GENETIC STUDIES ON YIELD & YIELD CONTRIBUTING CHARACTERS IN F_2 DIALLEL POPULATION OF *Brassica napus* L.

BY

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CERTIFICATE

This is to certify that the thesis entitled, *"GENETIC STUDIES ON YIELD & YIELD CONTRIBUTING CHARACTERS IN F_2 DIALLEL POPULATION OF Brassica napus L."* ***submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of*** *MASTER OF SCIENCE* ***in*** *GENETICS AND PLANT BREEDING*, ***embodies the result of a piece of bonafide research work carried out by*** *Mst. Atikunnaher, Registration No. 10-04213 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

(Dr. Firoz Mahmud)
Professor
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Dated: December 2012
Place: Dhaka, Bangladesh

Dedicated
to
My Beloved Parents

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LIST OF ABBREVIATIONS AND SYMBOLS

Abbreviations	**Full word**
%	Percent
°C	Degree Celsius
@	At the rate
$\boldsymbol{\sigma}_p^2$	Phenotypic variance
$\boldsymbol{\sigma}_e^2$	Environmental variance
$\boldsymbol{\sigma}_g^2$	Genotypic variance
h^2_b	Heritability in broad sense
AEZ	Agro-Ecological Zone
Agric.	Agriculture
Agril.	Agricultural
Agron.	Agronomy
ANOVA	Analysis of variance
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
BD	Bangladesh
BSMRAU	Bangabundhu Sheikh Mujibur Rahaman Agricultural University
CEC	Cation Exchange Capacity
cm	Centi-meter
CV%	Percentage of Coefficient of Variation
cv.	Cultivar (s)
DAS	Days After Sowing
df	Degrees of Freedom
et al.	And others
etc.	Etcetera
F_2	The second generation of a cross between two dissimilar homozygous parents
FAO	Food and Agricultural Organization
g	Gram (s)
G	Genotype
GA	Genetic advance
GCV	Genotypic Coefficient of Variation
GN.	Genotype Number
HI	Harvest Index
hr.	Hour (s)
IARI	Indian Agricultural Research Institute
ICARDA	International Centre for Agricultural Research in Dry Areas

Abbreviations	Full word
j.	Journal
kg	kilogram (s)
m	Meter
M.P.	Muriate of Potash
m^2	Square meter
MOA	Ministry of Agriculture
MSG	Mean square of the genotypes
MSE	Mean square of the error
NARS	National Agricultural Research System
No.	Number
NPB/P	Number of primary branches per plant
NSB/P	Number of secondary branches per plant
NS	Not Significant
NSP	Number of siliquae per plant
PCA	Principal Component Analysis
PCO	Principal Coordinate Analysis
PCV	Phenotypic Coefficient of Variation
PH	Plant height
ppm	Parts Per Million
R	Residual effect
RCBD	Randomized Complete Block Design
Rep.	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
Sci.	Science
SE	Standard Error
SL	Siliquae lenght
S/S	Seeds per siliquae
t/ha	Tons per hectare
T.S.P.	Triple Super Phosphate
Univ.	University
var.	Variety
Via	By way of
Viz	Namely
WP	Wetable powder
YPP	Yield per plant

ABSTRACT

An experiment on oleiferous *Brassica napus* L. was conducted at the experimental field to evaluate diallel analysis for ten different characters. Out of fifteen crosses, the parent Nap-9908 was the best general combiner for number of siliquae per plant, seed per siliqua and seed yield per plant. The parent Nap-205 was the best general combiner for plant height parent Nap-9901 was the best general combiner for days to maturity and Nap-108 for number of primary branches per plant. The parent Nap-9905 was the best combiner for siliqua length and parent Nap-130 for thousand seed weight.The higher magnitude of GCA variance was observed than that of SCA variance for plant height days to maturity, no. of primary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua, seed yield per plant and thousand seed weight. The SCA estimates of various characters revealed that Nap-9908 x Nap-130 was the best combination for plant height Nap-9905 x Nap-205 for no. of primary branches per plant, Nap-9901 x Nap-205 for secondary branches, Nap-9908 x Nap-9901 for number of siliqua per plant, Nap-9901 x Nap-205 for siliqua length, Nap-9901 x Nap-205 for seeds per siliqua, Nap-9905 x Nap-205 for seed yield per plant and Nap-108 x Nap-9908 for thousand seed weight were the best cross combinations. The Vr-Wr graph indicate over dominance for plant height, days to flowering, primary branches per plant siliquae per plant, seeds per siliqua, siliqua length and thousand seed weight. Partial dominance was observed for secondary branches per plant and seed yield per plant. The graphical analysis also indicates wide genetic diversity among the parents.

Chapter 1

INTRODUCTION

INTRODUCTION

The Brasscicaeae family (formerly Cruciferae) consists of approximately 375 genera and 3200 species of plants. The *Brassica* genus consists of approximately 100 species with highly diverse morphology. *Brassica* have great economic and commercial value and play a major role in feeding the world population.

All the major oleiferous species of *Brassica* genus are grouped into two; rapeseed and mustard. Rapeseed mainly include *Brassica napus*. Mustard encompasses the species like *Brassica campestris* (2n = 20AA), *Brassica nigra* (2n = 16BB), *Brassica Juncea* (2n = 36AABB), *Brassica carinata* (2n = 34BBCC).

Rapeseed (*Brassica napus* L.) is an important oil seed crop of the world. It is a cross pollinated crop. It is an amphidiploid containing 2n = 38 chromosomes through spontaneous hybridizations between tunip rape(*Brassica rapa* L.s.str.;AA.2n = 20) and cabbage (*Brassica oleracea* L.p.p;CC,2n = 18) genotypes (kimber and McGregor, 1995). The oil is mainly used as edible oil. Oil and fat are not only the source of energy (9 k. cal./g) but also contains fat-soluble vitamins A, D, E and K. Processing of rapeseed for oil production produces rapeseed meal as a by-product. The by-product is a high protein. Rapeseed "Oil cake" is also used as fertilizer which contains proteins of high biological value and applicable quantities of calcium and phosphorus and may be used for ornamentals, such as Bonsai, as well. Rapeseed leaves and stems are also edible.

Rapeseed was the third leading source of vegetable oil in the world after soyabean and oil palm, and also the world's second leading source of protein meal. Although only one-fifth of the production of the leading soyabean meal and about 16% of the world's oilseed production is obtained from this crop. Total oil seed crops cover 7.47 lakh acres of land. However, rapeseed and mustard cover 5.36 lakh acres of land and produces about 5.95 lakh MT of oil seeds. In India, *Brassica napus* is grown on 13% of cropped land. Rapeseed and mustard cover about 74.5% area of the total edible oil crops cultivated in Bangladesh which covers 4.04% area of the total cultivated land (BBS, 2006a).

Europian union, Canada, the united states, Australia, china and India are leading producers of rapeseed. World production of rapeseed is growing rapidly that 36 million tones of rapeseed was produced in the 2003-2004 season and estimates of 58.4 millons tones in the 2010-2011 season. In North America, the term "canola", originally a syncopated form of the abbreviation "Can.O.,L-A" (Canadian Oilseed, low-acid) and is now a tradename for "double low" low erucic acid and low glucosinolate) rapeseed.

The average yield of local varieties and high yielding varieties per hectare are 600-1000 kg and 1400-2000 kg respectively. Current oilseed production of Bangladesh is about 0.254 millon tones which is 40% of the country need (BBS, 2006c). As a result, more than 60% of the requirement of oil and oilseed has need imported every year by spending huge amount of foreign currency involving over 317 cores taka (BBS, 2006c).

In Bangladesh, among the oilseed cropped area 74% is covered by the mustard and rapeseed, 17% by sesame and 9% by groundnut (Anon., 2000). Present cultivated area of mustard and rapeseed is 4.81 lacs hectare with 5.36 lacs metric tones (BBS, 2006c). Its average yield per hectare was only 733 kg in Bangladesh compared to the world average of 1,575 kg (BBS, 2006c). Almost two-third of the edible oil consumed annually in Bangladesh is imported and foreign exchange spent for this was about 690 million US dollar (BBS, 2004).The per capita consumption of edible oil of the country is comparatively low, only 10-12 g/head/day against the optimum requirement of 35 kg/head/day.

The reason for such low yield are insufficient precipitation when the crops are cultivated under rainfed conditions, use of less improved cultivars, inappropriate crop production technology and almost low or no fertilizer use. The improved varieties already registered require somewhat longer duration to mature and hence are not easily acceptable to the farming. On the other hand, high population growth rate is also increasing pressure on per capita consumption rate of oils.

Meanwhile, about 27 mustard and rapeseed varieties have been released in Bangladesh, among these 16 from Bangladesh Agricultural Research Institute(BARI)(3 varieties for *Brassica napus*) , 5 from Bangladesh Institute of Nuclear Agrilture (BINA), 2 from Bangladesh Agricultural University (BAU), 3 from Sher-e-Bangla Agricultural University (SAU) and 2 from Bangladesh Agricultural Development Corporation (BADC) but most of them are not popular to the farming community because of their long duration, low to moderate yield and susceptibility to severe biotic and abiotic stresses.

In general the *Brassica napus* L. varieties have high seed and oil productivity with bold seed. They are more tolerant against *Alternaria* leaf bright and aphid than the varieties of *Brassica campestris* and *Brassica juncea*. High yield potential of *Brassica napus* is mainly due to elongated flower raceme with moderate number of large siliqua accommodating more number of bold seeds and also due to high number of plant that can be accommodated per unit area. Varieties of *Brassica napus*, however, have some weaknesses like prolonged flowering habit followed by longer maturity period, high rate of siliqua shattering and brownish black or black seed coat giving lower oil content and meal quality compared to yellow seeded ones.

In Bangladesh, the released varieties of *Brassica napus* (BARI sarisa 7, BARI sarisa 8, BARI sarisa 13) have early shattering of the siliqua. It has been recommended that when 60-70% of the siliqua become straw colour the harvesting should be done to escape shattering (Akbar et al., 1994).

Intra-specific hybridization is a good way of improving the varieties of different natures by combining desired traits followed by selection of desired types. The most impotant aspects for hybridization are the choice of parents and the selection of best genotypes from hybrid progenies.

Diallel analysis provides an effective means of obtaining rapid features of the inheritance of genes in homozygous lines. According to Crumpacker and Allard (1962), diallel analysis could successfully unravel the major features of a genetic system and predict the outcome of selection in early generations. The analysis allows for every conceivable variation in experimental design, including presence or absence of parental lines and reciprocal crosses (Yates, 1947; Hayman, 1954a; Griffing, 1956; Jones, 1965) and varying degree of replication of diagonal (parents) and off-diagonal (F1's or F2's) entries in the diallel table (Jones, 1965). Thus diallel analysis provides a more systematic approach to study the inheritance of continuously varying characters and to select parents having suitable combining ability (both general and specific) for hybrid breeding programme.

The present research was planned to the following objectives:

- To study the combining ability in the reference population for yield and yield contributing characters.
- To study the relationship among the different traits and their contribution to the yield.
- To select promising genotypes considering high yielding, early maturity and shading resistance plants.

Chapter 2

REVIEW OF LITERATURE

REVIEW OF LITERATURE

2.1 Taxonomy, origin and distribution

Brassica napus ($n = 19$) is an amphidiploid species derived from interspecific crosses between *B. oleracea* ($n = 9$) and *B. rapa* ($n = 10$).Wild forms of *B. napus* have been reported to occur on the beaches of Gothland, Sweden, the Netherlands and Britain. There are also reports that naturalized forms of *B. napus*, which are very distinct from any cultivated *B. napus*, were found on coastal cliffs of New Zealand, where *B. oleracea* and *B. rapa* grow wild. It is thought that *B. napus* was formed on the coast of northern Europe where both *B. oleracea* and *B. rapa* grow wild; other researchers believe that *B. napus* originated in the Mediterranean region or in western or in northern Europe (Tsunoda 1980). It is possible that *B. napus* could have formed at different places from crosses between different forms of *B. oleracea* and *B. rapa*. Both winter and summer annual forms of *B. napus* are grown as oilseeds in many countries of the world, and it is the most productive *Brassica* oilseed species under cultivation. Its high yield potential might be related to the high photosynthetic rate per unit leaf area which is positively related to chloroplast number per unit leaf area and to chloroplast volume. There are also root-forming *B. napus* types,known as rutabaga, grown as vegetables and fodder for animals.

Rapeseed (*Brassica napus*)

Scientific classification	
Kingdom:	Plantae
(unranked):	Angiosperms
(unranked):	Eudicots
(unranked):	Rosids
Order:	Brassicales
Family:	Brassicaceae
Genus:	*Brassica*
Species:	*Brassica napus*

2.2 Biology:

Habit: Usually annual or perennial herbs.

Root: Taproot system.

Stem: Herbaceous, erect, branched.

Leaves: Simple, alternate, radical or cauline, usually entire, sometimes lobed, petiolate, exstipulate, reticulate venation.

Inflorescence: Raceme or corymbose raceme.

Flower: Ebracteate, pedicellate, mostly actinomorphic, bisexual, heterochlamydeous, dimerous or tetramerous hypogynous.

Calyx: Sepals 4, polysepalous, in two whorls of two each imbricate aestivation.

Corolla: Petals 4, arranged in single whorl alternating with sepals, polypetalous, often with long claws and spread out to form a cross. Hence, the name cruciform corolla. Valvate aestivation.

Androecium: Stamens 6, polyandrous, arranged in two whorls of 4 and 2 (tetradynamous), outer two are short and the inner four are long, anthers bilobed, basifixed, introse.

Gynoecium: Bicarpellary, syncarpous, initially unilocular and later bilocular, (formation of pseudoseptum), one or more ovules on parietal placentation, style short, stigma bifid, sometimes bilobed, ovary superior.

Fruit: Siliqua or silicula.

Seeds: Endospermic

2.3 Diallel Analysis : Concept, Methodology and Application

Diallel analysis is a widely used genetic technique in the study of the inheritance of quantitative characters and assessing general and specific combining abilities of parents and their crosses. Schmidt (1919) first introduced the method of diallel crossing system. It implies all possible crosses between each of a group of male and female individuals. Sprague and Tatum (1942) analysed diallel cross with statistical technique first.

Diallel analysis provides for obtaining a rapid picture of the genetic control of quantitative characters. Crumpacker and Allard (1962) stated that diallel analysis could successfully reveal the major features of a genetic system and predict the outcome of selection in early generations. It allows for every conceivable variation in experimental design, including presence or absence of parental lines and reciprocal crosses (Yates, 1947; Hayman, 1954a; Griffing, 1956; Jones, 1965) and varying degrees of replication of diagonal (parents) and off-diagonal (F_1 s or F_2's) entries in diallel table (Jones, 1965).

Jinks (1954) defined the relationship between the parent-offspring array variance (Vr) and covariance between offspring and non-recurrent parent (Wr). The regression of Wr on Vr would give rise to a straight line of unit slope, provided the genes are independent in action. Hayman devised a graph almost similar to the one developed by Jinks (1954) which provides information about the adequacy of additive-dominance model, the average degree of dominance and characterizes parent containing proportion of the dominants and recessive genes. The effect of non-allelic interaction on the Vr-Wr graph has been described by Mather and Jinks (1987). They have shown that if the complementary kind of non-allelic interaction is present, the regression line is concave upward. If with duplicate type of non-allelic interaction, the regression line is concave downward.

Jinks and Hayman (1953) also proposed numerical approach to estimate genetic parameters based on Mather's notation. They outlined four components viz. D, H_I, H_2 and F assuming additive and dominance effects of genes but no epistasis or non-allelic interaction. Hayman (1954b) presented in detail the theory and algebraic basis of analysis and added two more statistics h_2 and Fr to those suggested by Jinks and Hayman (1953).

The main feature of diallel analysis is combining ability. The term combining ability introduced by Sprague and Tatum (1942). They used general combining ability (gca) to designate "average performance of a line in hybrid combination" and specific combining ability (sca) as "those crosses in which certain combination that do relatively better or worse than would be expected on the basis of average performance of the lines involved".

The statistical concept of general and specific combining ability effects and variance using diallel crosses was presented by Griffing (1956a,b). Four methods were suggested by Griffing (1956) depending upon inclusion or exclusion of parents and the reciprocal crosses in the analysis. The methods are as follows:

Methods	Materials involved
1	Parents +one set of F_1's +reciprocals
2	Parents +one set of F_1's
3	One set of F_1's + reciprocals
4	Only one set of F_1's

The last two models, where the parents are not involved, Griffing termed them as "modified model".

Griffing (1956) has described the method of analysis for combining ability considering Eisenhart's model-I (fixed effect) and model-II (random effect).

i. Model-I (Fixed effect model)-where the parental materials are selected and the results obtained are applicable to the material investigated. Here the main interest lies in the estimation of combining ability effects.
ii. Model-II (Random effect model)- where the parents are random sample from the population about which the inferences are to be drawn. Here interests lie in the estimation of genetic and environmental components of the population variance.

