GENE ACTION AND HETEROSIS FOR QUANTITATIVE TRAITS IN *Brassica rapa* L.

MST. SHAMIMA YESMIN

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

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GENE ACTION AND HETEROSIS FOR QUANTITATIVE TRAITS IN *Brassica rapa* L.

BY

MST. SHAMIMA YESMIN

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Approved By:

……..……	**….. ……**
Prof. Dr. Md. Harun-Ur-Rashid	**Prof. Dr. Md. Abdur Rahim**
Supervisor	**Co- Supervisor**

…….

Dr. Shahanaz Parveen

Chairman

Examination Committee

Dr. Md. Harun-Ur-Rashid
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207
Mob: +8801712-612417
E-mail: sumonsau@gmail.com

CERTIFICATE

This is to certify that thesis entitled, **"GENE ACTION AND HETEROSIS FOR QUANTITATIVE TRAITS IN *Brassica rapa* L."** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **MST. SHAMIMA YESMIN**, Registration No. **16-07120** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2022
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Harun-Ur-Rashid)
Supervisor

Dedicated
To
My Honorable Teachers
&
Beloved Parents
Whose Blessings Always
With Me

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SOME COMMONLY USED ABBREVIATIONS

ABBREVIATION	FULL WORD
%	Percentage
Agric.	Agriculture
ANOVA	Analysis of variances
AEZ	Agro-Ecological Zone
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
BP	Better Parent
BL	Beak Length
Via	By the way
cm	Centimeter
CV	Check variety
CV%	Coefficient of variation
df	Degrees of freedom
DFF	Days to First Flowering
D50%F	Days to 50% flowering
DAS	Days After Sowing
DM	Days to maturity
etc.	Etcetera
σ^2e	Environmental Variance
e.g.	For example
et al.	and others
FAO	Food and Agricultural Organization
F1	First Filial Generation
g	Gram
σ^2g	Genotypic Variance
GCV	Genotypic Coefficient of Variation
GCA	General Combining Ability
HYV	High yielding varieties
H^2b	Heritability in Broad Sense
i.e.	That is
viz.	For example
J.	Journal
LSD	Least Significant Difference
MoP	Muriate of Potash
MP	Mid parent
m	Meter
m2	Square Meter
No.	Number
ns	Not Significant
NPB	Number of primary branches per plant
NSB	Number of secondary branches per plant
PCV	Phenotypic Coefficient of Variation
σ^2p	Phenotypic Variance

SOME COMMONLY USED ABBREVIATIONS (CONT'D)

ABBREVIATION	FULL WORD
RCBD	Randomized Complete Block Design
SAU	Sher-e-Bangla Agricultural University
SCA	Specific Combining Ability
SL	Siliqua Length
SYP	Seed yield per plant
t/ha	Tonne per Hectare
TSP	Triple Super Phosphate

GENE ACTION AND HETEROSIS FOR QUANTITATIVE TRAITS IN *Brassica rapa* L.

ABSTRACT

The experiment was carried out to evaluate the seven parents and 21 F_1 hybrid that came from 7×7 half diallel cross of *Brassica rapa*, excluding reciprocals, for twelve yield and yield contributing attributes. The half diallel mating procedure was done during Rabi season 2021-2022 to develop 21 F_1 hybrids. A set of 7×7 half diallel cross (excluding reciprocals) of *B. rapa* along with their parents were evaluated to estimate genetic variability, correlation among the characters, path coefficient analysis, heterotic effects and general and specific combining ability of parents and crosses respectively at Sher-e-Bangla Agricultural University research field during Rabi 2022-2023 at Randomized Complete Block Design with three replications. Results revealed that all the observations exhibited high heritability in broad sense. Correlation revealed that at phenotypic level, plant height, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant showed positive and significant correlation with yield, while plant height and number of siliquae per plant showed significant positive association at genotypic level. Path analysis revealed that days to first flowering (0.049), days to 50% flowering (0.745), number of primary branches per plant (0.305), number of siliquae per plant (2.224), siliqua length (0.022), beak length (0.342), number of seeds per siliqua (1.734) and thousand seeds weight (0.821) has direct positive effects towards yield. Higher σ^2sca than σ^2gca was reported for all the characters, indicating non-additive gene action prevailing for the inheritance of the traits. The parental lines P5 and P6 were reported best general combiner for earliness, where P2 act as for dwarfness and P5 for yield. Among the hybrids, V15 (P3×P7), V3 (P1×P4) and V13 (P3×P5) found as best specific combiner for early maturity where V10 (P2×P6), V11 (P2×P7), V21 (P6×P7) and V7 (P2×P3) found best specific combiner for dwarfness. The crosses V2 (P1×P3) and V18 (P4×P7) found as best specific combiner for yield. In heterosis analysis, the hybrids V15 (-16.49%), V13 (-24.77%) and V19 (-16.49%) showed higher magnitude of negative heterosis over mid-parent, better parent and check variety, respectively for days to first flowering. For days to maturity, V14 (P3×P6) exhibited highest negative heterosis over mid parent (-7.98%), better parent (-10.69%) and check variety (-5.46%). For plant height, V10 (P2×P6) showed highest negative heterosis over mid parent (-16.41%), better parent (-17.91%) and check variety (-14.38%), which can be used for development of dwarf variety. For number of primary branches per plant, V7 (P2×P3) and V17 (P4×P6) represented significant amount of positive heterosis over mid parent, better parent and check variety. V18 exhibited significant positive heterosis for number secondary branches per plant over mid parent and better parent. The highest heterotic advantage for number of seeds per siliqua over mid parent and better parent was observed by V10 (P2×P6). The most heterotic hybrids over check variety for seed yield per plant were V4 (28.14%) which was followed by V2 (27.20%) and V13 (25.33%). Vr-Wr graph showed over dominance for days to maturity, number of primary branches per plant, number of seeds per siliqua and thousand seed weight, and thus heterosis breeding is important to improve those traits.

CHAPTER I

INTRODUCTION

Brassica rapa L. is an important rabi season oilseed crop in Bangladesh under the family Brassicaceae. *B. rapa* is a herbaceous cross-pollinated crop and commonly referred to as field mustard or rapeseed. Cytologically field mustard is a diploid (2n = 20) and originated in two separate regions: Asia and Europe (Zhao *et al*., 2005). A variety of mustard and rapeseed are grown in Bangladesh. Oleiferous *Brassica* holds three major species viz. *B. rapa* L. (AA, 2n = 20), *B. juncea* Czern and Coss (AABB, 2n = 36) and *B. napus* L. (AACC, 2n = 38). *B. juncea* (Indian mustard/Rai), *B. nigra* (black mustard), and *B. carinata* (Ethiopian mustard) are classified as mustard whereas, *B. rapa* and *B. napus* are considered as rapeseed (Yarnell, 1965).

There are mainly seven oilseed crops grown in Bangladesh. Mustard alone accounts for nearly 70% of the oilseed land in Bangladesh among the oilseed crops grown there. In Bangladesh total annual demand for edible oil and fat is around 3 million tonnes. Bangladesh imports around 90% of its annual demand for edible oil (Hassan, 2022). In Bangladesh the area under mustard cultivations are 330769.23 ha and the productions are 410000 mt (BBS, 2022).

Rapeseed and mustard oil is considered as a good source of vitamin A, D, E and K which are fat soluble and contains higher energy level. With that rapeseed seeds also contains almost 25% protein and 42% oil (Khaleque, 1985). The primary source of fatty acids, which are necessary for human nutrition, is edible vegetable oil. In Bangladesh, the most commonly consumed edible vegetable oils are sesame, groundnut, mustard, soybean, and sunflower. However, it is not possible for any vegetable oil solely to fulfill the requirement of the lipid soluble nutrients recommended by health agencies.

Rapeseed oil has anti-inflammatory properties as it contains a high level of selenium and magnesium (Akter, 2020). It also has the ability to lower body temperature and stimulate sweat glands. Furthermore, mustard oil is applied to relieve the discomfort associated with sprains and arthritis in the muscles (Sood *et al*., 2010). In terms of its health benefits, *Brassica* oil is advantageous. It contains oleic acid, which is excellent for cooking oil because of its thermostability, and linoleic acid, which is desirable for nutritional reasons (Vles,1989). The fatty acid's oxidative stability makes it useful for

a variety of industrial applications (Scarth,1999). In Bangladesh, native mustard oil seeds have erucic acid levels of 40–50% (Mortuza *et al.*, 2006). According to animal studies, feeding animals a diet high in erucic acid in mustard oil causes a number of degenerative alterations in their heart and skeletal muscles. Erucic acid content needs to be under 2% to be accepted internationally (Gami *et al.*, 2016).

Bangladesh's edaphic and climatic conditions are ideal for growing mustard and rape seeds (Haque *et al.*, 1987). Mustard and rape are Bangladesh's two most important oil crops, though farmers usually grow them on less productive land with little management and little investment. The maximum cultivars that they would cultivate are smaller and have brown seeds (2–2.5 g/1000 seed). According to Chakraborti (2020), yellow seeds are practically thinner in the seed coat and have a 1-2% higher oil content than brown seeds of the same size. Approximately 75% of Bangladesh's mustard crop is covered by *B. rapa* alone (Wahhab *et al.*, 2001). Tori 7 is a considered as a popular short durated mustard variety. There isn't a better short-duration *B. rapa* variant to take the place of Tori-7. Currently, though, producers are encouraged to grow the enhanced Tori and BARI Sarisha 14 and BARI Sarisha 15 types. The aforementioned scenario suggests that in order to meet the nation's demand for edible oils by expanding output, efforts should be made to produce short durated, high yielding cultivars with a higher oil percentage in seed and tolerance to biotic and abiotic challenges. The enhanced variety needs to fit into the intended cropping pattern, i.e. T. Aman-Mustard-Boro.

In the recent days, there is a huge hue and cry about unprecedented price hike of soybean oil. Bangladesh can easily become a self-dependent country in edible oil production. In the good old days, even during in 1970s, mustard oil used to be main cooking oil here. Almost 30 to 40 per cent oil present in the improved mustard seeds depending on the variety, climate and production condition (Rahman *et al.*, 1993). The overall production of mustard and rapeseed is much more below the requirement in Bangladesh. One of the most important reasons behind this is lack of genetic advancement of the crop keeping pace with the growing demand. Heterosis and combining ability analysis provides a significant role in genetic improvement of crop plants (De *et al.*, 2009). In case of mustard improvement of yield as well as oil content are the major breeding objectives.

