap130 and CMS4×nap130 were the best specific combiner for no. secondary branch per plant, thousand seed weight and seed yield per plant respectively.

Different type heterosis i.e. heterosis over mid parent (Hm), heterosis over better parent (Hb) and heterosis over standard check (HC) were estimated to evaluate eighteen hybrids for seed yield and yield related characters; where BARI Sharisha-7 was taken as check. The average heterosis for seed yield of eighteen hybrids over mid parent was 19.26% and that of better parent and standard check was7.96% and 73.90% respectively.

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

1. Nap94006×CMS2 and nap130×CMS4 pairs can be used for hybrid production,

2. The experiment was conducted with CMS lines which were back cross 4 generation so back cross should be continued to get better result,

3. It would be better if this experiment will be conducted at green house condition (controlled condition) and then in field condition and

4. Further research should be conducted to develop restorer line.

CHAPTER 6
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REFERENCES

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CHAPTER 7
APPENDICES

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-7

Parents	Days to 50%flowering	Plant height (cm)	No. of Silique per plant	Length of sliqua (cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant (g)	Yield /plant (g)
BARI Sharisa-7	32	104.2	134	6.60	20	3.33	4.33	3.8	7.12

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

Parents	Days to 50%flowering	Plant height (cm)	No. of Silique per plant	Length of sliqua (cm)	Seeds per siliqua	Primary branch/plan	Secondary branch/plant	Thousand seeds weight/plant (g)	Yield /pla (g)	GCA Group
Nap130	0	0	-1	0	0	0	0	0	-1	-2L
Nap94006	-1	0	1	0	0	1	1	0	1	3H
Nap9906	1	0	0	0	0	-1	-1	0	0	-1L
Total Significance	2	0	2	**0**	**0**	**2**	**2**	**0**	**2**	**Average**
										00
High Score	**1**	**0**	**1**	**0**	**0**	**1**	**1**	**0**	**1**	
Low score	**1**	**o**	**1**	**0**	**0**	**1**	**1**	**0**	**1**	

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

Parents	Days to 50%flowering	Plant height (cm)	No. of Silique per plant	Length of sliqua (cm)	Seeds per siliqua	Primary branch/plan	Secondary branch/plant	Thousand seeds weight/plant (g)	Yield /plant (g)	GCA Group
CMS1	0	1	-1	1	0	-1	-1	0	0	-2L
CMS2	-1	0	1	1	0	1	1	0	1	5H
CMS3	0	0	1	0	0	1	0	0	1	3H
CMS4	-1	-1	0	0	-1	0	0	0	1	-2L
CMS5	0	1	0	0	1	0	1	0	-1	2H
CMS6	1	0	-1	0	0	-1	-1	0	-1	-3L
Total significance	**3**	**3**	**4**	**2**	**2**	**4**	**4**	**0**	**5**	Average .50
High score	**1**	**2**	**2**	**2**	**1**	**2**	**2**	**0**	**3**	
Low score	**2**	**1**	**2**	**0**	**1**	**2**	**2**	**0**	**2**	

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

Parent	Days to 50%flowering	Plant height (cm)	No. of Silique per plant	Length of sliqua (cm)	Seeds per siliqua	Primary branch/plant	Secondary branch/plant	Thousand seeds weight/plant (g)	Yield /plant (g)	SCA group
CMS1×nap130	-1	0	1	0	-1	0	0	1	1	1H
CMS2×nap130	0	0	-1	-1	-1	-1	1	-1	-1	-5L
CMS3×nap130	0	-1	-1	1	1	-1	-1	1	-1	-2L
CMS4×nap130	1	1	1	0	1	1	1	0	1	7H
CMS5×nap130	0	0	0	0	0	0	0	0	-1	-1L
CMS6×nap130	0	0	-1	0	0	0	-1	0	0	-2L
CMS1×nap94006	0	0	-1	0	0	0	0	-1	-1	-3L
CMS2×nap94006	1	1	1	1	1	1	1	1	1	9H
CMS3×nap94006	1	1	1	-1	0	1	1	0	1	5H
CMS4×nap94006	-1	-1	-1	0	-1	-1	-1	0	-1	-7L
CMS5×nap94006	0	-1	-1	0	0	-1	-1	0	0	-4L
CMS6×nap94006	-1	0	1	0	-1	-1	1	0	-1	-2L
CMS1×nap9906	1	0	0	0	0	0	0	0	0	1H
CMS2×nap9906	-1	-1	0	0	0	-1	-1	0	0	-4L
CMS3×nap9906	-1	0	1	0	-1	-1	1	-1	1	-1L
CMS4×nap9906	1	0	-1	0	0	-1	-1	0	-1	-3L
CMS5×nap9906	0	1	1	-1	0	1	1	0	0	3H
CMS6×nap9906	0	0	-1	0	1	1	0	0	1	2H
Total Significance	10	8	15	5	9	13	13	6	13	Average
High Score	**5**	**4**	**7**	**2**	**4**	**5**	**7**	**3**	**6**	**-.33**
Low Score	5	4	8	3	5	8	6	3	7	