The contribution of each parent to general combining ability was measured by the estimates of gca effects (g_i) and the contribution of each parent to hybrids was given by estimates of sca effects (sij).

Arunachalam (1976) reviewed the genetic models employed in graphical analysis of Jinks and Hayman and combining ability analysis of Griffing. He concluded that methods given by Griffing alone provide all the information that a plant breeder needs from a diallel cross, in preference to the graphical analysis of Jinks and Hayman. In a full diallel, all parents are crossed to make hybrids in all possible combinations. Variations include half diallels with and without parents, omitting reciprocal crosses. Full diallels require twice as many crosses and entries in experiments, but allow for testing for maternal and paternal effects. If such "reciprocal" effects are assumed to be negligible, then a half diallel without reciprocals can be effective.

Common analysis methods utilize general linear models to identify heterotic groups, estimate general or specific combining ability, interactions with testing environments and years, or estimates of additive, dominant, and epistatic genetic effects and genetic correlations.

Amiri-Oghan *et. al* (2009) reported that twenty one F_2 progenies derived from a 7×7 diallel crosses along with parents were evaluated for grain yield, flowering and maturity time. Due to significant genotypic effects for all traits, genetic analysis were performed on F_2 progenies including analysis of combining ability and genetic components. The analysis of variance revealed that both additive and non-additive genetic effects were involved in controlling these traits. GCA/SCA ratios were 0.91 for days to flowering, 0.95 for days to maturity and 0.83 for grain yield which indicated that the additive gene effects were more important than non-additive gene effects for all these traits. Narrow-sense heritability was high for days to flowering (73.12%) and days to maturity (81.99%) and low for grain yield (30.15%). It could be concluded from the study that S_1 recurrent selection would be effective to improve the performance of these genotypes for grain yield, flowering and maturity time. The selected S_1 lines from each cycle can be used in a pedigree-breeding program to identify superior genotypes.

Wright (1921, 1935) defined three of variances as additive genetic variance, variance due to dominance and epistatic variance resulting from the interaction of non-allelic. Among the various mating designs developed for the determination of the architecture of quantitative characters, the diallel cross method, outlined by (1954, 1955) and Hayman (1954, 1958 and 1960), has received considerable of the geneticists and plant breeders.

Apart from measuring additive and dominance components of variation, appropriate model can be used to detect, though not measure, non-allelic gene interactions by using graphical representation (Vr-Wr graphs). The diallel has been extensively used in cross pollinated crops.

Griffing (1956, 1958) emphasized the statistical concepts of general and specific combining ability of Mustard, Bean and cereals.

Hayman (1954, 1957) attempted to obtain estimates of certain genetic parameters from statistics involving parents and off-springs. Variance for general combining ability, involves mostly additive gene effects while variance for combining ability depends on dominance and epistatic component of variation.

2.3.1Genetics analysis of *Brassica napus* L.

Little genetic research has been carried out in *Brassica napus* for improvement of the crop, especially through diallel mating system. Relevant information available on *Brassica napus* is presented here.

Huq (2006) conducted an experiment on *Brassica rapa* involving 7x7 half diallel cross. Heterosis and combining ability were estimated for seed yield and other related characters such as days to flowering, days to maturity, plant height, number of primary and secondary branches, length of siliquae, seeds per siliqua, seed yield per plant, thousand seed weight. Out of twenty one crosses Agroni x BARIsar-6, Agroni x Tori-7. Shafal x BARIsar-6 and Agroni x Tori-7 showed significant heterosis over mid and better parent. Agroni x Tori-7 best for number of primary branches/plant and siliquae/plant.

Shen *et al.* (2005) observed significant differences in seed yield per plant and seed oil content among the F_2, hybrids and between F_2, progenies and their parents of *Brassica campestris*. However, the heterosis for seed yield per plant was much greater than that for seed oil content. Mid parent heterosis and high parent heterosis of seed yield per plant ranged from 5.50 to 64.11 % and from -2.81 to 46.02%, while those of seed oil content ranged from -1.55 to 7.44% and -3.61 to 6.55%, respectively.

Yadav *et al.* (2005) found significant differences due to parents vs. crosses indicating the presence of heterosis in the crosses through conducted an experiment during the rabi seasons of 1998-2000 to study the nature of combining ability for seed yield and other yield-attributing characters through line × tester analysis in rape (*Brassica napus*) [*B. napus* var. *oleifera*]). They derived forty-five F_1 from the crosses of two cytoplsmic male sterile lines (Ogura, ISN-706a) and one normal fertile line (NDBN-1) used as females and 15 testers (Westar, FM-27,GSL-6267,GSL-8814, EC129120, PBN 9501, NRCG-7, GSL-6067, HNS-4, GSL-1, GSL-406, NRCG-2, GSL-6303, NRCG-13 and NRCG-14) as males. Among lines, they observed significant differences for plant height and number of secondary branches per plant. Higher magnitude of variances due to testers compared to lines were observed for seed yield per plant, plant height, primary branches per plant, days to flower initiation, days to maturity and oil content. They also found that the estimates of SCA variances were higher than GCA (average) for all the characters studied, indicating the preponderance of non-additive type of gene action in the inheritance of these traits and the cross Ogura × NRCG-13 showed high SCA effects for yield per plant which involved both good combining parents.

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

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

Mahak and lallu (2004) performed an experiment on Indian mustard strains/cultivars Varuna, Shekhar, Vardan, Laha 101, Pusa Bold, RH-30, Pusa, Basant, NDR -8501 and Kranti. These strains were crossed in a diallel mating design excluding reciprocals. The parents along with 36 F_1s and 36 F_2s were grown and data were recorded for plant height, branches per plant, siliquae on main raceme, seed yield per plant, thousand seed weight, seed oil content, de-fatted seed content and protein content. The crosses exhibited highly significant heterosis, for most of the characters studied.

Satyndra *et al.* (2004) evaluated twenty one Indian mustard hybrids and their parents for eight quantitative traits: days to flowering, days to maturity, plant height, number of primary branches, length of the main raceme, seed yield, thousand seed weight and oil content percentage, in an experiment. High heterosis (15.99, 15.51 and 12.37%) was obtained for seed yield in the crosses Basanti x NDR 8501, Basanti x Kanti and Basnati 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.

Ripley and Beversdorf (2003) reported that cultivars in *Brassica napus var. oleifera*, a self-pollinating, self-compatible species, have traditionally been developed as open-pollinated lines or populations. Significant yield gains in this species have been realized through the exploitation of heterosis. They stated that commercial hybrid production had been possible as a result of the development of a number of pollination control systems. They found self-incompatibility was transferred from *B. oleracea* var. *italics* to *B. napus* var. *oleifera* through interspecific hybridization. The response to interspecific pollination, as measured by siliquae elongation and initial stages of ovule development, was genotype dependent, and two highly responsive *B. napus* genotypes were identified. They used embryo rescue to produce the interspecific hybrids. Isoelectric focusing of stigma proteins was used to identify S-alleles in the interspecific hybrids to facilitate backcrossing. Segregation of the S-locus through a series of back-crosses to *B. napus* was complicated by aneuploidy; however, the S-locus was found to segregate as a single gene. They discussed usefulness of *B. oleracea* as a source of S-alleles for pollination control in *B. napus*.

Pietka *et al.* (2003) proposed that the general combining ability (GCA) values in terms of individual glucosinolates are important in breeding. Eleven inbred lines of winter oilseed rape (*B. napus* [var. oleifers]) characterized by very low glucosinolate contents were studied by them. These lines were crossed with five cultivars used as testers. Hybrids were grown in the field and statistical analyses of GCA values were performed separately for particular glucosinolates, as well as F_1 and F_2 generations.

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

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

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

Goffman and Becker (2001) stated that because of the nutritional and antioxidative properties, tocopherol production is an interesting trait for the liquid quality of oil crops. Total tocopherol content in rapeseed (*Brassica napus* L.) is medium to low, and therefore, higher levels of tocopherol are desirable in this species. The objective of the study was to determine the inheritance of alpha, gamma, and total tocopherol content and the alpha/gamma tocopherol ratio in seed of rapeseed. Two mating designs with six parents each were used. In Diallel I, the parents were high or low for total tocopherol content and in diallel II, the parents high or low for the alpha /gamma tocopherol ratio. Parents and F_1 hybrids tested in a screenhouse in 1998 and under field conditions in 1999 by means of a cmpletely randomized design with two replications. In addition, 10 selected F_1 were grown along with their respective parents. Compared with the the F_1 hybrids showed a significantly higher gamma -tocopherol content of 6 mg kg/seed for Diallel I and 24 mg kg/seed for diallel II. General combining ability effects in both diallels were highly significant ($P<O.01$) and much than specific combining ability effects for all traits studied. Reciprocal effects statistically significant. Gamma tocopherol was not correlated with alpha tocopherol. The results indicate that tocopherol content and composition inheritances strongly associated with additive gene action in rapeseed.

Huang *et al.* (2000) studied three rapeseed (*Brassica napus*) genotypes tolerant of resistant to *Sclerotinia sclerotiorum* and three susceptible genotypes differing in origin were used in reciprocal or complete diallel crosses and found that resistant genotype from

China 018, had the highest general combining ability (4.46) while the French variety Cobra had the lowest general combining ability (-10.54). They also found optimum cross combination in this study was Cobra 018, with high specific combining ability (10.41) and desirable agronomic characters

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

Krzymanski *et al.* (1999) made diallel (13x13) crossings of double low oilseed rape cultivars and strains. Parental forms and F_2, combinations of diallel were compared in yield trials in Poland. Two cultivars and four strains were the parental forms that mostuently occurred in F_2, combinations yielding considerably above the standard var (Bor), two strains gave combinations of the highest fat contents, considerably differing from the standard. The yields oscillated between 126.5 and 209.1% of the standard (38.2 q/ha) and the fat content between 103 and 108% of the standard (47%). Calculations were made to estimate the expected values of seed yield of synthetic varieties, which could be obtained from tested cultivars, and strains. Two or three component synthetics composed from the best combining cultivars and strains were taken into account by them.

Wos *et al.* (1999) presented general combining ability (GCA) and specific combining ability (SCA) for 23 cytoplasmic male sterile (CMS) ogura lines. Field trials were executed in four localities (Malyszyn, Marwice, Borowo and Bakow) in Poland.

The seed yield of hybrids, GCA and SCA of CMS lines and GCA of pollinators were significant. Twenty three ogura CMS lines were crossed using three pollinator cultivars Kana, Marita and MAH 1592. Obtained results were used to find the best combinations for hybrid production.

Liersch *et al.* (1999) conducted a breeding approach known as ogura CMS system of oilseed rape hybrid cultivars in Poland to evaluate yield and yield component variability of F_1, hybrids and their parental lines also heterosis effect, and qualitative traits such as oil and glucosinolate content in seeds. They found that composite hybrid cultivars yielded higher than restored hybrids.They stated that the yield of hybrids and qualitative traits such as oil and glucosinolate content in seeds are significantly dependent on genotypes and environmental conditions.

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

Sheikh and Singh (1998) analyzed combining ability in 10 × 10 half-diallel (excluding reciprocals) of Indian mustard for ten characters and found preponderance of non additive gene action for most of the characters including seed yield and oil content. They also observed that Additive genetic variance was more important for plant height and length of silliqua. Majority of the crosses showed high SCA effects for seed yield involved high × low GCA parents.

Varshney and Rao (1997) estimated combining ability, heterosis and inbreeding depression in yellow sarson for 11 quantitative characters including seed yield. Non-additive genetic variance was preponderant for all the characters in both F_1 and F_2 generations except for 1000-seed weight in F_2 generation. For seven characters, the best F_1s on the basis of sea involves one parent with high gca effect and the other with poor or average sca effects. The hybrids which exhibited highest heterosis also showed higher inbreeding depression.

A nine-parent diallel study was conducted by Thakur and Sagwal (1997) on the yield components and oil content in rapeseed *(Brassica napus* L.*)*. They reported the importance of both additive and dominance components. Estimates of heterosis over better parent (BP) for various traits indicated significant magnitude including seed yield (-14.8 to 82.8%). Unidirectional dominance was observed for most of the traits studied. Sheikh and Singh (1998) studied combining ability analysis, 10 x10 diallel including reciprocals in Indian mustard for ten characters and found preponderance of non-additive gene action for most of the characters including seed yield and oil content. Additive genetic variance was more important for plant height and length of siliqua for which high estimate of heritability was also observed. Majority of the crosses showed high sca effects for seed yield involved high x low gca parents.

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

Kudla (1996) investigated the combining ability of winter oilseed rape (*Brassica napus*) inbred lines, and heterosis effects of F_1 and F_2 hybrids in the growing season of 1994-95.

Analysis of variance showed that non-additive gene action had an advantage over additive gene action in the inheritance of plant height and number of primary branches. The significant effects of dominance genes in the F_1 for siliqua length, seeds/siliqua, seed yield/plant and 1000-seed weight did not occur in the F_2. The differentiation of GCA of inbred lines, based on F_1 hybrids, was significant for siliqua length, seeds/siliqua, seed yield/plant and 1000-seed weight. GCA based on the F_2 was significant for pod length and seeds/siliqua. Inbred lines T1056 and T1150 were good components for crossing to increase seed yield in the F_1. Both lines can be used for breeding high yielding oilseed rape hybrids varieties. In most of the F_1 and F_2 hybrids, significant positive effects of heterosis were found for plant height. F_1 of T1056 x Wotan showed the highest and significant heterotic effect (24.5%) for seed yield/plant. The mean heterotic effect in F_1 hybrids was 10% for seed yield, decreasing to 2% in the F_2 generation.

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

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

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

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

Ramsay *et al.* (1994) stated a complete diallel set of crosses, including selfs, was produced from eleven inbred lines of swedes and assessed in the field for both components of dry matter yield and neck length at Dundee, UK, during 1987. They found that there was a strong positive heterosis for dry matter yield with high yielding F_1s showing an improvement of more than 20% above the better parent. Reciprocal differences were also found. Both additive and non-additive genetic variation was found for dry matter yield and other quantitative traits. However a simple additive-dominance model with independence of action and distribution of the genes failed to describe the data adequately. Given the implications for the breeding of inbred or F_1, hybrid swede cultivars, further experiments, using triple test crosses are suggested.

Ahmed(1993) worked with parents and F_1, hybrids from crosses between resynthesized lines and improved 100 varieties. F_1, were earlier maturing than resynthesized lines and heterosis was observed for spring regrowth and plant height. In trails, the best resyn. line H128 could only produce 87% of the mean yield of the improved varieties.

Gupta *et al.* (1993) studied 56 hybrids of *Brassica napus* from a half diallel set of crosses involving eight genetic stocks with 28 hybrids being derived from crosses of the initial S_0 population and the rest from crosses of S_1 families from each of the parents.

Barua and Hazarika (1993) conducted a study during 1993 with five varieties representing two *Brassica napus* types and *Brassica compestris* var *toria* along with their hybrids from a half diallel set of crosses. Accroding to them, heterosis mainly due to non-additive gene effect was important for dry matter and seed yield/plant. The important heterotic crosses were BSHI ^{x} M27, B9 x PT303 and PK x M27.

Verma *et al.* (1989) studied the nature and magnitude of combining ability and heterosis in a set of 7 x 7 diallel crosses (excluding reciprocals) of yellow sarson

for yield, yield components and oil content. Predominance of additive gene action was observed for yield, primary and secondary branches per plant, siliquae on main shoot, 1000-seed weight and oil content while it was non-additive for siliquae per plant.
Singh *et al.* (1996) studied combining ability in eight diverse cultivars for ten characters including seed yield in *Brassica juncea (L.)* and found high magnitude of variance for most of the characters. He reported high gca only for plant height, siliqua length and 1000-seed weight for which high estimates of heritability was also recorded.

Singh and Chauhan (1987) worked with 60 triple test cross families produced by the crossing of 20 F_2 parents as males to the parents and F_1s. In Varuna × TM9 additive genetic variance appeared to be predominant for days to maturity, number of primary branch while dominance seemed to be mainly involved in the control of seed yield/plant. In Varuna x RW75-80-1, additive genetic variance was estimated to be predominant for plant height and dominant for days to maturity, number of seeds/siliqua, 1000 seed weight, yeild/plant.

Singh *et al.* (1987) reported data on yield and eight other agronomic characters involved from eight parent diallel cross in yellow sarson to indicate the presence of both additive and non-additive gene action, in the inheritance of all traits, with non-additive gene on being predominant for all traits, except plant height. YSK4 and YSKS were good general combiners for seed yield/plant while the best combinations were YSK5 ^{x} YST151 and K88 x YSK5.

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

Josefsson (1986) reported that shatter resistance was associated with increased thickness of lignified tissue at the junction of the valve and the replum. He stated that the forces leading to dehiscence are unlikely to arise within the siliquae. Kadkol *et al.*(1986a) studied orientation of cell layers in the siliqua valves of *B. campestris*, *B. juncea* and *B. napus* and showed an absence of differential orientation of the cell layers in all accessions studied, providing further proof that the dehiscence mechanism is most likely passive. Also, in all the lines studied, there was only one layer of sclerenchymatic tissue in the siliqua valves compared with legume pods, which have two, and which exhibit active dehiscence.