Information of variability, heritability along with genetic advance will help to fix the real potentialities of the genotypes. For efficient selection, estimation of the aforementioned parameters is pre-requisite. Heritability estimates followed by genetic advance is helpful in ascertain the reliability of the traits for selection. High heritability coupled with low genetic advance can be improved by intermating superior genotypes of the concerned segregating populations which was developed from combination breeding (Evangelin *et al.*, 2023).

Correlation coefficient reflects some ideas about yield and yield contributing characters. But the analysis of correlation does not meet the purpose solely, because it is not able to affects overall traits relating to indirect effects on seed yield. In this context, path analysis is an important tool. Thus character association followed by path analysis provides valuable information of yield contributing characters and plant breeder can practice selection using this information.

Intra-specific hybridization is a possible way for the improvement of rapeseed by combining and selecting for the desirable character(s). For this, the vital aspects are the choice of parents for hybridization program and selection of best lines from hybrid progenies. Information on heritability of materials in the very early generations, type of gene actions involved and different degrees of heterosis is very useful to select progenies among the hybrid populations. Heterosis breeding technique is one of the most successful and reliable breeding means being employed for the genetic improvement of crop varieties. Information about probable gene action and identify the desirable gene action from that was possible via heterosis analysis. A prerequisite of successful hybrid breeding work of rapeseed and mustard is the availability of heterotic germplasm. Heterotic investigations can provide basic information for the exploitation of valuable cross combinations from the breeding program (Ahmad *et al.*, 2009) and for this reason, the achievement of heterosis has become a major objective for the breeders of canola and the related species. Although mustard and rapeseed contribute a major proportion of oil requirement in our country, we have a limitation to accelerate total yield due to lack of poor performance of our cultivated varieties. So, we have ample opportunities to improve our cultivated varieties by exploiting heterosis for different yield and yield contributing characters. Increased yield, capacity for reproduction, adaptability, resistance to disease and insects, overall vigor, quality, etc.

are possible outcomes of heterosis. Therefore, determining prospective parents and promising cross breeding partners, as well as estimating heterosis for various yield and yield-contributing traits of rapeseed (*B. rapa* L.), are necessary steps towards creating high yielding varieties (HYV). Immense analysis of the combining ability which involved in the inheritance of quantitative characters and in the phenomenon of heterosis is prerequisite for the evaluation of various possible breeding procedure (Allard, 1960). Several researchers have attempted to increase seed quality, seed yield, and other yield-related aspects of the *Brassica* oil seed crop. Numerous authors used various techniques to increase the quantity and quality of *Brassica* seed production (Singh *et al.*, 2003 and Gami *et al.*, 2012). Different sorts of gene activity and combining ability have also been reported by Gami and Chauhan (2013) and Patel *et al.* (2013) in various sets of material studies. Combining ability experiments highlighted the dominant role of GCA for yield and most yield components, highlighting the importance of additive gene action (Wos *et al*., 1999). While Pandey *et al.* (1999) found evidence of non-additive gene action, they also found a significant SCA effect on yield and yield components. The assessment of variance and combining ability effects have been utilized to evaluate the breeding value of the parents using the various mating designs.

Diallel analysis is a systematic approach for identification of superior parents and cross combinations, which are the basic materials on which the success of a breeding program basis. It is widely used in crop plants for testing the performance of genotypes in hybrid combination and also for estimating the nature and extent of gene action which are involved in controlling quantitative characters (Griffing, 1956). Diallel mating design provides reliable information on the components of variance and on GCA and SCA variances and their effects. Combining ability analysis plays significant roles in determining the type of gene action involved in the inheritance of a character. GCA variances indicated additive type of gene actions where SCA variances revealed non-additive type of gene actions, originating mainly from dominance and epistasis deviations (Malek *et al.*, 2004). Consequently, it aids in the selection of appropriate breeding practices as well as suitable parents for hybridization (Hayman, 1954 and Griffing, 1956).

Therefore, the present studies was undertaken -

1. To identify potential parents and promising cross-breeding partners to develop high yielding *Brassica* genotypes
2. To explore the nature and extent of gene action that controls the traits
3. To estimate heterosis for different yield contributing traits of *Brassica rapa* L.

CHAPTER II

REVIEW OF LITERATURE

Diallel mating design has been extensively used in breeding of both self and cross pollinated species to understand the nature and magnitude of gene action involved in the expression of quantitative traits (Gami, 2016). In *Brassica* breeding, several researchers have contributed research works on heterosis over mid parental values or better parental values and combining ability by their work. To understand gene effects of yield and yield attributes combining ability studies are frequently utilized which helps in formulating proper breeding methodology. Evaluation of heterosis is a vital factor in developing a high yielding variety or cultivar. It also helps to find out the breeding potential of parents as well as different cross combinations which helps in the advancement of breeding programme (Chakraborti, 2020). The diallel analysis provides information of the genetic control of a set of parents in the very early generation (Jinks, 1954). A large volume of literature are available on these issues. Therefore, relevant information available in the literature pertaining to the combining ability, heterosis of rapeseed and mustard are reviewed in this section.

2.1 Genotypic and phenotypic variability

Afrin *et al.* (2016) conducted an experiment in order to study the variability among the fifteen F_4 population of *Brassica rapa* considering different morphological attributes. Highly significant variation was found among the genotypes for almost all of the characters under studied.

Parvin (2015) undertaken a research work with 30 BC_1 F_4 genotypes of *Brassica napus* L. to study the genetic variability. Significantly variable genotypes were found for most of the characters under study. Genotypic variances were comparatively lower than the phenotypic variances for all studied characters. PCV were higher than the GCV for all the studied characters.

Iqbal *et al.* (2014) worked on ten indigenous varieties of *Brassica rapa* with eight important yield contributing characters to study variability. They showed highly significant differences in almost all traits except siliqua width, which showed non-significant variation.

Khan *et al.* (2013) evaluated thirty F_7 segregating lines and two parents of *Brassica rapa* L. to study variability. The result showed significant variation among all the genotypes for all the characters except thousand seed weight. Plant height showed highest genotypic, phenotypic as well as environmental variances while lowest result were observed in length of siliquae. High heritability was observed in thousand seed weight, number of secondary branches per plant, seeds per siliquae and siliquae length which is coupled with low genetic advance in percent of mean. On the other hand, moderate heritability along with high genetic advance was observed in number of siliquae per plant.

Ara (2010) conducted an experiment where eight F_2 and eight F_4 populations were generated through inter-varietal crosses along with three check variety of *Brassica rapa* to study the variability. The result showed phenotypic variances were higher than corresponding genotypic variances. Days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, length of siliquae, seeds per siliqua, 1000-seed weight and yield per plant showed least significant differences between phenotypic and genotypic variances. The value of GCV and PCV indicated that there was least variation present among most of the characters under studied.

Mondal *et al.* (2022) conduct an experiment on genetic variability of twenty genotypes of Indian mustard (*Brassica juncea*) for 20 characters. They reported number of siliquae per plant, harvest index (%), seed yield per plant and number of secondary branches exhibited high to moderate GCV and PCV indicating the high amount variation present among the genotypes under studied. The value of PCV is higher than that of GCV suggested that the apparent variation is not only due to genotype but also due to the influence of environment.

Akoju *et al.* (2020) was made an experiment on *Brassica juncea* in order to estimate the genetic variability, trait association and path coefficient analysis among the Indian mustard genotypes during rabi, 2019. Highly significant was observed for all the characters studies indicating the existence of ample variability among the genotypes studied. The high GCV and PCV observed for number of siliquae per plant and secondary branches per plant indicated the influence of environment.

Dubey *et al.* (2019) conducted an experiment on phenotypic and genotypic coefficient of variation, correlation and path analysis, heritability and genetic advance (GA) for thirteen characters in seven genotypes of Indian mustard (*Brassica juncea*). Genetic variability indicated that the PCV was greater than GCV for all the traits that was majorly due to the influence of environment.

Bano *et al.* (2021) was conducted an experiment on 57 genotypes of brown sarson (*Brassica rapa*) during rabi 2019-2020 in order to estimate the genetic variability, genetic advance, heritability and correlation analysis. Higher amount of PCV and GCV as well as high values of broad sense of heritability and genetic advance was reported in no. of siliqua per plant, no. of seeds per siliqua followed by seed weight.

2.2 Heritability and genetic advance

Evangelin *et al.* (2023) carried out an experiment with 10 genotypes of Indian mustard for 11 quantitative traits to study the heritability and genetic advance as percent of mean. The observations like, number of seeds per siliqua, number of primary branches per plant, biological yield per plant and harvest index exhibited high heritability coupled with high genetic advance as percent of mean. High heritability coupled with high genetic advance as percent of mean indicated that most likely the heritability is due to the additive gene effects and selection directly based on this trait would be effective.

Lakra *et al.* (2020) conducted an experiment with thirty genotypes of Indian mustard to study the genetic variability, where they reported high to moderate heritability with high to moderate genetic advance for the characters- number of seeds per siliqua and number of primary branches per plant.

Khan *et al.* (2019) was conducted an investigation in order to study the correlation and path analysis of thirteen quantitative traits in 12 Indian mustard (*Brassica juncea*) where among the observations biological yield per plant, siliqua on main raceme, number of seeds per siliqua and grain yield per plant exhibited higher heritability along wih high genetic advance.

Kimbonguila *et al.* (2019) was investigated seven genotypes of Indian mustard (*Brassica juncea*) to study the genetic variability and degree along with direction of association between yield and yield contributing characters. Higher percentage of

heritability with high genetic advance as percent of mean was reported for plant height, yield per plant (g) and vitamin C content which indicated additive gene effects for controlling their expression and inheritance.

Shekhawat *et al.* (2014) conducted an experiment with 60 genotypes of Indian mustard (*Brassica juncea*) for thirteen quantitative characters which revealed high heritability along with high genetic advance for number of secondary branches per plant, number of siliquae per plant and seed yield per plant. The high estimates of heritability coupled with higher genetic advance indicated that inheritance of these traits is mainly due to the additive gene effects.

Muhammad and Waluyo (2019) reported high heritability in the observations viz. cotyledons, fresh weight, age of seed harvest, number of leaf consumption, number of siliquas per plant, length of siliquas, width of siliquas and number of seeds per siliqua by investigating on 57 genotypes of Indian mustard.

Dash (2007) investigated on 50 genotypes of toria for 14 yield component to study heritability for yield and yield attributing traits in (*Brassica rapa* L. var. toria). Higher estimates of heritability in broad sense coupled with high genetic advance as per cent of mean were reported for leaf area index, specific leaf weight and secondary branches per plant.

Khulbe *et al.* (2000) conducted an experiment on Indian mustard to study heritability and genetic advance for yield and its components. The findings revealed maximum variation was found in seed yield. All the characters exhibited high heritability with high or moderate estimates of genetic advance except oil content, indicating the role of additive gene action in conditioning the traits. Whereas non-additive gene action appeared to influence the expression of days to maturity, while on oil content environment had a major influence.