Vershney *et al.* (1986) found high heritability and high genetic advance for plant height in all three species; but high heritability and genetic advance were found for number of siliquae/plant only in *B. rapa* and in *B. juncea.* He reported high heritability and genetic advance in seed yield, 1000 seed weight and number of seeds/siliqua in *B. napus.*

Singh (1986) studied 22 genotypes of *B. napus*, *B. rapa* and *B. juncea* and observed high combining ability and genetic advance in seed yield, 1000 seed weight and number of seeds/siliqua.

Picart and Morgan (1984) reported that there is some possibility that different degrees of shrinkage on drying of the lignified inner layer of the valve compared with the nonlignified outer layers could give rise to some dehiscence forces, but this appears less likely because dry siliquae of highly shatter-susceptible varieties of *B. napus* can be stored intact if protected from internal impacts.

Sharma (1984) observed high heritability for plant height, days to flowering and low heritability for days to maturity. He also found low genetic advance for days to maturity and high genetic advance for yield/plant.

Lefort (1982) studied 140 F_1, hybrids of winter oil seed rape (Brassica napus L.) and found that for seed yield average hybrids vigour was 23.5% on the basis of the mid parent.. Ina few cross combinations the value reached up to 50% in relation to the best value. This emphasizes the interest of hybrids varieties for improving yield.

Working with 104 mutants of Indian mustard in *B. juncea* (Linn.) Czern and Coss Labana *et al.* (1980) found that plant height and number of seeds/siliqua were highly heritable where as siliqua length, number of primary branches/plant and seed yield per plant were less heritable. The yield variation is thus principally pouring to the environmental influence, for which selection would 'not be more practicable for plant height and number of seeds/siliqua. This confirmed the finding of Chaudhari and Prasad (1968). In the same experiment the GCA was highest for plant height followed by number of seeds/siliqua and seed yield/plant.

Katiyar *et al.* (1974) studied heritability and expected genetic advance in some varieties of Indian mustard *B. juncea* (L) Czern and Coss. Heritability value were high for yield per plant, plant height, days to first flowering and number of primary branches, moderate for the days to maturity but low for the number of secondary branches. High genetic advance was found for plant height, days to first flowering and yield per plant, where as low value was observed for number of primary branches.

2.3.2Genetic Analysis in other crops

Khan *et al.(*2007) conducted an experiment that 4 x 4 diallel cross of wheat were evaluated for combining ability at Wheat Research Institute, Faisalabad during 2004-05. Data were recorded from F_2, generation for plant height, number of tillers plant", biomass plant", 1000 grain weight, harvest index, number of grains spike" and grain yield plant". The additive gene effects were operating in plant height, biomass plant", number of grains spike" and grain yield plant' while number of tillers plant" and 1000-grain weight were controlled by non-additive gene effects. The genotypes of "Uqab 2000" proved to be good general combiner for grain yield, 1000-grain weight, biomass plant", number of tillers plant" and plant height. While V-00055 was found good general combiner for grain yield, biomass plant", plant height and number of grains spike". The cross "SH-02 x Uqab 2000" and its reciprocal and "V-00125 x V-00055" were the best specific combiners for grain yield plant" and yield components.

Inamullah *et. al* (2006) studied that the inheritance pattern of the important yield parameters viz.,tillers per plant, spike length, grains per spike, 1000 grains weight, harvest index and yield per plant of 8 bread wheat varieties. The component analysis indicated that the additive component was significant for all the traits except tillers per plant and yield per plant. The dominance component was significant for spike length, tillers per plant and yield per plant. Regression analysis revealed additive type of gene action for grains per spike, 1000 grains weight and harvest index and over dominant type of gene action for rest of the traits. Correlation analysis of dominant genes with the phenotype of the parents revealed recessive gene control for tillers per plant and spike length, while dominant gene control was indicated for rest of the traits studied.

Alam (2002) studied a 6 x 6 F_2 half-diallel of Lablab bean in two growing seasons (S_1 & S_2) and observed that the predominat role of additive gene action in all characters in both the growing seasons. Vr-Wr analysis showed complete dominance for pod yield in S_2, overdominance for days to first flowering inflorescences per plant and pod setting in both S_1 and S_2; and for 10-pod weight S_2 and for pod yield in S_1. Partial dominance was noticed for number of flowers per inflorescence, pods per inflorescence and pod length in S_2.

Islam and Newaz (2000) carried out a 7 x 7 diallel experiment on dry bean using F_2 populations in two cultural environments. Results suggest both additive and dominance genetic components were important in the genetic system controlling various yield related characters such as days to first flowering, days to first pod setting, days to maturity, plant height, pods/plant, pod length, seeds/pod, seeds/plant and 20-seed weight.

Sarker (2000) conducted an experiment on 6 x 6 half diallel in Lablab bean. The combining ability analysis suggested the importance of both additive and non additive components in the genetic system with the preponderance of additive part in expression of all the characters except pods/inflorescence. The Vr-Wr analysis and estimation of components of variation showed complete dominance for pod yield/plant. Partial dominance was noticed for flowers/inflorescence, inflorescence length, pod length, pod width, seeds/pod and 10-pod weight; while for days to 1st flowering, days to 1st pod setting, number of inflorescences/plant and pods/inflorescence overdominance was observed.

Carvalho *et* al.(1999) evaluated 8 agronomic characters in a diallel mating design without reciprocals of bush snap bean *(Phaseolus vulgaris)* cultivars. General combining ability (GCA) effects were significant for pod number, pod weight, pod length, pod diameter, days from sowing to flowering and plant height. Specific combining ability (SCA) effects were significant for all the 8 characters. They showed that dominance/epistatic effects were involved in the control of these characters.

Aher *et al.* (1999) found highly significant gca and sca variance for 13 traits in a 7 x 7 diallel analysis excluding reciprocals in mung bean *(Vigna radiata)* suggesting that both additive and non-additive components played role in the inheritance of these traits. The gca analysis showed that parents MP-2, E-65 and TARM-18 were the best general combiners making them suitable for further crop improvement research. The crosses BM-4 x TLN-5 and Kopargaaon x TARM-18 showed significant sca effects for seed yield/plant and most of the yield contributing characters.

Oliveira *et al.* (1999) evaluated the properties of an F_3 generation of dry bean *(Phaseolus vulgaris)* based on F_1 generation data form diallel crosses for pods per plant and seed weight per plant. They showed general combining ability in the F_3, generation was more efficient than performance in the F_1, generation to predict F_3 segregant- hybrid combinations.

Sharma (1999) crossed nine diverse genotypes of garden pea *(Pisum sativum)* in diallel fashion to determine combining ability for 5 quantitative traits viz. days to flowering, pods/plant, pod length, grains/pod and green pod yield. Analysis of variance revealed highly significant differences for all the traits. Significant negative gca effects were found in early maturity which is desirable in crop breeding programme. For pods/plant four genotypes exhibited significant and positive gca effects. None of the hybrids indicated significant positive sca effects for the characters under study.

Valu *et al.* (1999) fi-om a 7 x 7 half diallel cross in *Lablab purpureus*, reported that both additive and non-additive gene actions were in operation in the inheritance of all the traits studied. Further dominance ratio indicated the presence of overdominance in all the characters. Heritability estimates were high for pod length and number of seeds per pod indicated the prospect of involving these traits through selection while it was moderate to low for days to first picking, number of branches per plant, number of pods per plant and pod yield per plant.

Dasgupta *et al.* (1998) from combining ability analysis of a 6 x 6 half diallel in mung bean *(Vigna raidiata)* reported the role of both additive and non-additive components of variances in the control of plant height, days to 50% flowering, number of pods/plant and protein percentages. Additive gene effects were predominant for seed yield/plant, number of pods/cluster and harvest index.

Emygdio *et al.* (1998) studied combining ability for 4 yield related traits in an 11 x 11 F_2 diallel populations in Southern Brazil bean *(Phaseolus vulgaris L.)* cultivars. They found that both additive and non-additive genetic effects were important in the expression of each of the traits. Based on general combining ability and on specific combining ability, the most promising crosses for yield components were Macanudo x IAPARA, Macanudo x IAPR65 and IAPAR44 x Barrigaverde.

Uddin and Newaz (1997) evaluated fifteen hyacinth bean genotypes for eight flower and pod characters. Highly significant differences were observed among the genotypes for all the characters studied. High heritability and high expected genetic advance were recorded for pod yield, number of pods and inflorescences/plant, pod weight and flowers per inflorescence.

Oliveira *et al.* (1997) evaluated 11 hybrids form unbalanced partical and circulating diallel crosses of 7 cultivars of dry bean *(Phaseolus vulgaris* L.) for 3 yield components viz. plant height, pods per plant and seed weight/plant. They found the unbalanced circulating system was more efficient and it provided (gca) information on 3 other parents by using only one additional hybrid combination. Estimates of mean squares (gca) effects were higher than that of (sca) for all traits.

Kaul and Vaid (1996) evaluated an 8 *x* 8 diallel of faba bean *(Vicia faba)* for combining ability. Both gca and sca were highly significant showing the existence of both additive and dominance effects on yield per plant and seed protein content.

Halkude *et al.* (1996) studied combining ability in an 8 x 8 half diallel set for seed yield and its component characters in green gram *(Vigna radiata)*. The parent phule M-2 was the best general combiner for grain yield and most of the characters.' ML-337 and MB-112 were the other two good general combiners for grain yield and some of its components. Most of the parents which showed good general combining ability for grain yield were poor general combines of 1000-grain weight except KDM-1. Cl ahardi local was observed to be the best general combiner for 1000-grain weight followed by KBM-1 and Russian Mung. Phule M2 *x* Charhardi local, a combination of the best and the most poor general combiner proved to be the best specific combination for grain yield.

Singh and Mishra (1996) studied combining ability in a 6 x 6 diallel set of midseason peas. VP-7906 and VL-3 showed high gca effects for most of the characters. Bonneville *x* Rachna exhibited best for primary branches and pod yield.

Singh *et al.* (1986a) estimated genetic variance of and combining ability for number of flowers, pods per raceme and flowering by analysis of data from a 5 x 5 half diallel cross in *Dolichos lablab (Lablab purpureus)*. Non-additive gene action aria overedominance were important for all the three traits. The cross Rajani x 7001 was the best specific combination in all the cases.

Venkateswarlu and Singh (1982) analysed data for combining ability of 10 diverse cultivers of pea *(Pisani safivuni)* which indicated the importance of both general and specific combining abilities for pods/plant, pod length, seeds/pod, 100-seed weight and seed yield/plant.

Venkateswarlu and Singh (1981) evaluated the parents, F_1's and F_2's of 10 diverse cultivars of pea in diallel. They reported that both general and specific combining ability were important for all traits examined. However, additive effects were predominant in the inheritance of quantitative characters.

In a 5 x 5 diallel study with Lablab bean Singh and Singh (1981) found that in the F_1 and F_2 pod length was principally affected by additive gene action. The others characters were by and large affected by non-additive gene action, with the exception of pod width and days to flowering in the F_2.

Lal and Waldia (1980) studied an 8 x 8 diallel cross in urd bean *(Vigna mang* L. *hepper*) and reported predominance of additive genetic variance for all the characters, except grain yield, in which dominance variance was found to be high.

Singh and Gupta (1980), using a diallel experiment involving five varieties of *Lablab purpureus*, reported that four crosses showed heterosis over the better parent for leaf size. General combining ability variance was seven times higher than specific combining ability variance. The variety KT2 was a good general combiner and had the highest number of dominant genes. Additive gene effect was more important than non-additive gene effects.

Chikkadevaiah *et al.* (1979) investigated the mode of inheritance and segregation pattern in F_1, and F_2 generations of a Lablab bean cross. They found that traits twining habit and flowers in axillary clusters and flat, green pods were dominant. They also suggested that pod colour was conditioned by three duplicate genes.

Chapter 3

MATERIALS AND METHODS

MATERIALS AND METHODS

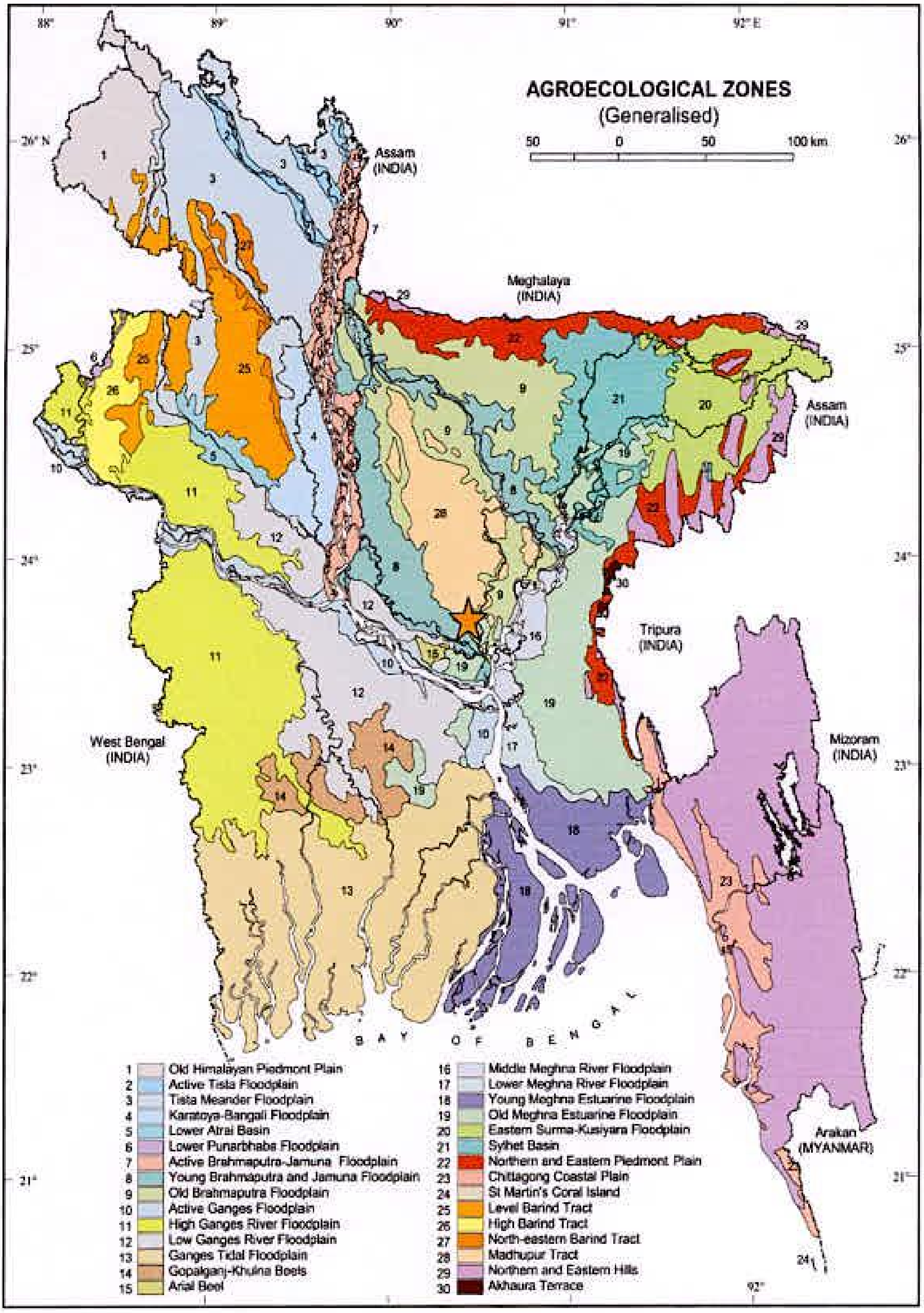
To conduct the experiment six selected cultivers were used as parents and these were (Nap-205, Nap-108, Nap-9901, Nap-9908, Nap-0130, Nap-9905). Fifteen crosses were done among parents in rabi season 2009-2010. In 2010-2011 rabi season, the parents and F_1's were grown in the experimental farm.

3.1 Experimental site

The present experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during November, 2010 to March, 2011. The location of the experimental site was situated at **23^0 74'** N latitude and **90^0 35'** E longitude with an elevation of 8.6 meter from the sea level. Photo graph showing experimental sites (Plate 1 and Plate 2).

3.2 Soil and Climate

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



★ The experimental site under study

Figure 1. Location of the experimental site under study

3.3 Plant materials

A total number of 21 (twenty) materials were used in this experiment where six were parents, fifteen were F_2 segregating generations. All the Materials were collected from Department of Genetics and Pant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The materials used in that experiment is shown in Table -1.