Shaukat *et al.* (2015) evaluated eight *Brassica napus* genotypes to study the heritability as well as genetic advance. High broad sense heritability estimates were appeared for plant height, primary branches per plant, pods per main raceme, seeds per pod, 1000-seed weight while pods per plant, pod length and seed yield per plant showed moderate heritability ranges.

Sultana (2015) performed an experiment by using sixty two F_4 genotypes of *Brassica napus* L. and reported highest value of heritability for number of secondary branches followed by seed yield per plant whereas days to maturity showed the lowest value of heritability.

2.3 Correlation analysis among variables

Analysis of correlation among different traits is important in breeding program. The correlation coefficient is a numerical measure of some interrelation to detect the direction and strength of the relationship between the relative movements of two or more variables. The range of correlation coefficient between -1.0 and 1.0. A calculated number higher than 1.0 or less than -1.0 indicates an error in the measurement of correlation. A correlation of -1.0 exhibits a perfect negative correlation, whereas a correlation of 1.0 shows a perfect positive correlation. A correlation of 0.0 exhibits no relationship between the movements of the two variables. Yield being the most important character is governed by polygene and it is highly influenced by the environment. So, selection based on only yield itself is bootless. When selection is made to develop any character highly correlated with yield, it affects some other correlated characters simultaneously. Therefore, knowledge regarding the association of character with yield and themselves provide a guideline to the plant breeder to improve through selection. Most of the cases it was obvious that genotypic correlation coefficients were higher than their respective phenotypic ones suggested that these traits were strongly correlated genetically and the environment less influenced the phenotypic expression of these traits. In many cases, the phenotypic correlation coefficient was higher than their corresponding genotypic correlation coefficient suggesting that both environmental and genotypic correlation performed in the same direction and finally maximized their expression at the phenotypic level.

Lavanya *et al.* (2022) conducted an experiment with fifty mustard genotypes to study the correlation and path coefficient analysis of twelve yield contributing characters. Correlation analysis revealed that seed yield per plant is positively and significantly correlated with harvest index followed by number of secondary branches per plant and number of siliquae per plant at genotypic level. Whereas days to 50% flowering, plant height, number of primary branches per plant and number of seeds per siliqua had direct negative effects on seed yield per plant both at genotypic and phenotypic levels.

Siddique *et al.* (2017) carried out an experiment to study correlation using six genotypes of *B. campestris* L. Results revealed that for plant height genotype S-9 (check) exceeded all other genotypes. Correlation results were positively significant among plant height with pods/plant, height with a yield of a single plant, pods per plant with seed index, days to flower with seed index, days to flower with a yield of a single plant, pods per plant with single plant yield, seed index with single plant yield. The negative and significant relationship was found between plant height and seeds per pod, branches per plant and ripeness days and pods per plant and seeds per pod.

Halder *et al.* (2016) conducted an experiment to study the interrelationship among the characters of eleven advanced lines and three popular check varieties of *B. rapa* L. on yield. The genotypic correlation coefficient observed that yield per hectare had a positive and highly significant correlation with days to first flowering, days to 80% flowering, and the number of primary branches per plant. In comparison, days to 50% flowering and length of siliqua were negatively correlated with yield.

Mahak *et al.* (2004) conducted an experiment on correlation for eight genotypes of Indian mustard. Where they recorded seed yield per plant showed the positive correlation with the number of primary branches per plant, length of the main raceme, 1000-seed weight and oil content. The recommendation was that the selection should be applied to the relative traits to improve seed yield in Indian mustard.

Rauf (2016) reported both significant and non-significant differences were observed while comparing correlation coefficient values of eleven variables on seed yield. He got genetic correlation coefficient was higher than phenotypic correlation coefficient of the concerned characters.

Paul (2017) carried out an experiment and observed that, seed yield per plant has significant positive correlation with days to 50% flowering (0.366) at genotypic level and siliquae per plant (0.746 and 0.643) at both genotypic and phenotypic levels.

Shakera (2014) conducted an experiment with twenty F_3 and F_4 populations obtained through inter-varietal crosses along with three check variety of *B. rapa* L. to study the correlation between pairs of different characters to select high yielding and early maturing plants. Yield per plant showed a significant positive correlation with plant

height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant and thousand seed weight.

Abideen *et al.* (2013) experiment on eight genotypes of *B. napus* and the result represented positive phenotypic correlation with plant height, pod length and seed yield. A significant positive association was also exhibited in seed yield per plant and pods per plant.

Tahira *et al.* (2011) conducted an experiment with ten variety of *B. juncea*, and the result represented a correlation among the different characters. The highest phenotypic correlation was observed between plant height, branches per plant, siliqua length and seeds per siliqua. Seed yield was only significantly associated with plant height and siliqua length. Plant height, branches per plant, siliqua length and thousand seed weight were associated with yield per plant at genotypic level. A highly significant positive genetic correlation was observed between plant height and branches per plant, siliqua length and seeds per siliqua.

Kashyap and Mishra (2004) experimented with studying correlation among 11 morphological characters of *B. campestris* Var. Toria using 16 genetically diverse genotypes and reported that seed yield showed a significant and positive correlation with plant height, branches per plant, siliqua per plant, seeds per siliqua and 1000 seed weight. He observed that these characters were also significantly and positively correlated with each other, suggesting the opportunity for their simultaneous improvement through selection.

Akbar *et al.* (2007) evaluated eight advanced lines and two check variety of *Brassica junea* and reported that siliqua per plant had strong and positive association with the seed yield which was followed by plant height while thousand grain weight showed non-significantly negative correlation. Significantly negative correlation was present in siliqua per plant and primary branches per plant.

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica* species to estimate correlation and reported highly significant positive correlation of yield per plant with number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

Tusar *et al.* (2006) observed that seed yield per plant was positively and significantly associated with plant height and total dry matter production. The number of siliquae per plant, number of branches per plant, crop growth rate during 60-75 days after sowing and 1000-seed weight were also positively associated with seed yield.

Zahan (2006) studied correlation and reported that yield/plant had highly significant positive association with plant height, length of siliqua, siliquae/plant and seeds/siliquae but non-significant negative association with days to 50% flowering, days to maturity.

Meena *et al.* (2020) investigated on Indian mustard to study the correlation and path co-efficient analysis. In the study highest positive correlation were observed between biological yield per plant and seed yield per plant.

2.4 Path coefficient analysis

The path analysis used to determine the direct and indirect contribution of traits towards the yield. Wright (1921) developed and described it as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components. The association between the various observations in rapeseed and mustard and their direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

Lakra *et al.* (2020) conducted an experiment with thirty genotypes of Indian mustard to study the path coefficient analysis. The path co-efficient analysis revealed that days to 50% flowering, plant height and seed yield per plot had positive direct effect on seed yield per plant which suggest that direct selection can be done for the concerned characters for the improvement of yield.

Ray *et al.* (2019) evaluated nineteen genotypes of Indian mustard to study path analysis. Path analysis revealed days to 50% flowering, number of primary branches per plant, plant height, number of siliquae per plant, biological yield per plant and harvest index had positive direct effect on seed yield per plant.

Uddin *et al.* (2013) experimented on seven parent and twenty one F_2 progenies of *Brassica rapa* to study path coefficient and reported that days to 50% flowering,

number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliquae length, seed per siliquae and thousand seed weight showed the direct positive association with seed yield per plant. On the other hand, the plant height and days to maturity had direct negative relationship.

Goswami *et al.* (2005) conducted experiment on variability analysis for number of secondary branches, siliquae on main shoot, seeds per siliqua, 1000-seed weight, and seed-yield per plant where the results exhibited that the coefficient of variation of pods per plant, filled grains per pod and 1000-grain weight on yield per plant were significant and there was considerable variability for the aforementioned character.

Sudan *et al.* (2004) conducted an experiment on Indian mustard to study path co-efficient. From this study number of primary branches was the most important character as it showed highest direct effect on seed yield. Characters like- days to flowering, 1000 seed weight and number of seeds per siliqua had highest positive effect on yield via other character.

Hasan *et al.*, (2014) worked on nine genotypes of *Brassica napus* to study path co-efficient analysis. Path coefficient revealed that the days to flowering, days to maturity, seeds/siliqua, 1000 seed weight, and seeds/plant had direct positive contribution towards seed yield per plant. For *Brassica* breeding seed per plant was the variable with maximum potential of selection for seed yield improvement because this trait possessed high heritability, highly significant positive correlation and maximum positive direct effects with yield.

2.5 Combining ability analysis

Sprague and Tatum (1942) defined the term general and specific combining ability. According to them "The term 'general combining ability' is used to designate the average performance of a line in a series of hybrid combinations. The term 'specific combining ability' is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved" (Adhikari *et al.*, 2018). The information obtained from combining ability analysis helps in partitioning the total genetic variation into two different component, one is general combining ability of parents and the other is

specific combining ability of the crosses. This information is useful to determine the nature and magnitude of gene action controlling different characters.

Griffing (1956) proposed a procedure for diallel analysis which makes provision for non-allelic interaction. This approach permits mean measurement of a cross is fragmented into two major components, a part from a general mean (p) and an environmental component, (i) the contribution of the parents, the general combining ability (GCA) effect analogous to main effect of a factorial designs, and (ii) the excess over and above the sum of the two GCA effects called the specific combining ability (SCA) effect, analogous to an interaction effect of a factorial design. The diallel approach has been extensively used, in cross pollinated crops.

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

Chowdhury *et al.* (2004) observed and investigate the nature and extent of combining ability of parents and crosses (F_1 s) in a 7 x 7 diallel cross analysis in turnip rape for seed yield, different yield contributing characters and oil content. GCA variances were observed higher than those of SCA variances for all the characters except siliquae per plant, seeds per siliqua and seed yield per plant. Maximum crosses showed high SCA effects for seed yield that involves high x low, average x average and average x low GCA parents.

Yadava *et al.* (2012) conducted an experiment in line × tester design which involves 14 lines and 5 testers and reported that both additive and non-additive gene actions were important in controlling yield-contributing traits. Among the parents, Pusa Mustard 25 was identified as best general combiner. Significant and positive SCA effects were observed for seed yield in 17 hybrids, 1000-seed weight in nine hybrids, number of siliquae on main shoot in nine hybrids, number of primary branches in six hybrids, point

to first siliqua in six hybrids, main shoot length in five hybrids and number of secondary branches in four hybrids; and significant negative SCA effects for point to first branch in four crosses and plant height in two crosses. Ten hybrids exhibited >15% heterobeltiosis, highly significant SCA effects and higher per se performance.

Sharma *et al.* (2008) conducted an experiment to estimate the combining ability and reciprocal effects of Toria (*Brassica rapa* L.) in 8 x 8 full diallel set for yield and its components along with protein and oil content. Open-pollinated and self-incompatible genotypes were bud pollinated to get the parental seed before inclusion into diallel mating. Significant SCA variances observed for all the traits except for oil content, while the GCA variance were non-significant for plant height, siliqua length and oil content and significant for rest of the characters. However, significant non-additive gene action was observed for all the traits as reflected by the ratio of GCA and SCA variances. Reciprocal variances were greater than both the GCA and SCA variances for plant height, number of primary branches/plant, siliquae on main shoot, siliquae length and seeds/siliquae indicating importance of maternal effects for the expression of these traits. The maternal effect, reflected in most of the crosses involved good general combiner as female parent. For seed yield and yield contributing characters genotypes PT-30, PT-9701, PT-9600 and PT-9700 were found good general combiners along with high per se performances.

Kumar *et al.* (2018) conducted an experiment on Indian mustard where Line × Tester effect showed positive significance for all the characters except days to maturity, plant height, siliqua length, and test weight. Both general combining ability and specific combining ability effects showed significant differences. For most of the trait IC-597919 found to be good general combiner. The cross combinations namely, IC597879 × IC-571648 was found to be most emerging for yield/plant. On the basis of estimates of heterosis and per se performance, the cross IC-597879 × IC-571648 found to be most promising which is followed by IC-597919 × IC-335852 and IC-589669 × IC-338586 for seed yield/plant. The above best parents and best crosses can be used in future hybridization program and heterosis breeding respectively.

Gami *et al.* (2016) observed an experiment on diallel analysis excluding reciprocals that comprises ten parents and their hybrids. The experiment was carried out to identify the highly heterotic crosses and their relationship in terms of general and specific

combining ability (GCA and SCA) in Indian mustard in 2013-14. Analysis of variance for GCA and SCA show significant differences for all the traits. The ratio of GCA and SCA variances was below unity for all the characters except days to flowering, plant height and harvest index. Among 45 specific crosses, five crosses observed highest economic heterosis viz., SKM 815 x RGN-303 (30.26 %), GDM 4 x RGN303 (26.67 %), GDM 4 x RH-0555 (27.72 %), GDM 4 x RGN-282 (25.06 %) and GDM 4 x SKM 518 (18.63 %). For seed yield and its component characters parents GM 3, GDM 4, RH-0555 and RSK-29 were found good combiners. Parents RGN-303 and RSK-29 were good general combiners for oil content. Similarly, Parents GM 3 and RGN-282 were found good general combiner for oleic acid content.

Bhakal *et al* (2018) conducted an experiment on combining ability where 10 x 10 half diallel crosses were done in Indian mustard for ten quantitative traits that indicated preponderance of non-additive gene action for all the characters in both generations as well as under both the environmental conditions (E1& E2). Higher extent of GCA and SCA effects reveals the presence of both additive and non-additive gene action for the inheritance of various traits. The parent Vardan and RN-393 in F_1 generation and parent GM-3 and RGN-229 in F_2 generations were found good general combiners for seed yield per plant under both the environments. Cross PBR-357 x Kranti, CS-52 x GM-3 and Bio-902 x RGN-229 exhibit good specific cross combiner, among the cross combinations for seed yield under both the generations and environments.

Ahsan *et al* (2013) investigate Line × tester analysis where three testers and five lines of *Brassica napus* L used in the experiment. In this experiment combining ability and heterosis were estimated for plant height, number of primary branches, number of secondary branches, 1000-seed weight and seed yield per plant. Significant genetic variations was found among the genotypes both parents and their crosses because significant mean squares of treatments for yield components and seed yield were found. Significant value was observed for all the traits in Line × tester mean square.

Kumar *et al.* (2022) carried out an experiment where 7-parents/strains (Varuna, Vardan, Basanti, Maya, NDR-8501-19, PR-21-15 and TPM-1) and 21crosses were obtained via diallel mating design that excludes reciprocal crosses. 28 genotypes (21 F_1 + 7 parents) were observed for 11 traits viz. days to 50% flowering, days to maturity, plant height (cm), length of main raceme (cm), number of primary branches per plant, number of

secondary branches per plant, number of siliquae per plant, 1000-seed weight (g), protein content (%), oil content (%), and seed yield per plant (g). In case of oil content the variety Basanti and Varuna were found best general combiners. The cross Basanti x PR-21-15 were found to be best for SCA for yield whereas, NDR-8501-19 x TPM-1 for oil content.

Arifullah *et al.* (2012) reported that eight promising genotypes were crossed in 8×8 full diallel system to investigate combining ability. Data was recorded for seed yield and yield contributing characters. Significant general combining ability was found for most of the traits except plant height and siliqua length. Genotypes UCD-8/4, KJ-119 and BRS-2 found good general combiners for yield attributing traits. In case of number of primary branches and siliquae per plant best desired SCA showed by the crosses BRS-2 × UCD-8/4. Crosses S-9 × Canola Raya, Canola Raya × UCD-8/4, KJ119 × BRS-2, BARD-1 × NIFA Raya and BRS-2 × UCD-8/4 showed good positive SCA for respectively siliqua length, number of seeds per siliqua, 1000-seed weight and seed yield which involves at least one of the promising general combiner parents. It was reported that due to highly significant genotypic mean square and pre-dominant role of nonadditive type of gene action selection should be delayed up to sixth segregating generation for number of primary branches, number of siliquae per plant, siliqua length and seed yield while selection in early generations would be suitable for number of seeds per siliqua and seed weight due to prominent of additive gene action.

Mahanta an Barua (2020) conducted an experiment where combining ability, heterosis and maternal effects were analyzed for the yield and yield related traits in three Yellow sarson varieties (B9, YSH 401 and NRCYS 05-03) crossed in full diallel fashion. For Combining ability analysis of variances revealed that variation due to GCA, SCA and reciprocals were significant for maximum characters. From the analysis it can be proposed that genotype YSH 401 was the best general combiner while YSH401 x B9 was the earliest genotype and best cross exhibiting good mean performance for various yield traits as well as highly heterotic.

Inayat *et al.* (2019) evaluated the performance of eight mustard genotypes and their cross combination in F_2 population derived from 8x8 full diallel. All the F_2 population along with parents were sown and data were recorded for plant height, primary branches plant^{-1}, pods main raceme^{-1}, pod length, seeds pod^{-1}, and seed yield/ plant. Highly

significant (P≤0.01) mean values showed for all the genotypes for all the traits except primary branches plant^{-1}. Significant general combining ability (GCA) effects were found for all the traits whereas significant specific combining ability SCA effects recorded except seed yield plant^{-1}. Significant reciprocal effects were found for all the traits.

Mumtaz *et al.* (2015) used the Hayman and Jinks model to investigate gene action on quality-related attributes (oil percentange, glucosinolate, protein percentage, erucic acid, linolenic acid, oleic acid and moisture percentage) using four lines (UAF-11, Toria, BSA and TP-124–1) and their hybrids in a diallel mating design. All traits were found to be controlled by dominant gene action except oil percentage and linolenic acid. Non-allelic interaction (epistasis) was absent for all the traits.

Iqbal *et al.* (2003) reported 6x6 diallel cross experiment on F_1 generation of Brown mustard (*Brassica juncea* L.) in order to estimate the genetic control of some important agronomic and quality parameters. From the analysis of variance highly significant differences was found among parents and their hybrids in F_1 generation for all the characters. Non-significant variations was found for days to maturity. Additive type of gene action was found for the characters like days to flowering and erucic acid. Characters such as glucosinolate content, oil percentage and days taken to maturity were found dominant type of gene action.

Adhakari *et al.* (2018) investigated ten diverse parents of Indian mustard (*Brassica juncea* L. Czern and Coss) in a diallel fashion which is suitable for different sowing conditions, in order to identify superior parents for different yield contributing traits and their relationship in terms of general combining ability and specific combining ability (GCA and SCA). Combining ability analysis revealed the higher magnitude of 2 S and 2 D values and over-dominance for all the characters under study. The results clearly indicated preponderance of non-additive gene effect in governing the traits. For days to maturity PM-25, RB-57 and Maya were good general combiners. In case of plant height and maya exhibited good GCA effects. PRL2012-13, Divya-55, NRCHB-101 and DRMR-675-39 were found as good general combiners for seed yield per plant. NRCHB101×Divya-55, NRCHB-101×PRE-2011-15 and NRCHB-101×RMM-09-4 were found promising cross combinations for the early flowering. Highest SCA effect was expressed by Divya-55×RRN-778 for seed yield per plant which is followed by

PRE-2011-15×Maya, PRL-2012-13×Divya-55, NRCHB-101 × RMM-09-4 and DRMR-675 -39 × RRN-778.

Akbar *et al.* (2008) studied combining ability in a 5 x 5 diallel cross of (*Brassica napus*) where data were recorded from F_1 generation for plant height, primary branches plant^{-1}, silique length, siliques plant^{-1}, seeds silique^{-1}, 1000-seed-weight and seed yield plant^{-1}. Mean Squares for all the traits were found highly significant for all the characters except for 1000-seed weight. RBN 96040 exhibited good general combiner for all the traits under study. KS-75 found good general combiner for all the traits except plant height and primary branches plant^{-1}. Best specific combiner for all the traits studied was found in the cross "RBN 96040/RBN 96038" which is followed by "RBN 96038//DGL/SHIRALEE" which proved good specific combiner for most of the traits including seed yield plant^{-1}.

Nassimi *et al.* (2006a) estimated combining ability of eight *Brassica napus* L. genotypes viz., NUR1, NUR 2, NUR 3, NUR 4, NUR 5, NUR 7, NUR 8 and NUR 9 by using diallel crosses where ANOVA revealed highly significant differences (p=<0.01) for all the traits. Combining ability analysis revealed that, highly significant (p=<0.01) GCA found for characters like- 50% flowering, number of primary branches/plant and number of pods main/raceme, while non-significant values found for maturity and plant height. Highly significant SCA and RCA effects were found for all traits. Majority of the traits revealed higher GCA effects than SCA and RCA which indicates additive gene effects controlled the expression of these traits. Reciprocal crosses have higher potential than direct crosses for maturity as RCA effects were greater than GCA and SCA for maturity.

Gautam and Chauhan (2016) analyzed twenty lines and three testers in Line × Tester of the Indian mustard (*B. juncea* L. Czern & Coss.) cultivars to determine the effects of general combining ability (GCA) and specific combining ability (SCA) on plant height and yield components and seed yield. Significant line-tester variance for features like pods per plant and seed yield demonstrating a significant impact for non-additive genetic effects for regulating these qualities. Most of the crosses have a negative SCA impact on plant height which had a substantial negative or negative GCA influence on at least one parent.