3.4 Methods

The following precise methods have been followed to carry out the experiment:

3.4.1 Land Preparation

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

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of Cowdung, 250 kg Urea, 175 kg Triple Super Phosphate (TSP), 85 kg Muriate of Potash (MOP), 250 kg Gypsum, 3 kg Zinc oxide and Boron 1 kg per hectare. The half amount of urea, total amount of Cowdung, TSP, MOP, Gypsum, Zinc Oxide and Boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

3.4.3 Experimental design and layout

Field layout was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was $20\text{m} \times 15\text{m} = 300\ \text{m}^2$. Each replication size was 24 m × 4 m, and the distance between replication to replication was 1 m. The spacing between lines to line was 25 cm. Seeds were sown in lines in the experimental plots on 8 December, 2010. The seeds were placed at about 2.5 to 3.5 cm depth in the soil.

Table1: Cross combinations in half diallel system of six varieties in *Brassica napus* L.

parents parents	**Nap-9905**	**Nap-108**	**Nap-9908**	**Nap-9901**	**Nap-205**	**Nap-130**
Nap-9905	**Nap-9905**	Nap9905× Nap-108 (C_1)	Nap9905× Nap-9908 (C_2)	Nap9905× Nap-9901 (C_3)	Nap9905× Nap205 (C_4)	Nap9905× Nap-130 (C_5)
Nap-108		**Nap-108**	Nap108× Nap9908 (C_6)	Nap108× Nap9901 (C_7)	Nap108× Nap205 (C_8)	Nap108 × Nap130 (C_9)
Nap-9908			**Nap-9908**	Nap9908× Nap9901 (C_{10})	Nap9908× Nap205 (C_{11})	Nap9908× Nap130 (C_{12})
Nap-9901				**Nap-9901**	Nap9901× Nap205 (C_{13})	Nap9901× Nap130 (C_{14})
Nap-205					**Nap-205**	Nap205 × Nap130 (C_{15})
Nap-130						**Nap-130**

3.4.4 Intercultural operations

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

3.4.5 Crop harvesting

Harvesting was done from 4th to 20th February, 2009 depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. Ten plants were selected at random from the parental line and 40 plants from F_2 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.

Plate 1: Field view at flowering stage (close view)

Plate 2: Field view at flowering stage (side view)

3.4.6 Data collection

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

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

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

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

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

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

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

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

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

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

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

3.10 Statistical Analysis of the Experimental Data

3.10.1 Genetic analysis of diallel population

The preliminary statistical analysis of the data was done according to standard texts and the subjects (Snedecor and Cochran, 1967; Clark, 1973). For the genetic analysis of daillel population, data were subjected to two main approaches viz. Griffing's approach and Hayman's approach. An understanding of general and specific combining ability, and the genetic system controlling important traits was thus attempted. The analytical methods and procedures of them, often quoted with worked out examples, may be found in several reference literature (Mather and Jinks, 1987; Singh and Chaudhary, 1985; Dabholkar, 1992; Narain, 1993 and Falconer and Mackay, 1996).

3.10.1.1 Combining Ability Analysis (Griffing's approach)

Griffing's (1956b) method-2, model-1(Fixed effect model) was used for combining ability analysis for each of the traits. In model 1 the experimental material is deliberately chosen and regarded as the population about which inferences are to be made; the general objectives are to compare combining abilities of the parents and, using parents as tester, to identify better cross combination (s).

The mathematical model for the combining ability analysis in model 1 is assumed to be as under

$$Xij = u + g_i + g_j + S_{ij} + \sum\sum eijkl$$

$$X_{ij} = u + g_i + g_j + S_{ij} + {}^{1}\!/_{bc}\sum_k\sum$$

Where,

ij = I -----------------------------p

k= I ----------------------------b

I=1-------------------------------c

p = number of parents

b = number of blocks

c = number of observations in each plot

Xjj is the mean of xijth genotype over k and 1; u is the population mean; gi (g) is the gca effect. Sij is the sca effect such that Sij = Sjj and e_{ij}kl is the environmental effect particular to the ijklth individual observation.

The restrictions imposed are :

$$\sum {}^{g}i = 0 \text{ and } \sum Sij + Sij = .0 \text{ (for each i)}$$

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

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

Where,

GCA = general combining ability

SCA = specific combining ability

p = Number of parents

b = Number of blocks or replications

e = Number of entry (family)

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

Y_{ii} = Mean value of the ith parent

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

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

S_e = Sum of square due to error

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

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

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

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

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

The variance of GCA and SCA were,

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

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

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

j Var(g;) and jVar(s.)

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

3.10.2 Graphical diallel analysis

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

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

Wr =covariance between parents and their offspring in each array

V_{OLI}=Variance of parents

Vo_{LO}=Variance of the means of array

Wr =The Wr for constructing the limiting parabola

bWr Vr= Regression of Wr on Vr

a= TheY- intercept

V_1L_1= Mean of all the Vr values
W_{oLol}= Mean of all the Wr values

Yr=Standardized mean for each parent

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

ry$_r$. (Wr+ Vr)=*)* Correlation between parental order of dominance

$(M_{LI} — M_{Lo})$ = Dominance relationship

r= Possible limit of selection of parents showing dominance

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

3.10.2.1 Test of homogeneity of Wr-Vr variances

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

Here,

Vr = Variance of the array variance

Wr = Variance of the parent and array covariance

y (Vr, Wr) = covariance of the variance and covariance Number of parents involved in the diallel crosses equivalent to a F-test with 4 and (n-2) degrees of freedom.

3.10.2.2 Test of deviation of regression slope from unity

i.Deviation from 0

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

ii.Deviation from unity

t=(1-b)/SE (at n-2 df)

Where,

B=regression co-efficient of Wr on Vr

SE_b= standard error

3.11 Proportion of Genetic Components

The different proportions of the genetic components are worked out according to the procedure given below:

a) Degree of dominance

The mean degree of dominance in F2 is $[1/4\ (HI/1))]^{*2}$ following Verhalen and Murray (1969).

if $[\ 1/4\ (H_I/D)]\ _=1$ (complete dominance)

> 1 (overdominance)

< 1 (Partial dominance)

Proportion of genes with positive and negative effects in the parents.

It is calculated as the ratio $H_2/4H_1$. It denotes the mean product of u_i and vi averaged over all the parents of a diallel set of crosses. When u and v symmetrically distributed, i.e. $u = v = 0.5$, the ratio will give the value of $H_2/4H, = 0.25$.

Proportion of dominant and recessive genes in the parents

It is calculated as :

$$\frac{\frac{1}{4}(4DH1)1/2+F/2}{\frac{1}{4}(4DH1)1/2-F/2}$$

If the dominant and recessive genes are symmetrically distributed among the parental lines, this ratio equals unity within the limits of sampling variance.

Number of groups of genes which control the character and exhibit dominance It is calculated as h^2/H_2. It is an approximate measure of sets of genes exhibiting dominance.

Estimation of heritability:

In F_2 heritability in narrow sense is calculated following Verhalen and Murray (1969) as:

$$\text{Heritability} = \frac{\frac{1}{4}D}{\frac{1}{4}D+\frac{1}{16}H1-\frac{1}{8}F+E}$$

Chapter 4

RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

The present study was conducted with a view to determining the combining ability among six parents and fifteen F_2 materials of *Brassica napus* genotypes and also to study the heritability for seed yield and different yield contributing characters. The data were recorded on different characters such as plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, days to 50% flowering, days to 80% maturity, pod per plant, length of pod (cm), number of seeds per pod, 1000 seed weight (g) and yield per plant (g). The data were statistically analyzed and thus obtained results are described below under the following heads:

4.1 Mean performance

Mean performance of ten agronomic and yield related traits of parents and hybrid combinations are presented in Table 2.

4.1.1 Plant height

For parent, the lowest plant height was observed in Nap-130 (105.60 cm) and for hybrid Nap – 205 x Nap-130 (95.20 cm) showed lowest plant height followed by Nap-108 x Nap-9901 (97.20 cm). Where as the parent Nap- 205 (118.81) exhibited the highest plant height. The highest plant height was found from the hybrid Nap-9908 x Nap-130 (124.87 cm). This hybrids were approximately 4-6 cm higher than the parents (Table 2).

4.1.2 Days to 50% flowering

In case of days to 50% flowering, it ranged from 28 to 33 days for parent. However, the parent Nap-9905, Nap-9908 and Nap-130 (29 days) flowered within the lowest time but the parent Nap-205 (34 days) took the highest duration. On the other hand, the hybrid combination Nap-9905 x Nap-130 (29 days) produced fifty percent flower with the lowest growth duration (Table 2).

4.1.3. Days to 80% Maturity

Considering earliness, the parent Nap-130 (97 days) showed the lowest duration for maturation but the parent Nap-205 (102 days) had taken the highest duration. On the other hand, the hybrid combination Nap-9905 x Nap-130, Nap-9908 x Nap-9901, Nap- 9908 x Nap- 130 (97 days) matured with lowest growth duration which was required same days for maturity (Table 2).

4.1.4. Number of primary branches per plant

For this character the parent showed the value ranging from 2.77 to 6.07. The parent Nap- 108 (4.91) showed the highest value. In the hybrid, the highest value was provided by the combination Nap- 9908 x Nap – 9901 (6.7) which is higher than parents (Table 2).

4.1.5. Number of secondary branches per plant

For the number of secondary branches per plant, the parent Nap-108 (2.63) showed the highest value. Similarly in the hybrid, the highest value of number of secondary branches per plant was provided by the combination Nap-108 x Nap-9901 and Nap-9908 x Nap- 9901 (3.90) which were almost double than the average value of the parents (Table 2).

4.1.6. Number of siliquae per plant

Number of siliquae per plant was varied from 94.53 to 151.10 where the parent Nap-205 (94.53) produced the lowest and Nap-9908 (151.10) produced the highest number of siliquae per plant considering the hybrid performance, it was ranged from 98.94 to 220.17. The hybrid combination Nap-9905 x Nap-205 (220.17) provided the highest number which was much higher than its parent (Table 2).

4.1.7. Siliqua length

Siliqua length of parent was ranged from 7.41 to 8.58. The parent Nap-9908 (8.58 cm) produced the longest siliqua while the parent Nap-108 (7.41 cm) produced the shortest siliqua. On the other hand, the values varied from 7.17 to 8.87 cm from hybrids. In this regard, the hybrid combination Nap-9905 x Nap-9908 (8.87 cm) exhibited the highest length of siliqua and that was higher than that of its' either parent (Table 2).

Plate 3: Nap-108 showing flowering status

Table 2: Mean performance for 10 different characters in 6 parents and their 15 F_2s of *Brassica napus* L.

Treatments	**Plant height (cm)**	**Days to 50% flowering**	**Days to 80% maturity**	**No. of primary branches/ plant**	**No. of secondary branches/ plant**
Nap- 9905	115.47	**29**	100.00	4.23	2.53
Nap- 9901	105.82	30	99.00	4.43	1.93
Nap- 205	118.81	**34**	102.00	4.07	**1.53**
Nap- 108	107.14	30	98.00	4.91	2.63
Nap- 9908	114.67	**29**	98.00	3.17	2.57
Nap- 130	105.60	**29**	**97.00**	4.10	2.30
Nap-9905 x Nap- 108	117.47	30	98.00	3.20	3.97
Nap-9905 x Nap- 9908	106.08	31	98.00	4.78	1.80
Nap-9905 x Nap- 9901	114.83	30	98.00	4.63	3.53
Nap-9905 x Nap- 205	110.90	**29**	**97.00**	5.57	3.53
Nap-9905 x Nap- 130	100.79	**29**	**97.00**	3.67	2.57
Nap-108 x Nap- 9908	117.90	32	98.00	3.07	2.30
Nap-108 x Nap- 9901	**97.20**	30	98.00	5.73	3.90
Nap-108 x Nap- 205	105.77	33	100.00	5.20	3.80
Nap-108 x Nap- 130	106.97	30	99.00	**2.77**	2.63
Nap-9908 x Nap- 9901	102.37	**29**	**97.00**	**6.07**	3.90
Nap-9908 x Nap- 205	121.23	32	101.00	5.50	2.97
Nap-9908 x Nap- 130	**124.87**	31	**97.00**	4.43	3.30
Nap-9901 x Nap- 205	106.66	32	103.00	5.89	**5.03**
Nap-9901 x Nap- 130	99.47	30	99.00	4.08	2.88
Nap-205 x Nap- 130	95.20	31	**108.00**	3.70	1.74
Grand Mean	109.30	30	98.00	4.44	2.85
Hightest value	124.87	34	108.00	6.07	5.03
Lowest value	97.20	29	97.00	2.77	1.53

Table 2. (Continued)

Treatments	No. of siliquae/ plant	Siliqua length (cm)	Seeds/ siliqua	Seeds yield/plant (gm)	1000 seed weight (gm)
Nap- 9905	122.50	8.51	24.11	23.73	4.60
Nap- 9901	147.23	7.72	24.69	27.23	4.42
Nap- 205	**94.53**	8.38	26.16	19.83	4.29
Nap- 108	102.57	7.41	23.09	**16.62**	4.21
Nap- 9908	151.10	8.58	25.53	32.38	4.53
Nap- 130	116.10	7.65	22.36	18.34	4.57
Nap-9905 x Nap- 108	173.19	8.34	26.87	35.06	4.19
Nap-9905 x Nap- 9908	179.94	8.87	28.13	40.27	4.35
Nap-9905 x Nap- 9901	117.90	8.61	25.65	19.98	4.16
Nap-9905 x Nap- 205	**220.17**	8.40	26.80	**107.54**	4.39
Nap-9905 x Nap- 130	107.80	8.02	24.15	17.21	4.54
Nap-108 x Nap- 9908	123.88	8.20	24.25	20.92	4.63
Nap-108 x Nap- 9901	170.33	**7.17**	25.89	24.92	**4.14**
Nap-108 x Nap- 205	198.57	7.55	**21.80**	29.19	4.26
Nap-108 x Nap- 130	164.47	8.26	21.85	21.61	**4.67**
Nap-9908 x Nap- 9901	215.97	7.89	23.67	32.45	4.44
Nap-9908 x Nap- 205	137.33	8.55	24.45	20.83	4.34
Nap-9908 x Nap- 130	195.80	7.96	23.76	29.39	4.34
Nap-9901 x Nap- 205	217.35	**8.80**	**27.81**	29.77	4.56
Nap-9901 x Nap- 130	108.21	7.74	23.25	21.80	4.58
Nap-205 x Nap- 130	98.94	8.25	26.79	20.27	4.18
Grand Mean	150.66	8.14	24.81	29.02	4.41
Hightest value	220.17	8.80	27.81	107.54	4.67
Lowest value	94.53	7.17	21.80	16.62	4.14

Plate 4: Hybrid Nap-9905 × Nap-205 showing bearing status

Plate 5: Nap-205 × Nap-130 showing bearing states

4.1.8. Seeds per siliqua

Seed per siliqua also varied from 22.36 to 25.53 and from 21.80 to 28.13 in hybrids. The hybrid Nap-9905 x Nap- 9908 (28.13) produced an excellent number of seeds per siliqua which was higher than any one parent in this programme (Table 2).

4.1.9. Seed yield per plant

Seed yield per plant of the genotype varied from 16.62 to 32.38 gm in parents and from 17.21 to 107.54 gm hybrids. The highest seed yield of the parent was found in Nap- 9908 (32.38 gm) where as lowest in Nap-108 (16.62 gm). Similarly, the highest seed yield was also observed in the hybrid Nap-9905 x Nap- 205 (107.54 gm) which was almost three times higher than both its parent (Table 2).

4.1.10. 1000 seed weight

1000 seed weight in *Brassica napus* varied with some extent *i.e.* from 4.21 to 4.60 gm in parent and from 4.14 to 4.67 gm in hybrids. However, the heaviest seeds were produced by the parent Nap- 9905 (4.60) and also by the hybrid combination Nap-108 x Nap- 130 (4.67). The hybrid produced the highest weighted seeds which was higher than it's both parents (Table 2).