Rameeh (2010) assessed 15 F_2 progenies of *Brassica napus* that were produced from a half diallel cross of six parents for their number of main axis, number of plants, length of pods, number of seeds per pod, weight of 1000 seeds per pod, grain yield, and oil content. For all of these variables, analysis found significant GCA and SCA, showing both additive and non-additive gene action. However, degree of dominance less than unity was reported for pod length and 1000-seed weight, indicating predominance effects of additive gene action.

Krzymanski *et al.* (1994) reported a diallel set of crosses between 10 best strains to compare F_1 and F_2 generations. In the first generation, SCA for seed yield was significant but not in the second.

Meena *et al.* (2015) investigated combining ability where mean squares due to lines, testers, and line × testers were highly significant for all the traits, except for the number of primary branches in testers and plant height, number of siliquae on main shoot and number of primary branches. Considerable amount of genetic variability was found in the experimental material as well as GCA and SCA were involved in the genetic expression of studied traits. The 17 high yielding cross combinations can further be exploited for their commercial utilization.

Azizinia (2011) studied combining ability of eight genotypes in a complete diallel design. Among the genotypes significant variance was reported for plant height, number of lateral branches, number of pods in the main raceme, number of seeds per pod, 1000- seed weight, seed yield and oil contents. Significant GCA and SCA was found for 1000-seed weight, oil contents and seed yield.

Tomar *et al.* (2015) studied combining ability effects where the parents namely; Vaibhav, Varuna, Durgamani and Kranti reported good general combiners for seed yield per plant (g). Crosses Vaibhav × Mathura Rai, Pusa Jai Kisan × Pusa Agrani and KR-5610 × Pusa Agrani were found good specific combiners for seed yield per plant (g).

Parmar *et al.* (2011) performed line × Tester analysis in order to estimate the general and specific combining abilities for days to flowering, days to maturity, number of primary and secondary branches, plant height and oil contents, from that they concluded that additive as well as non-additive genetic variance were important for controlling

these traits. Significant ratio of GCA variances over SCA variances proved that non additive gene action present for all the traits except for days to maturity.

2.6 Heterosis

Superiority of F_1 hybrids over both of its parents in relation to height, yield and so on is termed as heterosis. Several researchers worked on heterosis of mustard and reported varying extent of heterosis for yield and yield contributing traits. Both intra and inter-specific crosses of mustard showed considerable extent of heterotic effects.

Heterosis and combining ability information jointly considered more meaningful. According to Mahantesh (2006), the parental contribution to heterosis is primarily through additive gene action if the heterotic hybrids include both parents who have strong general combining ability effects.

Singh *et al.* (2003) observed that Varuna × Rohini (56.74%), Vardan × Rohini (53.43%), Varuna × RK-9501 (52.86%), Vardan × NDR-8501 (36.73%), Pusa Bold × Rohini (37.68%) and Varuna × NDR-8501 (32.54%) showed high heterosis for the characters seed yield per plant. The extent of inbreeding depression was very low in these hybrids, as a result these hybrids can be grown for 2 or 3 generations without losing yield.

Singh *et al.* (2022) carried out a study in order to estimate heterosis and gene action for physiological traits in Indian mustard (*Brassica juncea*) with 45 F_1 hybrids along with 10 parents. The ANOVA for combining ability revealed the significance of mean squares due to GCA and SCA for most of the traits. Out of 10 parents, only one parent EC 511664 exhibited significantly positive GCA effects while three F_1 crosses exhibited significantly positive SCA effects for thousand seeds weight.

Monalisa *et al.* (2005) reported that cross combination TM-4 × Local Yella, Varuna × TM-4, Varuna × NPJ-100 and Pusa Bold × Local Yella exhibited highest heterosis respectively for siliquae per plant, 1000-seed weight, seed yield per plant and oil content.

Aher *et al.* (2008) reported the extent of heterosis in *B. juncea* and observed medium heterosis for number of secondary branches, number of siliquae per plant and seed yield in *B. juncea* and found lower extent of heterosis in the remaining traits. For seed yield,

highest heterosis produced by RSK-87 × GM-2, SKM-95-85 × GM-2 and RSK-87 × Varuna.

Goswami *et al.* (2004) conducted an experiment on 30 crosses of Indian mustard in order to estimated heterosis for yield and yield components. The cross RH9404 x RH30 exhibited maximum heterosis for seed yield per plant (92.88 and 106.23%) during E1 and E2, respectively and also showed high heterosis for thousand seed weight. RH9617 x RWH1 and RH9621 x RWH1 crossed showed high heterosis for all the parameters tested.

Qi *et al.* (2000) looked into heterosis in hybrids of 6 *Brassica campestris* cultivars. They discovered that the hybrid's yields ranged from 46 to 125 kg. Some hybrids showed notable yield heterosis, with the highest value coming in at 96.4%. The majority of hybrids displayed lower levels of heterosis, with 1.4% being the lowest.

Meena *et al.* (2015) conducted an experiment on *Brassica juncea* to determine combining ability of parents and heterosis over better parents of 36 F_1's. Hybrids DRMR 2243/NRCHB 101, DRMR 2269/NRCHB 101, DRMR 2326/NRCHB 101, DRMR 2341/NRCDR 2, DRMR 2398/NRCHB 101, DRMR 2486/Ashirwad and DRMR 2613/NRCDR 2 showed highly significant SCA effects with higher extent of better parent heterosis as well as better performance for seed yield.

Mahto and Haider (2004) reported that crosses made in *B. juncea,* some parameters like - days to 50% flowering, days to maturity, plant height, primary and secondary branches per plant, harvesting index, 1000- seed weight, seed yield per plant and oil content exhibited high heterosis. High relative heterosis and heterobeltiosis was observed by the cross combinations RH-843 × RH 851 and RH 18 × BR-40 respectively, for most of the characters under study.

Meena *et al.* (2015) investigate Line × tester analysis of Indian mustard in order to elucidate combining ability and heterosis of 18 hybrids which were developed by crossing 9 lines with 2 testers. The hybrids were evaluated for twelve parameters, including days to flowering, days to maturity, plant height (cm), number of primary & secondary branches / plant, main shoot length (cm), number of siliquae on main shoot, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g), seed yield (kg/ha) and oil content (%). For most of the traits sufficient genetic variability among parents,

hybrids and parent vs. Hybrids were revealed by ANOVA values. High magnitude of better parent, standard parent and mid parent heterosis with highly significant SCA effects was exhibited by the cross combinations NRCHB 101× NPJ 112, RH-749× NPJ 112 and RH-406× RRN-727.

For the line x tester examination of 10 quantitative features in Indian mustard, Ghosh *et al.* (2002) used 29 promising female and seven male parents. The crosses combination YSRL-10 × Pusa bold as well as DBS-10 × Pusa bold demonstrated strong heterosis for seed yield and some of the features that contribute to yield.

Mahmood *et al.* (2003) conducted an experiment on *Brassica juncea* where five crosses viz., SMP 13-78 x Zem-I, DL 8 x Zem-I, SM 83000 x Zem-I, SML 31E x Zem-I, Pr 171-71 x Zem-I were made. Heterosis was estimated from the crosses (F1's) and their parents for characters such as- plant height (cm), branches per plant, number of siliquas and yield per plant (g) in F_1 generation. It was found that a cross of SMP 13-78 x Zem-I showed maximum heterosis and heterobeltiosis for all the characters studied. Therefore, this cross combination can fruitfully be utilized for improving yield and its components in future breeding programmes.

Chaurasia and Bhajan (2015) recorded high heterobeltiosis in six crosses namely CS 609B-10 × NDRE-4, PRQ -2005 × NDRE-4, RGN142 × PRB-2006-12, CS 609B-10 × Kanti, PRB-2006-12 × Kanti and PAB-9534 × Kanti. These crosses also exhibited significant heterosis over mid-parent and standard variety. Three crosses namely SKM-401 × Vardan, PRB-2006-12 × Vardan and NDRE-4 × PWR-9541, showed significant low heterosis over MP over Standard variety for oil content.

Bhinda *et al.* (2020) evaluated the extent of standard heterosis for seed yield, its component traits of Indian mustard generated by crossing of fifty lines with five testers in a line x tester mating design for thirteen yield and yield contributing characters. The maximum values of standard heterosis recorded were 47.87% for seed yield per plant and the highest value of standard heterosis was found in case of yield components was 41.43% for harvest index.

Wolko *et al.* (2019) estimated heterosis of oilseed rape (*Brassica napus*) where 600 double haploid lines and 2 generations of hybrid were evaluated. Plant height, siliqua length and number of seeds per siliqua for a large number of hybrids showed significant

positive heterosis. Whereas number of branches and silique per plant and 1000 seed weight, hybrids exhibited both positive and negative significant heterosis.

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted in the experimental field of Sher-e-Bangla Agricultural University, Dhaka. In first year, 7×7 half diallel crossing of the parental lines were performed during November 2021- March 2022 to develop twenty one (21) F_1 hybrid. These 21 F_1 hybrids were then evaluated to understand the gene action and heterosis during November 2022- March 2023. The experimental site was in Agro-ecological region of "Madhupur Tract" (AEZ No. 28) and it was located at 23°4′ N latitude and 90°22′ E longitude with an elevation of 8.6 meter from the sea level (Appendix I).

3.2 Soil and Climate

The soil type of the experimental plots was clay loam in texture, olive gray colour with common fine to medium distinct dark yellowish brown mottles, land type was medium high along with medium fertility level. The experimental site was situated in the subtropical climatic zone where the general climatic feature of this region was wet summer and dry winter. The pH range of the experimental site was between 5.6 to 5.8 and the amount of organic carbon is 0.82%. The physical and chemical nature of the soil have been presented in Appendix-II. Meteorological data on rainfall, temperature, relative humidity from November 2021 to March 2023 were collected from the Department of Meteorological Centre, Agargaon, Dhaka which have been shown in Appendix III.

3.3 Materials

A total number of 28 (twenty eight) plant materials were used in this experiment which included the twenty-one (21) F_1 hybrids (Table 2) which was developed from (7×7) half diallel fashion excluding the reciprocals and their 7 parents (Table 1). The parental line P7 (BARI Sarisha14) used as check variety (CV) which was also used as a parent. All the plant materials were collected from Bangladesh Agricultural Research Institute, Gazipur.