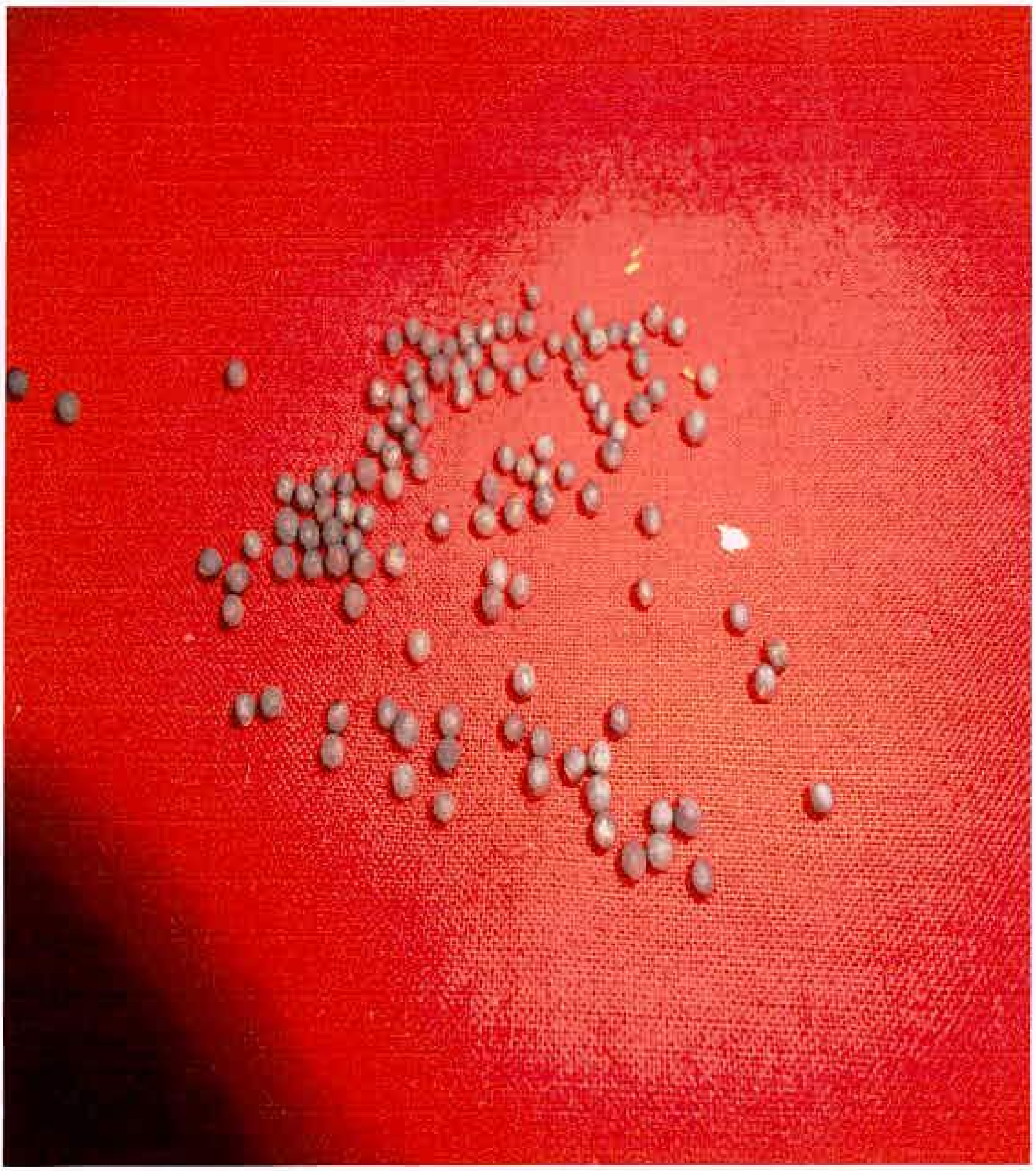


Plate 6: Hybrid Nap-108× Nap-130 showing seed size

4.2 COMBINING ABILITY

The analysis of variance for the genotypes, combining ability variances, ratio of GCA and SCA variances, sum of square, estimates of general and specific combining ability effects are presented in Table 3 to Table 6. The analysis of variance carried out for ten characters are presented in Table 3 which indicated that the genotypes differed significantly for all the characters studied. Treatment mean sum of squares (mean of genotypes) were further partitioned into parents crosses (hybrids) and parent vs crosses. Parent showed highly significant variances for siliqua length and thousand seed weight. Crosses have showed significant variances for plant height. Number of primary branches per plant, Number of secondary branches per plant, Number of siliqua per plant, siliqua length, seed per siliqua, seed yield per plant and thousand seed weight (Table 3). Variances due to parent vs cross interaction were also observed significant for most of the traits except plant height, days to 50% flowering, days to 80% maturity, siliqua length, seed per siliqua and seed yield per plant.

The general and specific combining ability effects are effect genetic parameters in the breeding program. Analysis of variances for yield and yield contributing characters (Table 3) revealed highly significant variation among the parents and hybrids indicating the presence for variability in the material. Variance due to genotypes was significant for most of the traits. Combining ability analysis of six parents and fifteen F_2s in half diallel cross coross was for ten quantitative traits. The variances due to general and specific combining ability were estimated for amassing the contribution of the additive and non-additive type of gene action involved in the inheritance of different characters. The mean sum of square due to general combining ability (GCA) was significant for all the traits except days to maturity, days to 50% flowering. Number of secondary branches per plant, Number of siliqua per plant, seed yield per plant and thousand seed weight indicating that the additive gene action was predominant for the expression of these characters (Table 4). The significant mean sum of square due to specific combining ability (SCA) was also observed for plant height, Number of primary branches per plant, Number of secondary branches per plant, Number of siliqua per plant, seed yield per plant and thousand seed weight indicating that the non-additive gene actions were predominant for the expression of these characters (Table 6). The results showed the agreement with the findings of

Malik *et al*. (1995); Thakur and Sagwal (1997) in rape seed. Similar findings were also veported by Tamber *et al* (1991) in Indian mustard.

The higher magnitude of GCA variance was observed than that of SCA variance for plant height, days to 50% flowering, days to maturity, no. of primary branches/plant, no. of secondary branches/plant, no. of siliquae/plant, seed yield/plant and thousand seed weight. In an earlier study of verma (2000), reported that SCA variance was higher than GCA variance (non-additive type) for seed yield per plant. Verma *et al*. (1989) and Labana *et al*. (1978) reported non-additive type of gene action for siliquae per plant, seed yield per plant in yellow sarson.

Table 3:Analysis of variances (MS values) for seed yield and yield contributing characters in *Brassica napus* L.

Source of variation	df	plant height	Days to 50% flower-ing	Days to 80% matur-ity	No. of primary branches / plant	No. of secondary branches/ plant	No. of siliqua/plant	Siliqua length	Seed/ siliqua	Seed yield/ plant	1000 seed weight
Replication	2	203.53**	1.063	3.111	0.575	0.484	2878.957	0.228	1.750	845.965	0.037
Genotype	20	201.63**	1.863	1.430	2.874**	2.467*	5334.491**	0.656*	10.409*	1093.593*	0.103**
Parent	5	98.988	1.922	0.989	0.983	.609	1589.985	0.764**	6.227	107.357	0.128**
Cross	14	245.805**	1.975	1.676	3.608**	2.540*	5609.016**	0.648*	12.215*	1459.26**	0.096**
Parent vs cross	1	96.378	0.014	0.192	2.060*	10.742**	20213.08**	0.224	6.025	905.423	0.079**
Error	40	83.842	1.497	1.794	1.102	1.146	1905.537	0.302	5.129	600.514	0.027

**** P<0.01, *p<0.05**

Table 4: Analysis of variances (MS values) for GCA and SCA for seed yield and yield contributing components in *Brassica napus* L.

Source of variation	df	plant height	Days to 50% flowering	Days to 80% maturity	No. of primary branches / plant	No. of secondary branches/ plant	No. of siliqua/ plant	Siliqua length	Seed/ siliqua	Seed yield/ plant	1000 seed weight
GCA	5	99.589**	0.304	0.937	1.298**	0.312	1041.368	0.490**	4.260*	361.192	0.021
SCA	15	56.417*	0.727	0.323	0.844*	0.992**	2023.76**	0.128	3.206	365.644*	0.039**
GCA/SCA	-	1.765	0.418	2.9	1.538	0.315	0.515	3.828	1.329	0.988	.308
Error	40	27.947	0.499	0.598	0.367	0.382	635.179	0.107	1.71	200.171	0.009

** $p < 0.01$, * $p < 0.05$

4.2.1 General combining ability (GCA) effects

The additive nature and magnitude of gene action for a trait could be measured by estimation of GCA effects. Similarly the magnitude and nature of non-additive ie. dominance and epistasis nature of gene actions could be measured by estimation of SCA effects. A parent with higher significant GCA effects is considered as a good general combines. A parent showing high GCA and SCA variances is a better parent for creating high yielding specific combination. Parents with significant high GCA effect could be used in conventional breeding programme and crosses with significant high SCA effect could be used in hybrid development. The estimates of GCA effect are presented in Table 5. The magnitude and direction of the significant GCA effects for six parents provide meaningful comparisons and would given a clue to design the future breeding programme. The results of GCA effects of different characters are presented as follows:

4.2.1.1 Plant height

The GCA mean square was highly significant indicating that additive gene action was responsible for the expression of the trait (Table 4). The ratio of GCA/SCA effects (>1) indicated however predominance of additive component for this trait. The GCA effects for six parents ranged from -3.322 to 5.626. Out of six parental GCA three parents showed negative GCA effect. The highest negative GCA effects (-3.782) was provided by Nap-108. The other parents which represented negative GCA were Nap-9901 (-1.017) and Nap-103 (-3.322). Those parents with positive and significant GCA effects were considered as good general combiner for the traits aimed to promote desireable plant height in their crosses (Table 5). The parent Nap-205 showed positive GCA effects. Chowdhury *et al.* (2004) obtained dwarfness in YSK-8501 in *Brassica campestris* L. Singh *et al.* (1996) observed dwarfness in glossy mutant in *Brassica juncea* L.

4.2.1.2 Days to fifty percent flowering

For the trait days to 50% flowering, a significant positive GCA effect is useful for shorter growth duration. Out of six parents, three parents exhibited insignificant and positive

GCA effect. Other three parents showed insignificant and negative GCA values. (Table 5) Chowdhury *et al.* (2004) found earliness in Din-2 in *Brassia napus* L. Singh *et al.* (2000) obtained earliness in YSK-8501 in *Brassica campestris*.

4.2.1.3 Days to eighty percent maturity

The parent Nap-9901 (0.556) provided highest positive GCA effects for days to maturity hence the parent were desireable general combiners to promote the earliness in *Brassica napus* L. (Table 5). Three parent Nap-9905 (-0.069) Nap-205 (-0.319), Nap-9908 (-0.153) and Nap-130 (-0.278) showed insignificant and negative GCA effects.

4.2.1.4. Number of primary branches per plant

The GCA mean square was highly significant indicating that additive gene action was responsible for the expression of the trait and parents are the combiner for further breeding approach (Table 4). The ratio of GCA/SCA effects (>1) indicated however predominance of additive component for this trait. The GCA effects for six parents ranged from -0.319 to 0.556. There was only one parent viz. Nap-108 (0.644) provided significant and positive GCA effects out of six parents which indicated that this parent was good general combiners for promising primary branches. So thus parent was considered as good to use in the breeding programme for more primary branches (Table 5). Other parents showed insignificant positive and negative GCA effects. Chowdhury *et al.* (2004) obtained more primary branches on sampan in *Brassica napus* L. Singh *et. al* (2000) observed maximum number of primary branches on YSP-842 in *Brassica campestris* L.

4.2.1.5 Number of secondary branches per plant

For number of secondary branches per plant four parents exhibited insignificant and negative effect. Other two parents showed insignificant and positive GCA values. None parent could be used to improve this character. Singh *et al* (1996) obtained the highest secondary branches in BJ-1235 in *Brassica juncea* L.

Table 5: **General combining ability (GCA) effects for 6 parents in 6 x 6 half diallel crosses of *Brassica napus* L.**

Parents	Plant height (cm)	Days to 50% flowering	Days to 80% maturity	No. of primary branches/plant	No. of secondary branches/ plant
Nap- 9905	1.992	-0.069	-0.069	-0.094	-0.228
Nap- 9901	-1.017	0.264	0.556*	-0.278	0.009
Nap- 205	5.626*	0.097	-0.319	0.114	0.047
Nap- 108	-3.782	0.056	0.264	0.644*	0.079
Nap- 9908	0.503	-0.028	-0.153	0.141	0.301
Nap- 130	-3.322	-0.319	-0.278	-0.527	-0.209
SE (gi)	1.706222	0.227976	0.249614	0.195585	0.19948
SE (sij)	4.686014	0.62612	0.685546	0.53716	0.547857

** $p < 0.01$, *$p < 0.05$

Table 5: **Continued**

Parents	No. of siliqua/plant	Siliqua length (cm)	Seeds/ Siliqua	Seed yield/plant (gm)	1000 seed weight (gm)
Nap- 9905	-1.328	0.287*	0.767	8.051	0.042
Nap- 9901	8.785*	-0.249	-0.458	-2.119	-0.015
Nap- 205	-1.579	0.160	0.363	-2.450	-0.023
Nap- 108	-2.467	-0.239	-0.154	-5.119	-0.070
Nap- 9908	14.991*	0.218	0.629*	8.657*	-0.006
Nap- 130	-18.402	-0.177	-1.147	-7.020	0.073*
SE (gi)	8.134155	0.102375	0.422002	4.566308	0.03091
SE (sij)	22.33986	0.281166	1.158996	12.54103	0.084892

** $p < 0.01$, * $p < 0.05$

Plate 7: Nap-9908 showing branching status

4.2.1.6 Number of siliquae per plant

The parent Nap-9908 exhibited the highest (14.991) significant GCA effects for this charater. This parent was selected as the best general combiner and desireable to use in hybridization program to improve the number of siliquae per plant in *Brassica napus* L. (Table 5). Other significant and positive GCA value was provided by Nap-9901 (8.785). The other parent showed insignificant and negative GCA effects. The ratio of GCA/SCA effects (<1) indicated however predominance of non-additive component for this trait. Chowdhury *et al.* (2004) found the highest number of siliquae in Din-2 *Brassica rapa.* Singh and Murty (1980) obtained maximum number of siliquae per plant in SS-1 in *Brassica campestris* L.

4.2.1.7. Siliqua length

The GCA mean square was highly significant and indicated the additive gene action was responsible for the expression of the trait (Table 4). The ratio of GCA/SCA effects (>1) indicated however predominance of additive component for this trait. The GCA effects for six parents ranged from -0.249 to 0.287. Out of six parents, Nap-9908 (0.629) showed significant and positive GCA effects which was selected as the best general combiner to use in breeding program (Table 5). Other parent showed insignificant positive and negative GCA effect. Sheikh and singh (1998) obtained different result (maximum siliquae length) in glossy mutant.

4.2.1.8 Number of seeds per siliqua

The GCA mean square was significant indicating that additive gene action was responsible for the expression of the trait (Table 4). The ratio of GCA/SCA effects (>1) indicated however predominance of additive component for this trait. The GCA effects for six parents ranged from -0.458 to 0.629. Out of six parents, only Nap-9908 exhibited significant and positive GCA effect (0.629). So, the parent would be considered as general combiner for the character and could be used for hybrid production with more seeds per siliqua development in breeding programme. Rest of the parent provided insignificant GCA effects. Chowdhury *et al.* (2004) found maximum seeds per siliqua in

Dhali in *Brassic rapa* L. Singh and Murty (1980) obtained more seeds per siliqua m YPS-842 in *Brassica campestris* L.

4.2.1.9 Seed yield per plant

Significant and positive GCA effects were observed in Nap-9908 (8.657). This parent might be selected as promising general combiner for high yield. On the other hand, Nap-9901 (-2.119), Nap-205 (-2.450), Nap- 108 (-5.119) and Nap-130 (-7.020) showed insignificant and negative GCA effect and were not fit for increasing seed yield (Table 6). Chowdhury *et al.* (2004a) found highest seed yield per plant in *Brassica rapa* L.

4.2.1.10 Thousand seed weight

Most of the parents showed insignificant positive and negative GCA effects except Nap-130 (0.073). Nap-130 showed significant and positive GCA effects and considered as the best general combiner for this trait. Other parents Nap-9901, Nap-205, Nap-108 and Nap-9908 had negative GCA effects suggesting them to be poor general combiner. Chowdhury *et al.* (2004a) found highest seed weight in Dhali in *Brassica rapa* L.

4.2.2 Specific combining ability (SCA) effects

The specific combining ability effects signify the role of gene action in the expression of the characters. It denotes the highly specific combining ability leading to highest performance of some specific cross combinations. For this reason it relates to a particular cross. The specific combining ability effects are also seen in relation to their size. High SCA effects may arise not only on cross involving high x high combinations, but also in those involving low x high and also from low x low. Thus in practice, some of the low combiners should also be accommodated in hybridization programme. The specific combining ability effects of fifteen crosses for the different characters studied are presented in Table 6. The magnitude and direction of the significant effects for the fifteen crosses provide meaningful comparisons and would give a clue to the future breeding programme. The results of SCA effects for different characters are given below.