Table 1. List of seven (7) parents used in the experiment

SL No.	Parents	Name of Parents	Sources
01	P1	BARI Sarisha 15	BARI
02	P2	BARI Sarisha 6	BARI
03	P3	BARI Sarisha 17	BARI
04	P4	SS 75	BARI
05	P5	BARI Sarisha 12	BARI
06	P6	Tori 7	BARI
07	P7	BARI Sarisha 14	BARI

Table 2. List of F_1's developed from 7×7 half-diallel crosses excluding reciprocals

SL No.	F_1 hybrids of half-diallel crosses	Cross Combinations
01	P1 × P2	BARI Sarisha 12 × BARI Sarisha 6
02	P1 × P3	BARI Sarisha 15 × BARI Sarisha 17
03	P1 × P4	BARI Sarisha 15 × SS75
04	P1 × P5	BARI 15 × BARI Sarisha 12
05	P1 × P6	BARI Sarisha 15 × Tori 7
06	P1 × P7	BARI Sarisha 15 × BARI Sarisha 14
07	P2 × P3	BARI Sarisha 6 × BARI Sarisha 17
08	P2 × P4	BARI Sarisha 6 × SS75
09	P2 × P5	BARI Sarisha 6 × BARI Sarisha 12
10	P2 × P6	BARI Sarisha 6 × Tori 7
11	P2 × P7	BARI Sarisha 6 × BARI Sarisha 14
12	P3 × P4	BARI Sarisha 17 × SS75
13	P3 × P5	BARI Sarisha 17 × BARI Sarisha 12
14	P3 × P6	BARI Sarisha 17 × Tori 7
15	P3 × P7	BARI Sarisha 17 × BARI Sarisha 14
16	P4 × P5	SS 75 × BARI Sarisha 12
17	P4 × P6	SS75 × Tori 7
18	P4 × P7	SS75 × BARI Sarisha 14
19	P5 × P6	BARI Sarisha 12 × Tori 7
20	P5 × P7	BARI Sarisha 12 × BARI Sarisha 14
21	P6 × P7	Tori 7 × BARI Sarisha 14

3.4 Land Preparation

To ensure good tilth condition, the experimental plot was prepared by multiple ploughings, cross ploughings, and cleaning from previous crop stubbles. Laddering and harrowing with a power tiller came next. The experimental plot was meticulously cleared of weeds and other stubble before being leveled appropriately.

3.5 Fertilizer application

Inorganic fertilizers like urea, triple super phosphate (TSP), muriate of potash (MP), gypsum, boric acid, zinc oxide and organic fertilizer (cow dung) were applied at the rate shown in Table 3. Total amount of TSP, MP, gypsum, boric acid, zinc oxide and cow dung along with half of the urea were applied at the time of final land preparation as a basal dose. Urea was applied by two installments. The second half of the urea was top-dressed at the time of flower initiation.

Table 3. List of fertilizers with doses and application procedures

Sl. No.	Fertilizer	Doses (kg/532 m2)	Application procedure
01	Urea	17kg	Half as basal and half at the time of first flower initiation
02	TSP	10kg	As basal dose
03	MoP	5kg	As basal dose
04	Gypsum	8kg	As basal dose
05	Boric acid	0.6kg	As basal dose
06	Zinc oxide	0.6kg	As basal dose
07	Cowdung	100kg	As basal dose

3.6 Experimental design and layout

After final land preparation, field layout was done. The total area of the experimental plot was 19m×28m = 532m^2. Twenty-one F_1s along with their seven parents were grown in the experimental plot. Seeds were sown continuously in a randomized block design with 3 replications. The plot size was 10m × 30m. A distance of 0.75m from replication to replication was maintained. Distance between two rows was 30cm and plant to plant distance was 10cm. F_1 seeds were sown in lines in the experimental plots on 01 November, 2022. About 1.5 cm depth in the soil, seeds were sown and the germination of seeds started after 3 days of sowing.

Plate 1. Photograph showing final land preparation

Plate 2. Photograph showing seed sowing operation

3.7 Intercultural operations

Necessary intercultural operations, such as weeding, thinning, irrigation etc. were done uniformly in all the plots during the crop period. Sprinkler irrigation was used to bring proper moisture condition of the soil to ensure uniform germination of the seeds. For immediate release of rainwater from the experimental plot a good drainage system was maintained. The first weeding as well as thinning was done after 15 days of sowing. Second weeding was done after 35 days of sowing. Urea top dressing was done after second weeding. Immediate after seed sowing, there was severe presence of ant. To control ant, sevin dust 75WP was used. There was also aphid infestations during the siliqua developmental stage. To control aphid, Diazinon 60 EC at the rate of l ml per liter was applied. No remarkable disease attack was observed during the growing season. Various intercultural operation was presented in plate 3.

Plate 3a. Fertilizer application

Plate 3b. Weeding

Plate 3c. Thinning

Plate 3d. Spraying of insecticide

Plate 3. Various types of intercultural operations

3.8 Half diallel mating procedure

In half diallel mating design, all possible crosses among the selected parents were made in one direction only (direct cross). Seven selected varieties of *B. rapa* were crossed among themselves followed by half diallel mating design. Pictorial demonstration of different crossing step is shown in Plate 4.

Plate 4a. Emasculation

Plate 4b. Collection of pollen

Plate 4c. Hand pollination followed by bagging

Plate 4d. Tagging

Plate 4e. Field view after completing the crossing

Plate 4f. Siliqua setting after crossing

Plate 4: Half diallel (7×7) crossing program among selected genotypes of *Brassica rapa*

3.8.1 Selection of parents

At the time of flowering 20 plants were selected on the basis of stem color, stem thickness, leaf hairiness, leaf apex shape and size for doing crossing program for each cross combination.

3.8.2 Emasculation

For emasculation, ready to open floral buds were selected. Removal of petal, sepal and anther was done at morning usually 6:30 am to 9:00 am at the same time, special care was taken to remain the stigma unaffected.

3.8.3 Hand pollination

Hand pollination was done to get the desired cross combinations. Pollen was collected from the selected plant when it started shedding. Desired pollens were dusted on each of the stigma of the emasculated bud, and it is demonstrated in Plate 4c.

3.8.4 Bagging

Bagging was done immediate after hand pollination to protect the crossings from unwanted pollination. Ensuring optimum growth of siliqua, the bag was removed after a week.

3.8.5 Tagging:

Tagging was done carefully in each of the cross combinations to collect the true seeds (Plate 4d). Siliqua setting is represented in (Plate 4f).

3.8.6 Seed collection:

A total number of 21 cross combination's seeds were gained from the above procedure and allow them to grow F_1 hybrids.

3.9 Harvesting

Harvesting was started from mid of January, 2023 depending upon the maturity of the plants. The maturity indices for *Brassica* is 80% of the plants showed straw colour of siliqua, leaves, stem and desirable seed colour in the matured siliqua. Ten plants were selected at random from each parental line and ten plants from F_1 progeny's line in each

replication avoiding the two border plants. The plants were harvested by uprooting and then they were tagged properly. Data were recorded from these plants.

Plate 5. Experimental field during seedling stage

Plate 6. Experimental field during flowering stage

Plate 7. Experimental field during harvesting period

3.10 Collection of data

Data were collected for the following parameters:

30.10.1 Days to first flowering: Days to first flowering was recorded when at least one plant showing anthesis in a line.

30.10.2 Days to 50% flowering: Days to 50% flowering was counted when about 50 percent plants had at least one open flower of each F_1, s or parents.

30.10.3 Plant height (cm): During harvesting it was measured in centimeter from the base of the plant to the tip of the longest inflorescence.

30.10.4 Number of primary branches/plant: Number of branches produced from the main stem of a plant was recorded as the number of primary branches per plant.

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

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

30.10.7 Siliqua length (cm): Five siliqua was selected at random from every selected plant in order to measure the length of siliqua. The measurement was done in cm and it was measured the length between pedicel of siliqua and top of beak.

30.10.8 Beak length (cm): Five siliqua was selected at random from every selected plant in order to measure the length of beak. The measurement was done in cm and it was measured the length between top of siliqua and top of beak.

30.10.9 Number of siliquae/plant: Mean number of siliquae obtained from ten selected plant was considered as the number of siliquae/plant.

30.10.10 Number of seeds/siliqua: Well filled seeds were counted from five representative siliqua, which was considered as the number of seeds/siliqua.

30.10.11 Thousand seed weight (g): Weight in grams of randomly counted thousand seed were recorded.

Plate 8. Data collection

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

3.11 Statistical analysis

Ten plants were selected randomly and their mean values were used for recording the data. The observed data were computed for each of the twelve traits for each genotype in each replication and were subjected to statistical analysis. Duncan Multiple Range Test (DMRT) was performed for all characters to estimate the differences between the means of the genotype. Genotypic and phenotypic coefficient of variation, heritability, genetic advance, correlation coefficient and path analysis was estimated using R 4.2.1 software. Combining ability analysis was done with Model II and Method 1 of Griffings (1956) and obtained estimates of GCA and SCA. Heterosis expressed as percent increase or decrease in hybrid (F_1) over its mid parent value, better parent value and check variety in the desirable direction was calculated though microsoft excel. Vr-Wr graph were plotted by using Hayman (1954) graphical approaches.

3.11.1 Analysis for variance

All the observation were subjected to analysis of variance (ANOVA). The total variances of each character were partitioned into three different components namely- replication, genotype and error differences. The genotypic variances were also partitioned into parent and F_1. The level of significance was tested at 5% and 1% using F-test. The mathematical model used in the analysis was as follows:

$$Yij = \mu + \tau i + \rho j + \varepsilon ij \begin{pmatrix} i = 1,2,3 \dots t \\ j = 1,2,3 \dots r \end{pmatrix}$$

Where,

Yij: The value of observation belongs to the experimental unit designated

μ: The general mean value,

τi: The value of the actual effect of the treatment "i",

ρj: The value of the actual effect of the block "j", and

εij: The value of the actual effect of the experimental error belongs to the observation designated as treatment "i" in the block "j".

$\varepsilon ij \sim$ NID $(0, \sigma^2 E)$

3.11.2 Genotypic and phenotypic variance

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

Genotypic variance $(\sigma^2 g)$ = GMS-EMS/r

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Where, GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares

r = Number of replications

$\sigma^2 g$ = Genotypic variance

$\sigma^2 r$= Error variance

3.11.3 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation were calculated by the formula suggested by Burton (1952).

Genotypic coefficient of variation (GCV %) = $\sqrt{\sigma^2 g}/\bar{x} \times 100$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula,

Phenotypic coefficient of variation (PCV %) = $\sqrt{\sigma^2 p}/\bar{x} \times 100$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$= Population mean

Categories of GCV and PCV:

Low: Less than 10%; Moderate: 10-20%; High: More than 20%

3.11.4 Heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability in broad sense, $h^2 b = \sigma^2 g/\sigma^2 p \times 100$

Where,

h^2 = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Similarly, narrow sense heritability was calculated from the following formula, Heritability in narrow sense, $h^2 n = \sigma^2 g(\text{additive}) /\sigma^2 p \times 100$

Where, $h^2 n$ = Heritability in narrow sense

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ (additive) = Variance due to additive genetic action

Estimation heritability in cultivated plants could be placed in the following categories as suggested by the Robinson *et al.* (1966).

Categories of Heritability in broad sense

Low: 0-30%; Moderate: 30-60%; High: >60%

3.11.5 Genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, GA = K. h^2b. σp

Or, Genetic advance, GA = K. σ^2g/σ^2p. σp

Where, K = Selection intensity, the value which is 2.06 at 5% selection intensity

σp = Phenotypic standard deviation

h^2b = Heritability in broad sense

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

Categories of Genetic advance:

High (>20%); Moderate (10-20%) and Low (20%)

3.11.6 Genetic advance as percent of mean

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952).

Genetic advance (% of mean) = Genetic advance/Population mean × 100

Genetic advance as per cent mean was categorized into following groups as suggested by Johnson *et al.* (1955).

Categories of Genetic advance as percentage of mean:

Low (10%); Moderate (10-20%) and High (>20%)

3.11.7 Correlation coefficient

The calculation of genotypic and phenotypic correlation coefficient for all possible combinations through the formula suggested by Miller *et al.* (1958) and Johnson *et al.*

(1955) were adopted. The genotypic covariance component between two traits and have the phenotypic co-variance component were derived in the same way as for corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows: Genotypic correlation, $r_{gxy} = GCOV_{XY}/\sqrt{GV_x}.GV_Y = \sigma_{gxy}/\sqrt{(\sigma^2_{gx}.\ \sigma^2_{gy})}$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

Phenotypic correlation, $(r_{pxy}) = PCOV_{XY}/\sqrt{PV_x}.\ PV_Y = \sigma_{pxy}/\sqrt{(\sigma^2_{px}.\ \sigma^2_{py})}$

Where, σ_{pxy} = Phenotypic co-variance between the traits x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait

3.11.8 Path coefficient analysis

According to the procedure employed by Dewey and Lu (1959), Path coefficient analysis was done utilizing simple correlation values. In path analysis, the correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

Where, r's denote simple correlation coefficient and P's denote path coefficient. P's in the above equations may be conveniently solved by arranging them in matrix from. Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = the indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = the indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below:

$P^2_{RY} = 1 - \sum P_{iy} \cdot r_{iy}$

Where, $P^2_{RY} = (R^2)$

Hence, residual effect, $R = (P^2_{RY})$ ½

P_{iy}= Direct effect of the character on yield

r_{iy}=Correlation of the character with yield

Categories: Negligible (0.00 to 0.09); Low (0.10 to 0.19); Moderate (0.20 to 0.29); High (0.30 to 1.0) and Very High (>1.00)

3.11.9 Combining ability in relation to diallel analysis:

Griffing (1956) designed two main models and four methods for the analysis of diallel data. In this study, analysis of the combining ability for each character was done following Griffing's method I Model II, which the inbred lines, F_1's without reciprocals were included. The data was analyzed with using a fixed model. If the fixed effects model is used, the sampling error becomes the effective residual for testing combining ability mean squares and estimating variance components and standard errors. The mathematical model for the analysis was:

$Yij = m + gi + gj + Sij + 1/bc \sum \sum kl €ijkl$

Where, i,j = 1,2,3,…….., p

k = 1,2,3,……., b

l = 1,2,3,……., c

P = Number of parents

B = Number of blocks or replications

C = Number of observations in each plot

Yi =The mean of i×jth genotype over k and l

m = The population mean

g_j =The general combining ability effects to ith parent

g_j = The GCA of jth parent

S_{ij} =The SCA effects such that $S_{ij} = S_{ji}$

1/bc ∑ ∑ kl €ijkl = The mean error effects

The restriction imposed are: $\sum g_i = 0$ and $\sum S_{ij} + S_{ii} = 0$

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

ANOVA

Sources	**d.f.**	**Sum of squares**	**Mean sum of squares**	**Expected MSS**
GCA	p-1	Sg	Mg	σ^2e +(P+2).1/(P-1) Σ gi 2
SCA	P(p-1)/2	Ss	Ms	σ^2e+2/p(p-1) Σ i Σ j Sij2
Error	(b-1) (e-1)	Se	Me	σ^2e

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 i^{th} parent

Y_{ii} = Mean value of the i^{th} parent

Y_g = Grand total of the P(P-1) crosses and parental lines

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

Se = Sum of square due to error

Sg = 1/(P+2) [∑I (Yi+ Yii) 2 -4/p.y2]

Ss = ∑i∑j Yij2 1/(P+2) ∑ (Yi+ Yii) 2 + 2/(P+1) (P+2).Y2

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

gi = 1/(P+2) [∑I (Yi+ Yii) 2 -2/p.y]

S_{ij} = Yij -1/(P1+P2) ∑i (Yi + Yii + Yg + Yij) +2/(P+1) (P+2).

Y The variance of GCA and SCA were,

Var (gi) = (P-1)/P(P+2). σ^2e

Var (Sij) = 2(P-1)/(P+1) (P+2). σ^2e

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

√Var (gi) and √Var (Sij)

3.11.10 Estimation of heterosis:

The amount of heterosis was estimated as the percentage of F_1's hybrid from mid parent value.

Heterosis over mid parent (%) = $(\bar{F_1}\text{-}\overline{MP}\ /\overline{MP}) \times 100$

Where,

$\bar{F_1}$= Mean value of F_1 hybrid

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

The amount of heterosis was estimated as the percentage of F_1's hybrid from better parent value.

Heterosis over better parent (heterobeltiosis in %) = ($\overline{F_1}$-$\overline{BP}$/ $\overline{BP}$) × 100

Where,

$\overline{F1}$= Mean of F_1 hybrid

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

Heterosis over check variety was calculate by the same was,

Heterosis over check variety (Standard heterosis in %) = ($\overline{F_1}$- $\overline{CV}$/ $\overline{CV}$) × 100

Where,

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

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

CD (Critical Difference) values were used for testing significance of heterotic effects. Critical differences (CD) = t × √2EMS/√r

Here, EMS = Error mean sum of squares

r = Number of replications

t = Tabulated t value at error d.f

CD values were compared with the values obtained from (F_1-BP) and (F_1-CV) to test the significance of respective heterotic effects obtained from equation.

3.11.11 Estimation of genetic components

Following genetic components of variance were estimated according to Hayman (1954a).

D = Component of genetic variance due to additive effects of the genes

H_1 = Component of genetic variance due to dominant effects of the genes

H_2 = Component of genetic variance due to dominance effects corrected for the genes distribution

F = The mean of Fr over the arrays, where Fr is the dominance effects in single array and

h^2 = Overall dominance effects of heterozygous loci

3.11.12 Vr-Wr graph

The graphical analysis was done according to Hayman (1954). The Vr, Wr points for the parental were depicted along the Vr, Wr axes. For drawing parabola V_{ri} values and an initial value were calculated as per formula: $W_{ri} = (V_{ri} \times V_0L_0)^{0.5}$

Where,

Vr = Variance of the r^{th} array

V_0L_0 = Variance of parental value.

For drawing regression line, expected Wrei values were calculated as per: $W_{rei} = W_r - bV_r + bV_r$

The point of interception (a) on W_r ordinate by the regression line is obtained by the formula: a = Wr – bVr

The point of interception and the position Vr, Wr points for the different parents along the regression line would lead to draw the conclusion regarding degree of dominance and type of gene action involved in the parents.

CHAPTER IV

RESULTS AND DISCUSSION

Observations were recorded on days to first flowering, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length (cm), beak length (cm), number of seeds per siliqua, thousands seed weight (g) and seed yield per plant (g) from selected plants of seven parent and their 21 F_1s derived from half diallel mating procedures. The data were undergone to biometrical analysis and the obtained results from mean performance, genetic variability, heritability and genetic advance, correlation among yield attributing parameters, path coefficient analysis, combining ability effects among parents and hybrids and heterotic estimate of the hybrids were demonstrated in this section.

4.1 Varietal performance and genetic parameters

In order to ensure the success of the crop breeding program, the breeders removed the environmental components of phenotypic variation before collecting and selecting highly heritable and yield-associated traits (Mather, 1949). To estimate heritability and perhaps anticipate the expected genetic advancement through character selection, data on both the genotypic and phenotypic coefficient of variation are required. To achieve this, the experiment's results were subjected to analysis of variance (ANOVA), mean performance, genotypic variance, phenotypic variance, and environmental variance among the variables, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) as well as genetic advance and expected genetic advance as a percentage of mean for twelve characters of both the seven parental genotypes and their crosses that were obtained through diallel design. These results are shown in Tables 4, 5, and 6.

Among the observations of the experiment viz., plant height, number of primary branches per plant, number of secondary branches per plant were regarded as growth promoting characters while days to first flowering, days to 50% flowering and days to maturity were considered as phenological characters. Number of siliquae per plant, length of siliqua (cm), beak length (cm), number of seeds per siliqua and thousands

seed weight (g) were the reproductive traits whereas yield per plant (g) was considered as economic traits.

4.1.1 Days to first flowering

With a mean sum of square of 17.76, there was a highly significant variation among the genotypes for the observation days to first flowering (Table 4). The range varied from 27.00 DAS to 36.33 DAS. The foremost duration for days to first flowering was recorded in P3 (36.33 DAS) followed by P1 (36.00DAS) and P4 (32.67 DAS) where P2 and V19 required 27.00 DAS to bloom first flower, (the shortest duration among the genotypes) (Table 5). The genotypic and phenotypic coefficients of variation were 7.98 and 8.48, respectively, and the phenotypic variance was (6.41), which was slightly greater than the genotypic variance (5.68). This small difference in the coefficient of variation between genotype and phenotype suggested that there was very little environmental interaction and that genotypes accounted for the majority of the variation observed in the experiment. The highest heritability (88.55%) and medium genetic advance were shown by the days to first flowering, whereas genetic advance in percentage of mean was recorded medium (15.46%) which indicated additive gene effects governed the inheritance of these traits (Table 6). The results were in conformity with Shekhawat *et al.* (2014), who reported high heritability (62.05%) and moderate genetic advance (15.36%). Their findings implied that additive gene action may be the cause of the high to moderate heritability and moderate genetic advance, and for that simple selection may be an effective strategy.