Table 6: **Specific combining ability (SCA) effects for 15 crosses in 6 x 6 half diallel crosses of *Brassica napus* L.**

Cross combination	Plant height (cm)	Days to 50% flowering	Days to 80% maturity	No. of primary branches/ plant	No. of secondary branches/ plant
Nap- 9905 x Nap- 108	7.20*	0.06	0.15	-0.86	-0.33
Nap-9905 x Nap- 9908	-10.84	1.23	0.36	0.32	1.30*
Nap- 9905 x Nap-9901	7.33*	0.27	0.11	-0.35	-0.90
Nap- 9905 x Nap-205	-0.89	-0.32	-0.14	1.08**	0.61
Nap- 9905 x Nap- 130	-7.18	-0.69	-0.68	-0.15	0.16
Nap- 108 x Nap-9908	4.00	-0.77	0.40	-1.21	-0.60
Nap-108 x Nap-9901	-7.30	-0.07	-0.18	0.93*	0.97
Nap-108 x Nap-205	-3.02	1.02	-0.10	0.90*	0.64
Nap-108 x Nap- 130	2.01	0.31	0.69	-0.87	-0.02
Nap-9908 x Nap-9901	-8.77	-0.57	-0.64	0.87	0.93
Nap-9908 x Nap-205	5.81	-1.15	-0.89	0.81	-0.23
Nap-9908 x Nap- 130	13.27**	-0.86	-0.43	0.41	0.62
Nap-9901 x Nap-205	0.64	-0.44	0.52	-0.66	1.80**
Nap-9901 x Nap- 130	-2.72	0.52	0.65	-0.48	0.16
Nap-205 x Nap- 130	-11.28**	1.60	0.73	-0.35	-1.20
SEd (gi-gj) =	2.643268	0.353179	0.3867	0.30299	0.309033
SEd (sij-sik) =	6.993431	0.934424	1.023113	0.80166	0.817625
SEd (sij-skl) =	6.474659	0.865108	0.947218	0.74219	0.756973

**** p <0.01, * p<0.05**

Table 6. Continued

Cross combination	No. of siliquae/ plant	Siliqua length (cm)	Seeds/ siliqua	Seeds yield/ plant (gm)	1000 seed weight (gm)
Nap- 9905 x Nap- 108	15.07	0.16	1.75	0.11	-0.24
Nap-9905 x Nap- 9908	32.19	0.28	2.19	5.65	-0.07
Nap- 9905 x Nap-9901	-28.97	0.43	0.22	-11.96	-0.22
Nap- 9905 x Nap-205	55.84*	-0.24	0.60	61.82**	-0.05
Nap- 9905 x Nap- 130	-23.13	-0.23	-0.28	-12.84	0.02
Nap- 108 x Nap-9908	-33.98	0.15	-0.47	-3.53	0.26**
Nap-108 x Nap-9901	13.35	-0.48	1.69	3.14	-0.18
Nap-108 x Nap-205	24.13	-0.56	-3.18	-6.36	-0.12
Nap-108 x Nap- 130	23.42	0.55	-1.36	1.73	0.20*
Nap-9908 x Nap-9901	69.35**	-0.16	-1.35	11.00	0.12
Nap-9908 x Nap-205	-26.74	0.04	-1.35	-14.39	-0.04
Nap-9908 x Nap- 130	65.12**	-0.16	-0.27	9.84	-0.12
Nap-9901 x Nap-205	54.16*	0.69*	2.53*	-2.78	0.23*
Nap-9901 x Nap- 130	-21.58	0.02	-0.27	4.92	0.17
Nap-205 x Nap- 130	-48.31**	0.07	2.50	-10.39**	-0.29
SEd (gi-gj) =	12.60138	0.158599	0.653762	7.074094	0.04788
SEd (sij-sik) =	33.340	0.419614	1.729692	18.71629	0.12669
SEd (sij-skl) =	30.86695	0.388487	1.609384	17.32792	0.11729

** p <0.01, * p <0.05

4.2.2.1 Plant height

The SCA mean square was significant indicating that non-additive gene components with additive genetic components were responsible for the expression of the character. Out of 15 crosses, Nap-9908 x Nap-130 (13.27) showed the highest significant positive SCA effects and Nap-205 x Nap-130 (-11.28) showed the highest significant negative SCA effects for plant height and could be considered as the best combination. Nap-9905 x Nap-108 and Nap-9905 x Nap-9901 were good specific combiner. Thus, the cross combination Nap-9908 x Nap-130 could be used for tallness of this crop (Table 6). Chowdhury *et al.* (2004a) observed dwarf ness in PT-303 x Tori-7 in *Brassica rapa*. Acharya and Swain (2004) obtained dwarfness in Varuna x Pusa Bahar in *Brassica juncea*.

4.2.2.2 Days to 50% flowering

The highest positive SCA value was exhibited by Nap-205 x Nap-130 (1.60) followed by Nap-9905 x Nap-9908 (1.23) for days to 50% flowering but it was insignificant (Table 6). On the other hand, the highest negative SCA value was provided by Nap-9908 x Nap-205 (-1.15) but it was also insignificant indicating that most of the crosses are not responsible for the character. Singh *et al.* (2000) obtained earliness on YSK-8501 x SS-2 in *Brassica campestris*.

4.2.2.3 Days to 80% maturity

The highest positive SCA value was exhibited by Nap-205 x Nap-130 (0.73) followed by Nap-108 x Nap-130 (0.69) for days to maturity but it was insignificant (Table 6). On the other hand the highest negative SCA value was provided by Nap-9908 x Nap-205 (0.89) but it was also insignificant. Acharya and Swain (2004) found early maturity in JC 26 x Jai Kisan in *Brassica juncea*.

4.2.2.4 Number of primary branches per plants

The SCA mean square was significant indicating that non-additive gene action was responsible for the expression of the character. The SCA value ranged from -1.29 to 1.08. The cross combination Nap-9905 x Nap-205 (1.08) was found to be the best to improve this crop with more number of primary branches as it showed the highest significant and positive SCA effects for this trait. Nap-108 x Nap-9901 and Nap-108 x Nap-205 were good specific combiner. The rest of the crosses were average specific combiner (Table 6). Chowdhury *et al.* (2004a) found more primary branches in Sampad x Tori-7 in *Brassica rapa*. Sheikh and Sing (1998) observed best positive effect in Pusa x Barani in *Brassica juncea*.

4.2.2.5 Number of secondary branches per plant

The SCA mean square was significant indicating that non-additive gene action was responsible for the expression of the character. The SCA value ranged from -1.20 to 1.80. The highest significant and positive value for this character was revealed by Nap-9908 (1.30). Thus, Nap-9901 x Nap-205 (1.80) and Nap-9905 x Nap-9908 (1.30) were the best cross combinations to improve plants with more numbers of secondary branches and Nap-205 x Nap-130 (-1.20) was the best combinations to obtain plants with minimum secondary branches (Table 6). Chowdhury *et al*. (2004a) found maximum secondary branches in Sampad x Din-2 in *Brassica rapa*. Acharya and Swain (2004) obtained more secondary branches in BM 20-12-3 x JC 26 in *Brassica juncea*.

4.2.2.6 Number of siliqua per plant

The SCA mean square was highly significant indicating that non-additive gene action was responsible for the expression of the character. The SCA value ranged from -48.31 to 69.35. Among the cross combinations, Nap-9908 x Nap-9901 (69.35) showed the highest significant and positive SCA effects followed by Nap-9908 x Nap-130 (65.12), Nap-9905 x Nap-205 (55.84) and Nap-9901 x Nap-205 (54.19). On the other hand, Nap-205 x Nap-130 (-48.31) showed the significant but negative SCA effects (Table 6). So, Nap-9908 x Nap-9901 was the best combination for this trait. Singh and Murty (1980) observed more siliquae per plant in YSP-842 x SS-3 in *Brassica rapa*. Acharya and Swain (2004) obtained highest siliquae per plant in Pusa Bahar x JC 26 in *Brassica juncea*.

4.2.2.7 Siliqua length

Among the cross combinations, Nap-9901 x Nap-205 (0.69) showed the significant and positive SCA effects. On the other side, the remaining combinations showed insignificant positive or negative SCA effects for the trait (Table 6). Hence, the cross combination Nap-9901 x Nap-205 was the best for siliqua length. Sheikh and Singh (1998) and Acharya and Swain (2004) observed maximum siliqua length in Pusa Barani x Glossy mutant and BM 20-12-3 x Pusa Bahar respectively in *Brassica juncea*.

4.2.2.8 Number of seeds per siliqua

Among the cross combinations, Nap-9901 x Nap-205 (2.53) exhibited the highest significant and positive SCA value. The other cross combinations showed either insignificant or negative SCA effects. Hence, Nap-9901 x Nap-205 was the best cross combination to increase the number of seeds per siliqua (Table 6). Singh *et al.* (2000) obtained more seeds per siliqua in YSP-842 x YSK-8501 in *Brassica campestris*. Acharya and Swain (2004) observed maximum number of seeds per siliqua in BM 20-12-3 x Pusa Bahar in *Brassica juncea*.

4.2.2.9 Seed yield per plant

The SCA mean square was significant indicating that non-additive gene action was responsible for the expression of the character. The SCA value ranged from -11.96 to 61.82. The cross combination Nap-9905 x Nap-205 (61.82) exhibited the highest significant and positive SCA effects for seed yield per plant. The other cross combinations Nap-205 x Nap-130 (-10.39) showed the significant and negative SCA effects (Table 6). Chowdhury *et al.* (2004a) obtained highest seed yield in M-27 x Din-2 in *Brassica rapa*. Singh *et al.* (2000) observed more seed yield per plant in YSP-842 x YSK-8501 in *Brassica campestris*. Acharya and Swaim (2004) found maximum seed yield per plant in Pusa Bold x Pusa Bahar in *Brassica juncea*.

4.2.2.10 Thousands seed weight (g)

The SCA mean square was highly significant indicating that non-additive gene action played important role for the expression of the character. The GCA/SCA effects (<1) showed however predominance of non-additive components. The SCA value ranged from -2.9 to 0.26. The cross combination Nap-108 x Nap-9908 (0.26) exhibited the highest significant and positive SCA effects followed by Nap-108 x Nap-130 (0.20) and Nap-9901 x Nap-205 (0.23). The remaining combinations showed insignificant effects i.e. poor specific combiner for the trait. Sheikh and Singh (1998) and Acharya and Swain (2004) observed high 1000-seed weight in Pusa Barani x Glossy mutant and BM 20-12-3 x Pusa Bahar respectively in *Brassica juncea*. Singh *et al.* (2000) observed more seed yield per plant in YSP-842 x YSK-8501 in *Brassica campestris*.

Plate 8: Hybrid Nap-9908 × Nap-9901 showing branching status

4.2.3 Vr-Wr graph

Vr-Wr graphs, the two dimensional depiction made based on the parental variance (Vr) and parent off spring co-variance (Wr) are presented in the Fig. 2 to Fig. 11. Hayman's graphic approach to diallel analysis is based on monogenic additive model. The regression coefficient differ significantly from zero and approaching to unity for all the traits studied suggesting that there was no epistasis for most of the traits indicated the validity of such type of analysis. Vr-Wr graphs for the ten characters are described below:

4.2.3.1 Plant height

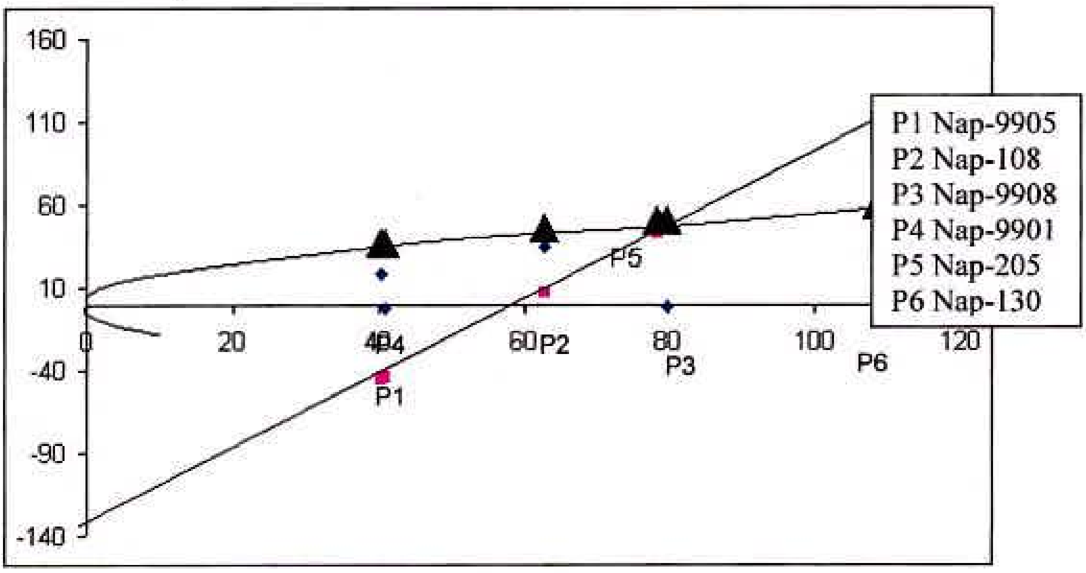


Fig 2: Vr-Wr graph for plant height in *Brassica napus*

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 2). The distribution of array points indicated two parents Nap-9901 (p_4) and Nap-9905 (p_1) contained most dominant alleles as they fell closer to the point of origin. The parents Nap-108 (p_2) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. Whereas, rest of the parents fallen far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) observed complete dominance in *Brassica rapa* .

4.2.3.2 Days to flowering

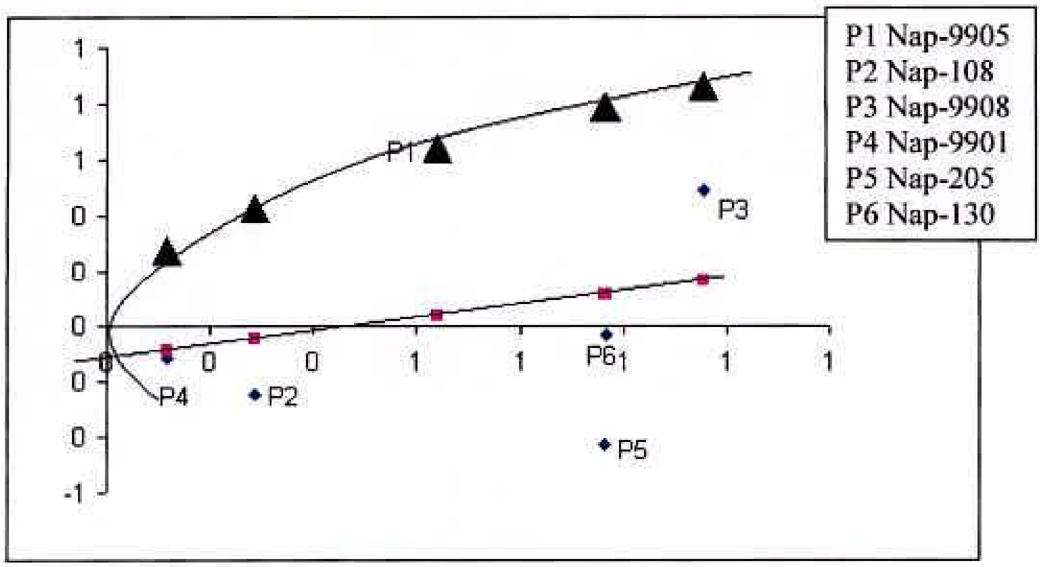


Fig 3: Vr-Wr graph for days to 50% flowering in *Brassica napus*

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 3). The distribution of array points indicated two parents Nap-9901 (p_4) and Nap-108 (p_2) contained most dominant alleles as they fell closer to the point of origin. The parents Nap-9905 (p_1) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. Whereas, rest of the parents fallen far from the origin indicated that they possess maximum frequency of recessive alleles. Singh *et.al* (2000) obtained earliness on YSK-S501× SS-2 in *B.campestris/rapa*. Singh *et al.* (1996) observed earliness in PR-1108 × BJ-1235 in *Brassica juncea* L.

4.2.3.3 Days to 80% maturity

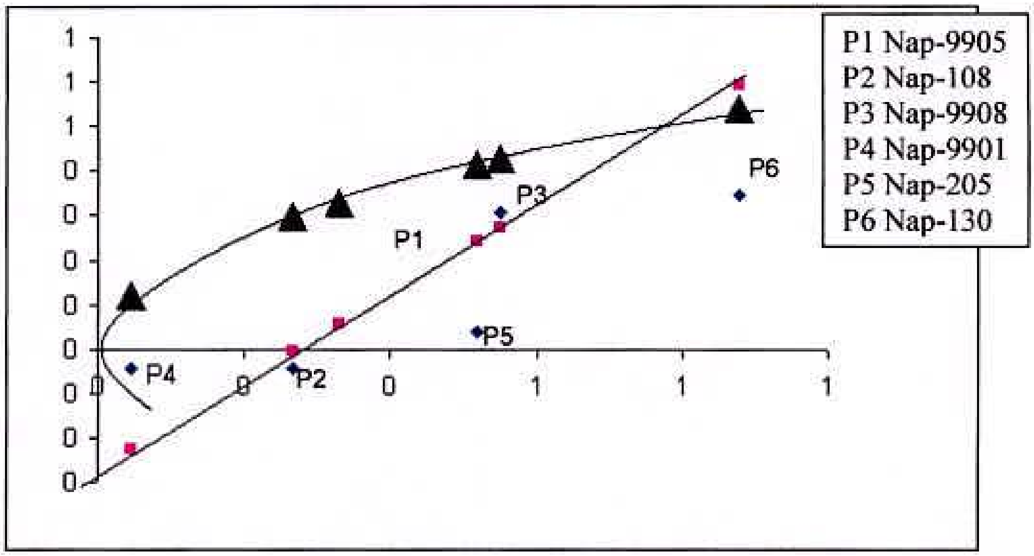


Fig 4: Vr-Wr graph for days to 80% maturity in *Brassica napus*

The regression line intersected above the point of origin suggesting partial dominance gene action for controlling the trait (Fig. 4). The parents Nap-9901 (p_4) and Nap-108 (p_2) contained maximum dominant alleles as they fell very closer to the point of origin. The parent Nap-130 (p_6) fell far from the origin and thus it contained maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) observed partial dominance in *Brassica rapa*, Trivedi and Mukharjee (1986) found over dominance in *Brassica juncea*.

4.2.3.4 Primary branches per plant

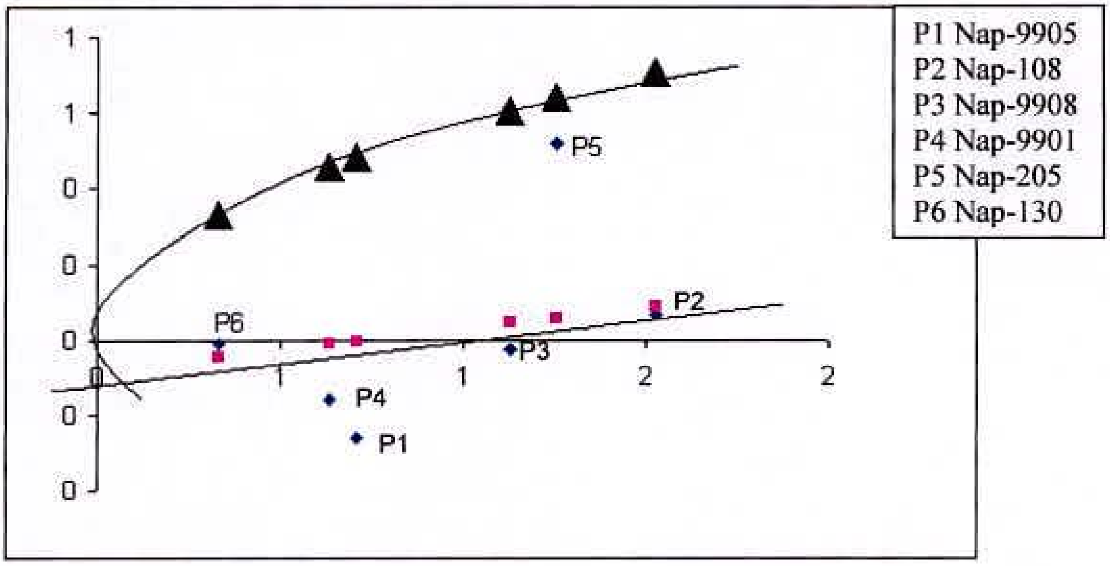


Fig 5: Vr-Wr graph for primary branches per plant in *Brassica napus*

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance gene action for controlling the trait (Fig 5). The parent Nap-130 (p_6) and Nap-9901 (p_4) fell close to the origin means they contained maximum frequencies of dominant alleles. The parent Nap- 9905 (p_1) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The other parents fallen far from the origin and thus it contained maximum frequency of recessive alleles. Yadav and Yadava (19960 found over dominance in *Brassica campestris* respectively.

4.2.3.5 Secondary branches per plant

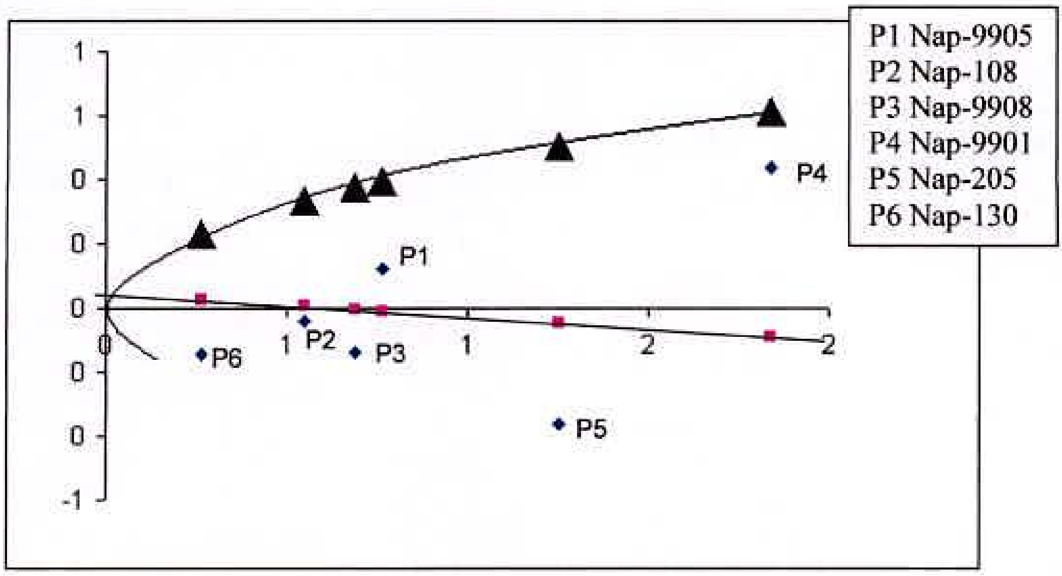


Fig 6: Vr-Wr graph for secondary branches per plant in *Brassica napus*

The regression line intersected the Wr axis below the point of origin indicating the existence of partial dominance gene action for controlling the trait (Fig 6). The parent Nap-130 (p_6) and Nap-108 (p_2) fell closer to the point of origin suggesting they contained maximum number of dominant alleles. The parent Nap- 9908 (p_3) and Nap-9905 (p_1) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parent Nap- 9901 (p_4) and Nap- 205 (p_5) fell far from the origin indicating the presence of maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) obtained partial dominance in *Brassica rapa*, Yadav and Yadava (1996) observed over dominance in *Brassica campestris.*

4.2.3.6 Siliquae per plant

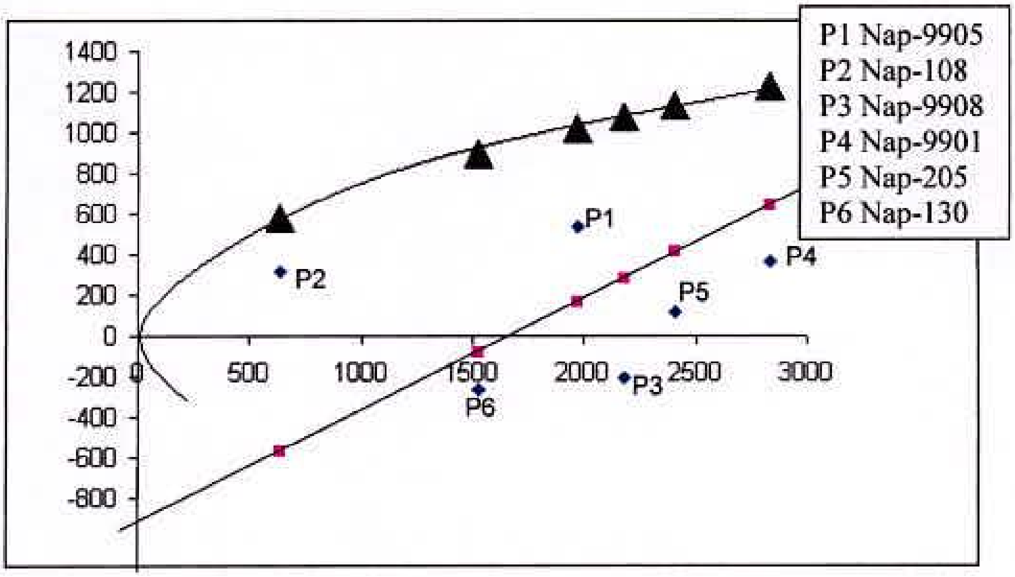


Fig 7: Vr-Wr graph for no. of siliquae per plant in *Brassica napus*

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance gene action for controlling the trait (Fig 7). The parent Nap-108 (p_2) contained maximum number of dominant alleles as it fell closer to the point of origin. The parents Nap- 130 (p_6) and Nap-9905 (p_1) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parent Nap- 9908 (p_3), Nap- 205 (p_5) and Nap- 9901 (p_4) fell far from the origin indicating the presence of maximum frequency of recessive alleles in that parent. Chowdhury *et al.* (2004b) and Trivedi and Mukharjee (1986) obtained over dominance in *Brassica rapa* and *Brassica juncea* respectively.

4.2.3.7 Length of siliqua

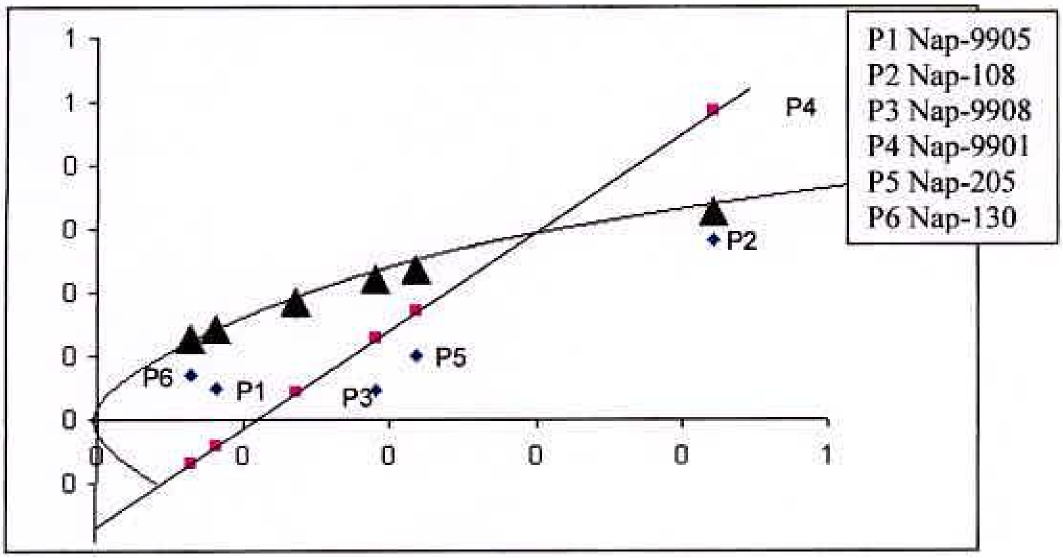


Fig 8: Vr-Wr graph for length of siliqua in *Brassica napus*

The regression line intersected the Wr axis above the point of origin suggesting partial dominance gene action for controlling the trait (Fig 8). The parent Nap-130 (p_6) and Nap-9905 (p_1) contained maximum dominant alleles as it fell closer to the point of origin. The parents Nap- 9908 (p_3) and Nap-205 (p_5) fallen at the nearly middle portion means they contained nearly equal frequencies of dominant and recessive alleles. The parent Nap-108 (p_2) and Nap- 9901 (p_4) fell far from the origin and thus it contained maximum frequency of recessive alleles. Trivedi and Mukharjee (1986) found over dominance in *Brassica juncea.*

4.2.3.8 Seeds per siliquae

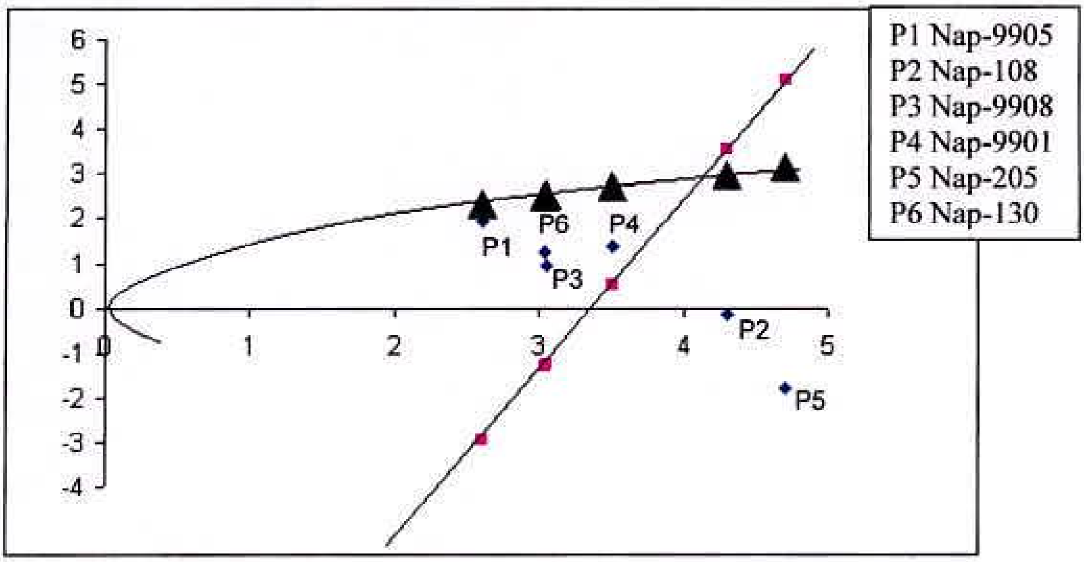


Fig 9: Vr-Wr graph for seeds per siliquae in *Brassica napus*

The regression line intersected the Wr axis above the point of origin suggesting over dominance gene action for controlling the trait (Fig 9). The parent Nap-9905 (p_1) contained maximum dominant alleles as it fell closer to the point of origin. The parents Nap- 205 (p_5) fallen far from the origin indicating the presence of maximum frequency of recessive alleles in this parent. Chowdhury *et al.* (2004b) observed over dominance in *Brassica rapa,* Trivedi and Mukharjee (1986) found over dominance in *Brassica juncea.*

4.2.3.9 Seed yield per plant

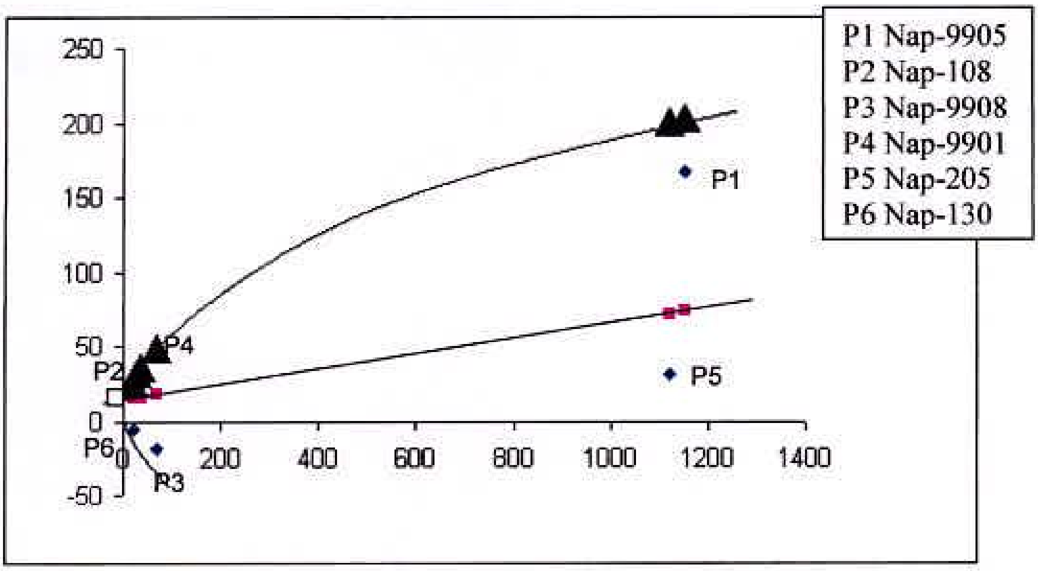


Fig 10: Vr-Wr graph for seed yield per plant in *Brassica napus*

The regression line intersected the Wr axis below the point of origin suggesting partial dominance gene action for controlling the trait (Fig 10). The parents Nap-108 (p_2), Nap-9908 (p_3), Nap-9901 (p_4) and Nap-130 (p_6) fell closer to the point of origin indicating that it contained maximum dominant alleles. The parent Nap- 9905 (p_1) and Nap- 205 (p_5) fell far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) obtained over dominance in *Brassica rapa*, Trivedi and Mukharjee (1986) observed over dominance in *Brassica juncea* respectively.

4.2.3.10 Thousand seed weight (g)

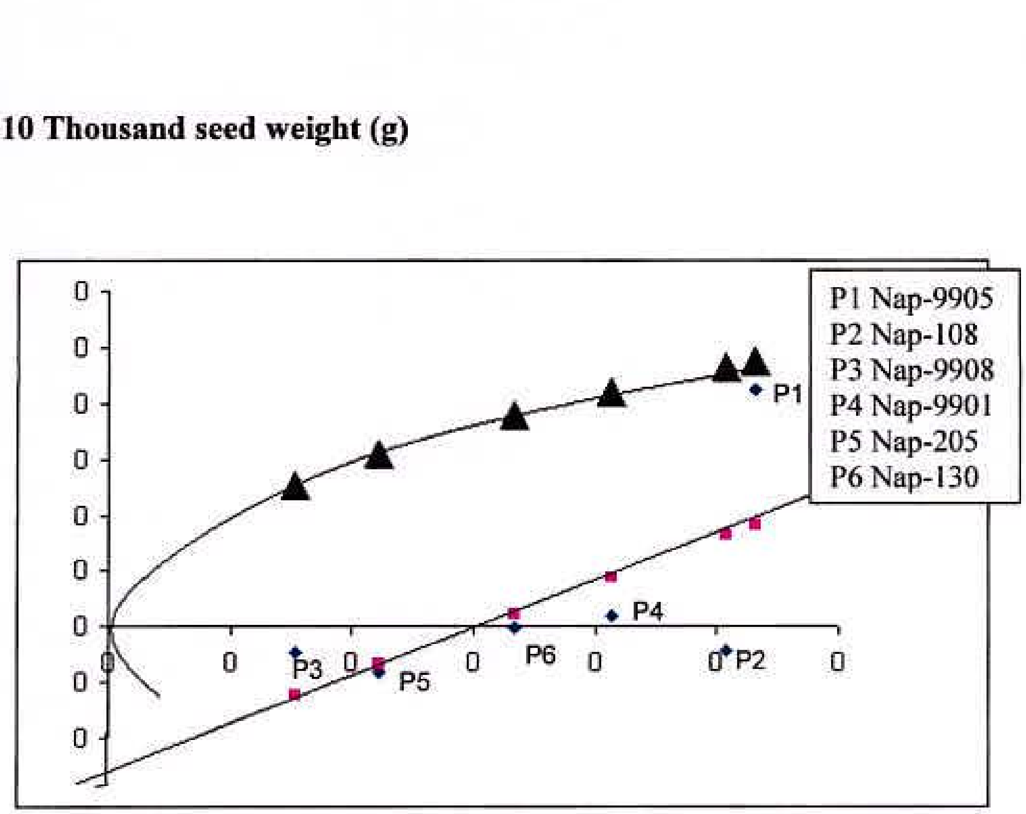


Fig 11: Vr-Wr graph for thousand seed weight in *Brassica napus*

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig 11). The distribution of array points indicated that two parents Nap-9908 (p_3) and Nap-205 (p_5) contained most dominant alleles as they fell closer to the point of origin. Nap- 205 (p_6) and Nap- 9901 (p_4) fallen at the middle portion suggesting they contained equal frequencies of dominant and recessive alleles. The parents Nap- 9905 (p_1) and Nap- 108 (p_2) fell far from the origin indicated that they possess maximum frequency of recessive alleles. Chowdhury *et al.* (2004b) found partial dominance in *Brassica rapa*, Trivedi and Mukharjee (1986) observed over dominance in *Brassica juncea.*

Regression line intersected the Wr-axis below the origin for all the characters except secondary branches per plant and seed yield per plant indicating the presence of over dominance. Such serious inflation of dominance has been postulated by Hayman (1954) and Jinks (19550. A further support to the existence of pseudo-over dominance was visualized in the estimates of D and H components and relative magnitude of GCA and SCA in variance component analysis for these traits. This was supported by the earlier findings reported by Chowdhury *et al.* (2004b) in turnip rape, Trivedi and Mukharjee (1986) in Indian mustard. The over dominance might not be an index of real over dominance at gene level, since particular combination of positive and negative genes or a complementary type of gene interaction of simply correlated gene distribution could have caused serious inflation in particular combinations of unidirectional dominance which might have resulted in over-estimation of partial dominance (Comstock and Robinson, 1952; Hayman, 1954; Grafius, 1959). The presence of over dominance in the various components of oil yield and seed yield in the parent study has also been substantiated by the findings of Singh *et al.* (1970, 1971) in B. *campestris*, Rawat (1975) in B. *juncea* and Trivedi and Mukharjee (1985) in B. *juncea*, Chowdhury et al. (2004b) in B. *rapa*.

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

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

4.3 Components of variation and genetic parameters

4.3.1 Plant height

Both additive and dominant component were significant, but due to higher magnitude dominant gene effects the latter appeared to have more control of the character. Negative F value indicated that the recessive alleles were predominantly in excess in its inhentance (Table 7), the estimate was however nm-significant. The dominance effect (h^2) was negative and non-significant. Over dominance was found for plant height. The value of $H_2/4H_1$ indicates asymmetrical distribution of positive and negative alleles. The analysis gave narrow sense heritability (h^2n) estimate of 7.92% (Table 7).

4.3.2 Days to 50% flowering

Dominance component was significant and H_1 was greater in magnitude than additive component, indicating greater role of dominance component in the inheritance. Positive value of F revealed that the dominant alleles were predominantly in excess in its inheritance (Table 7); but then the estimate was significant H_2 value differed from H_1 suggesting that there was unequal frequency of increasing and decreasing alleles. The results of dominants effect (h^2) were positive and significant. Over dominance was found for days to 50% flowering. The analysis gives narrow sense heritability as 7.9% (Table 7).

4.3.3 Days to maturity

The components H_1 and H_2 are significant but D is not significant for days to maturity (Table 7). This indicates the importance of dominance effect of genes in the days to maturity. the magnitude of H_1 was much higher than D, suggesting the preponderance of dominance type of gene action for this trait. Dominance effect (h^2) was found positive and significant. The $[\frac{1}{4}\ (H_1/D)_4]^{\frac{1}{2}}$ value was zero that means complete dominance for the character. The analysis gives narrow sense heritability as – 9.3% (Table 7).

4.3.4 No. of primary branches per plant

The components H_1 and H_2 are significant but D is not significant and the magnitude of H_1 was much higher than D, suggesting the preponderance of dominance type of gene action for this trait. Positive value of F revealed that the dominant alleles were predominantly in excess in its inheritance (Table 7); and the estimate was significant. Dominance effect (a^2) were positive and significant. The analysis gives narrow sense heritability as- 2.5% (Table 7).

4.3.5 No of secondary branches per plant

Result suggested that only additive component played role in the expression of the trait. Significant and positive indicates that the dominant alleles were predominantly in excess in its inheritance and significant. Dominance effect was significant. The narrow sense heritability was – 17.9% (Table 7).

4.3.6 No. of siliquae per plant

Results suggested that only additive component played roe in the expression of the trait. Significant and positive F value revealed that the dominant alleles were predominantly in excess in its inheritance overall difference between parent and cross were substantiated by significant h^2 value. The $H_2/4H_1$ value is not equal to unity that positive and negative value were asymmetrically distributed. The narrow sense heritability was – 3.9% (Table 7).

Table 7: Components of variation and genetic parameters for ten characters in a 6 x 6 F_2 half diallel crosses of *Brassica napus* L.

Items	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches/ plant	No. of secondary branches/ plant	No. of siliquea/ plant	Siliqua length (cm)	Seed/ siliqua	Seed yield/ plant (gm)	1000 seed weight (gm)
D	3.149**	0.149**	-0.289	-0.031	-0.169	-120.635	.155**	0.420**	-168.28**	0.033**
F	-61.146	1.507**	-0.746	0.673**	0.492**	130.610**	-0.065	1.324**	-403.89**	0.123**
H_1	359.059**	2.051**	2.147**	0.674**	-0.532	2628.69**	2.657**	13.428**	148.854**	0.215**
H_2	797.434**	9.500**	3.307**	9.817**	12.394**	6786.61**	1.764**	42.191**	4968.88**	0.527**
h^2	-53.087	0.171**	1.286**	5.138**	11.981**	167.214**	1.704**	8.207**	-1.480	-1.057
E	29.847**	0.492**	0.619	0.359**	0.371**	650.630**	0.099**	1.656**	204.067	0.009**
$\frac{1}{4}[(H_1/D)_4]^{1/2}$	5.339	1.857	0	0	0.888	0	2.068	2.828	0	1.272
$H_2/4H_1$	0.555	1.158	0.385	3.643	-5.829	2.548	0.166	0.785	8.345	0.012
h^2/H_2	-0.06657	0.01801	0.38881	0.52336	0.9666	0.00624	.96632	0.19452	-0.0003	-2.0058
h^2n	0.01296	0.0792	-0.0935	-0.025	-0.1797	-0.039	0.1242	0.0431	-.1896	0.528

**** p <0.01, * p <0.05**

4.3.7 Siliqua length

Both additive and dominance components were significant for the trait. But dominance component was preponderant. Negative value of F suggested that the presence of recessive alleles but the estimate was non-significant. The result of dominance effect (h^2) was positive and significant over dominance was found for this trait. The $H_2/4H_1$ was asymmetrical distribution of positive and negative alleles in the parent. The narrow sense heritability was 12.42% (Table 7).

4.3.8 Seed per siliqua

For seed per siliqua most of the genetic parameters (D, H_1, H_2) were significant (Table 7). Both additive and dominant effects of genes were important for the character expression. But H_1 was greater than D indicating greater role of dominance component in the inheritance of the trail. Positive and significant F value revealed that the dominant alleles were predominantly in excess in its inheritance. Dominance effect was significant. Positive and negative alleles were more or less asymmetrically distributed as $H_2/4H_1$ value was not exactly 0.25. The narrow sense heritability was 4.3% (Table 7).

4.3.9 Seed yield per plant

Dominance component was significant and H_1 was greater in magnitude than additive component, indicating greater role of dominance component in the inheritance. Significant and negative F value indicated that the recessive alleles were predominantly in excess in its inheritance (Table 7). Dominance effect was negative and significant. The $H_2/4H_1$ value indicates that there was asymmetrical distribution of positive and negative alleles in the parents. The narrow sense heritability was – 18.96% (Table 7).

4.3.10 Thousand seed weight

For thousand seed weight most of the genetic parameters (D, H_1, H_2) were significant (Table 7). Both additive and dominant effects of genes were important for the character expression. But H_1 was greater than D indicating greater role of dominance component in the inheritance of the trait. Positive F value revealed that the dominant alleles were predominantly in excess in its inheritance. Negative and non-significant result was found for dominance effect. Over dominance was found for thousand seed weight. The $H_2/4H_1$ value indicates positive and negative alleles were more or less asymmetrically distributed. The narrow sense heritability was 52.8% (Table 7).The results agree with Yadav and Yadava (1996) in toria; Trivedi and Mukharjee (1986) in Indian mustard.

Chapter 5

SUMMARY

SUMMARY

An experiment was conducted during the period of 8th December, 2010 to March 2011, at the experimental farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University using six parents and fifteen F_1 progenies of *Brassica napus*. The experiment was carried out to study combining ability, heritability, genetic components in percentage of mean and mean square direct and indirect effect of different traits on yield and yield contributing characters. All progenies varied significantly with each other for all the characters studied. The results of the present study are summarized as follows:

A six parents (Nap-9905, Nap-9901, Nap-205, Nap-108, Nap-9908 and Nap-130) half diallel cross hybrids were evaluated for estimating the magnitude of general and ospecific combining ability effects with Vr-Wr graphs..

It was observed that all the hybrids obtained did not perform well for many of the important characters and to find out the desireable hybrids. Analysis of combining ability following Griffing approach showed significant GCA and SCA variance for all the charactess studied, indicating the role of both additive and non-additive components in the genetic system controlling these characters. The higher magnitude of GCA variance was observed than that of SCA variance for plant height days to maturity, number of primary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua, seed yield per plant and thousand seed weight.

Estimates of GCA effects for different characters suggested that the parent Nap-9908 was the best general combiner for number of siliquae per plant, seed per siliqua and seed yield per plant. The parent Nap-205 was the best general combiner for plant height. The parent Nap-9901 was the best general combiner for days to maturity and Nap-108 for number. of primary branches per plant. The parent Nap-9905 was the best combiner for siliqua length and parent Nap-130 for thousand seed weight.

The SCA estimates of various characters revealed that Nap-9908 x Nap-130 was the best combination for plant height Nap-9905 x Nap-205 for no. of primary branches per plant, Nap-9901 x Nap-205 for secondary branches, Nap-9908 x Nap-9901 for number of siliqua per plant, Nap-9901 x Nap-205 for siliqua length, Nap-9901 x Nap-205 for seeds per siliqua, Nap-9905 x Nap-205 for seed yield per plant and Nap-108 x Nap-9908 for thousand seed weight were the best cross combinations.

In the Hayman's approach of diallel analysis a graph is drawn with the help of variance of arrays (Vr) and co-variances between parents and their offspring (Wr) for each trait. Results showed by and large simple additive-dominance genetic model to be adequate without presence non-allelic interaction. The Vr-Wr graph indicates over dominance (when the regression line passes below the origin cutting the Vr axis) for plant height, days to flowering, primary branches per plant siliquae per plant, seeds per siliqua, siliqua length and thousand seed weight. Partial dominance (when the regression line passes above the origin cutting the Wr axis) was observed for secondary branches per plant and seed yield per plant. The graphical analysis also indicates wide genetic diversity among the parents.

The components of variation revealed that both additive and dominance genetic component were important in plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length, seed per siliqua, seed yield per plant and thousands seed weight. For number of secondary branches per plant and number of siliquae per plant, additive genetic components were important while for days to 50% flowering, days to 80% maturity, number of primary branches per plant, siliqua length and seed yield per plant. The components of variation due to dominance effect of the gene (H_1) was greater than D, suggesting the preponderance of dominance type of gene action for days to 80% maturity, number of primary branches per plant, seeds per siliqua, seed yield per plant and thousands seed weight (g). Dominant and recessive genes were unequally distributed in the parental genotypes for all the characters studied. These genotypes could be effectively used in future for developing varieties of rapeseed (*Brassica napus* L.)

Chapter 6

CONCLUSION AND RECOMMENDATION

CONCLUSION AND RECOMMENDATION

The research work in this thesis which a 6x6 F_2 diallel population of *Brassica napus* excluding reciprocals was carried out with the aim of obtaining various genetic information on yield and yield contributing characters and, also of identifying the best parents and specific crosses.

The parental genotypes used in the study are Nap-9905, Nap-9901, Nap-205, Nap-108, Nap-9908 and Nap-130 which are chosen for their genetic differences and diverse origin. Among parents, the parent Nap-9908 showed best performance for number of siliquae per plant, seeds per siliqua and seed yield per plant, Nap-205 for plant height, Nap-9901 for days to 80% maturity, Nap-108 for number of primary branches per plant, Nap-9905 for siliqua length and parent Nap-130 for thousands seed weight i.e. all the parents highly contribute to yield. Out of fifteen crosses, Nap-9908 x Nap-9901 for number of siliqua per plant, Nap-9901 x Nap-205 for siliqua length, Nap-9901 x Nap-205 for seeds per siliqua, Nap-9905 x Nap-205 for seed yield per plant showed the best performance.

According to investigation, there are some recommendations as follows:

- Yield potentiality of *Brassica napus* is high but high rate of siliqua shattering is occurred. Further research is necessary for improving siliqua shattering problem.
- Brownish black or black seed coat gives lower oil content compared with yellow seed coat. Future effective research is necessary to improve this character.
- More and more research is necessary for variability, combining ability, heterosis and, also gene analysis for improvement.
- Among the genotypes, the parents had high GCA and SCA effects and higher percentage of heritability should give maximum emphasis. These genotypes could be effectively used in future for developing varieties of rapeseed (*Brassica napus* L.)
- Further research is necessary for shorter maturity period to fit in the existing cropping pattern of Bangladesh.

Chapter 7

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REFERENCES

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APPENDICES

APPENDIX

Appendix I: Monthly record of year temperature, rainfall, relative humidity and Sunshine of the experimental site during the period from October 2010 to March 2011

Year	Month	Air temperature (°c)			Relative humidity (%)	Rainfall (mm)	*Sunshine (hr)
		Max.	Min.	Mean			
2010	October	31.4	23.8	27.6	77	320	5.7
	November	29.0	19.9	24.45	69	111	5.5
	December	25.8	15.0	20.4	73	00	5.6
2011	January	24.7	12.5	18.6	67	00	5.8
	February	27.2	16.8	22	67	31	5.8
	March	31.5	19.7	25.6	55	12	8.3

*Monthly average
Source: Bangladesh Meteorological Department (Climate division)- Agargoan, Dhaka

Appendix II: Physical and chemical characteristics of initial soil (0-15 cm depth)

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

Appendix III:Total cultivated area and production of oil seed crops of Bangladesh from 2001-2002 to 2006-2007

Name of crops	2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007	
	Area	Prod^n.	Area	Prod^n.	Area	Prod^n.	Area	Prod^n.	Area	Prod^n.	Area	Prod^n.
Rape and mustard	749	233	735	218	690	210	597	191	536	183	-----	188
Til	91	22	96	25	96	25	96	37	76	39	-----	29
Linseed	11	3	11	2	11	3	12	3	34	8	-----	8
Groundnut	64	30	66	34	64	34	71	39	73	38	-----	46
Coconut	76	87	77	88	96	133	13	907	22	325	-----	-----

Note : Area calculated in thousand acres, prod^n (production) are in thousand metric ton

Source : Agricultural statistics, BBS (2008)

Statistical pocket book Bangladesh, 2008.