4.1.2 Days to 50% flowering

Highly significant differences was found for days to 50% flowering among the genotypes with the mean sum of squares 23.36 (Table 4). Days to 50% flowering ranged from 29.33 to 40.67 DAS. The maximum duration was observed in P4 (40.67 DAS) followed by P3 (39.33 DAS) and P1 (39.00 DAS) while the minimum days required for V19 (29.33 DAS) (Table 5). Environmental factors had a slight influence on the expression of this trait, as indicated by the genotypic variance (7.65) being lower than the phenotypic variance (8.08) (Table 6). Significant variability was found within the genotypes, as evidenced by the value of genotypic coefficient of variation and the phenotypic coefficient of variation of 8.30 and 8.53, respectively.

Table 4. Analysis of variances (Mean Square) value for twelve characters of *Brassica rapa*

Sources of variation	d.f.	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
Replication	2	0.19	0.11	1.76	6.78	0.09	0.01	23.71	0.34	0.03	0.39	0.01	0.26
Genotypes	27	17.76**	23.36**	24.25**	199.21**	0.84**	5.96**	2352.82**	0.82**	0.16**	48.21**	0.16**	2.41**
Error	54	0.73	0.43	1.08	10.93	0.06	0.01	27.43	0.11	0.030	1.52	0.01	0.22

* = Significant at 5% level of probability, ** = Significant at 1% level of probability

Here,

DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousand seeds weight (g), YPP= Yield per plant (g).

Table 5. Mean performance of twelve characters of both seven parents and their 21 F_1's in mustard (*Brassica rapa*)

Genotype	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
P1	36.00a	39.00b	87.00 c	97.53j-l	5.97a-e	0.17i-k	93.47ij	4.91d-i	1.00f	21.17d-f	2.96f-h	5.90d-g
P2	27.00j	32.33h-j	86.00 cd	105.58f-i	5.20 b-f	1.15d	137.87c	5.61a-c	1.41b-d	16.37h-j	2.93gh	5.00h-l
P3	36.33a	39.33b	90.33b	98.70jk	5.23b-f	0.20h-k	68.30n	4.87e-j	1.47bc	29.13a	3.02e-h	6.13b-f
P4	32.67b	40.67a	92.33a	114.36a-c	6.20 a-d	0.12kl	101.08hi	5.27c-f	1.48bc	17.28hi	3.73a	6.37a-d
P5	27.67h-j	32.00i-k	86.00cd	106.73e-g	6.33 a-c	5.23a	173.87a	5.32c-e	1.47bc	14.37jk	2.88h	6.95a
P6	27.67h-j	31.67i-l	85.00 d-f	101.79g-j	6.04 a-e	4.76b	161.99b	5.19c-f	1.48bc	13.93k	2.67i	5.64d-h
P7	32.33b	37.00c	85.33c-e	101.23h-j	5.08 c-f	0.00l	66.93n	5.16c-f	1.46bc	24.93bc	3.10d-g	5.33g-k
V1(P1×P2)	28.67f-i	32.33h-j	81.00 jk	95.52k-m	5.23 b-f	0.28g-i	93.89h-j	3.83m	1.11ef	15.36i-k	3.52b	4.81i-m
V2(P1×P3)	30.33c-e	33.33f-h	81.67 i-k	105.40f-i	5.40 a-f	0.10kl	92.83i-k	4.61g-l	1.02f	24.53bc	2.95f-h	6.78ab
V3(P1×P4)	29.33d-g	34.67de	83.00 g-i	105.87e-h	4.60 f	0.00l	68.20n	4.37j-m	0.97f	22.30de	3.07d-h	4.66k-m
V4(P1×P5)	31.67bc	35.00d	84.00 e-g	116.73ab	5.97 a-e	1.03de	134.80cd	4.29k-m	1.01f	16.17h-j	3.13d-f	6.83ab
V5(P1×P6)	27.33ij	32.00i-k	80.67k	98.20jk	6.13 a-e	0.33f-h	92.87i-k	4.16lm	0.97f	19.57fg	3.03e-h	5.49e-i
V6(P1×P7)	31.67bc	33.67e-g	83.00g-i	104.20f-i	5.67 a-f	0.13j-l	84.60kl	4.57h-l	1.05f	23.07cd	3.07d-h	5.90d-g
V7(P2×P3)	30.00d-f	33.33f-h	83.00g-i	90.27m-o	5.57 a-f	0.43f	68.03n	5.94ab	1.55ab	15.90h-j	3.23cd	3.51n
V8(P2×P4)	30.33c-e	33.33f-h	83.67e-g	100.20i-k	5.27 b-f	0.13j-l	83.00lm	5.16c-f	1.35b-e	19.63fg	3.03e-h	4.69j-m
V9(P2×P5)	29.00e-h	31.00k-m	82.00h-k	101.87g-j	5.73 a-f	0.37fg	102.83h	4.99d-i	1.23c-f	17.27hi	3.07d-h	5.42f-j
V10(P2×P6)	28.33g-j	30.67lm	81.00jk	86.67o	4.63 f	0.00l	94.53h-j	6.13a	1.62ab	20.00f	2.60i	4.93h-l
V11(P2×P7)	30.00d-f	31.67i-l	82.00h-k	89.90no	5.33 a-f	0.00l	86.13j-l	5.27c-f	1.17d-f	15.93h-j	2.97f-h	4.07mn
V12(P3×P4)	31.67bc	34.33d-f	85.33c-e	108.53d-f	4.87 ef	0.13j-l	68.13n	5.28c-f	1.47bc	22.27de	3.43b	5.33g-k
V13(P3×P5)	27.33ij	30.33mn	81.67i-k	108.17d-f	5.03 d-f	0.00l	122.43ef	5.13c-g	1.14d-f	16.20h-j	3.37bc	6.68a-c
V14(P3×P6)	27.33ij	31.00k-m	80.67k	95.53k-m	5.73 a-f	0.27g-j	120.73e-g	4.89e-j	1.13ef	14.67jk	2.97f-h	5.27g-k
V15(P3×P7)	28.67f-i	30.67lm	81.00jk	119.47a	5.13 c-f	0.20h-k	75.20mn	4.45i-l	1.06f	25.67b	3.07d-h	5.92d-g

Table 5 (Cont'd)

Genotype	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
V16(P4×P5)	30.67cd	34.67de	84.33d-g	105.40f-i	5.43 a-f	0.93e	112.33g	5.39c-e	1.50bc	17.83gh	3.17de	6.34a-d
V17(P4×P6)	30.00d-f	32.00i-k	82.67g-j	108.90d-f	6.57 a	0.23g-k	98.13hi	5.45b-d	1.54ab	15.17jk	3.03e-h	4.42lm
V18(P4×P7)	30.33c-e	32.67g-i	83.33 f-i	112.90bcd	5.63 a-f	0.37fg	97.47hi	4.74f-k	1.37b-e	20.50ef	3.06d-h	5.99c-g
V19(P5×P6)	27.00j	29.33n	80.67 k	111.00c-e	6.43 ab	3.83c	129.10de	5.28c-f	1.52b	16.07h-j	3.00e-h	6.22a-e
V20(P5×P7)	28.67f-i	31.33j-m	81.67 i-k	105.67e-h	5.03 d-f	1.07de	116.60fg	5.03d-h	1.79a	14.53jk	3.07d-h	5.43f-j
V21(P6×P7)	28.33g-j	33.67e-g	84.33 d-g	92.77l-n	5.27 b-f	0.00l	82.00lm	4.47i-l	1.17d-f	15.77ij	3.17de	4.10mn
Max	36.33	40.67	92.33	119.47	6.57	5.23	173.87	6.13	1.79	29.13	3.73	6.45
Min	27.00	29.33	80.67	86.67	4.60	0	68.03	3.83	0.97	13.93	2.60	3.51
CV%	2.87	1.96	1.24	3.20	14.01	10.09	5.18	6.65	12.59	6.59	3.55	8.32
LSD	1.40	1.07	1.70	5.4	1.27	0.13	8.56	0.54	0.27	2.02	0.19	0.76

Here,

DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousand seeds weight (g), YPP= Yield per plant (g).

High heritability (94.70%) was observed for this trait with a low genetic advance (5.54) and a moderate genetic advance as percentage of mean (16.64), indicating, selection based on improvement of this trait will be rewarded and the inheritance of the characters was controlled by additive gene effects (Table 6). For days to 50% flowering, Akoju *et al.* (2020) investigated the lowest GCV (8.54%) and moderate PCV (10.51%). Higher heritability estimates and a moderate genetic advance as a percentage of mean were noted by Jahan (2008) for this trait.

4.1.3 Days to maturity

For days to siliqua maturity, the mean sum of squares was 24.25 which showed significant variation (Table 4). For maturity, 92.33 DAS were required for P4 which was the highest duration for days to siliqua maturity which was followed by P3 (90.33 DAS), however, the shortest duration was observed in V5, V14 and V19 and the value was (80.67 DAS) (Table 5). Low genotypic variance (7.72) as well as low phenotypic variance (8.80) along with lower phenotypic coefficient of variation (3.55) and genotypic coefficient of variation (3.32) was observed for days to maturity. Little difference between phenotypic variance and genotypic variance revealed slightly influences of environmental factors in the expression of this characters (Table 6). High heritability (87.70) along with low value of genetic advance (5.36) and genetic advance as percentage of mean (6.41) indicated involvement of non-additive gene action in the inheritance of this trait and selection for this character are not rewarding. High heritability and low genotypic advance in percent of mean for days to maturity were found by Ara *et al.* (2010) and Jahan (2008); as a result, selection for this trait may not be beneficial.

4.1.4 Plant height (cm)

Highly significant variation was reported among the genotypes for plant height, analysis of variance revealed the mean sum squares for plant height was 199.21. Among the genotypes the tallest plant was observed in in V15 (119.47 cm) followed by V4 (116.73 cm) and P4 (114.36 cm). The shortest plant height was found in V10 (86.67 cm) followed by V11 (89.90 cm) (Table 5). Genotypic and phenotypic variance was recorded as 62.76 and 73.69, respectively for the aforementioned character (Table 6) with an environmental variance (10.93).

Table 6. Estimation of genetic parameters for twelve yield and yield contributing characters of both seven parents and their crosses

Parameters	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
Genotypic variance (σ^2g)	5.68	7.65	7.72	62.76	0.26	1.98	774.78	0.24	0.05	15.56	0.05	0.73
Phenotypic variance (σ^2p)	6.41	8.08	8.80	73.69	0.32	1.99	802.14	0.35	0.07	17.08	0.06	0.95
Environmental variance (σ^2e)	0.73	0.43	1.08	10.93	0.06	0.01	27.37	0.11	0.03	1.52	0.01	0.22
Genotypic coefficient of variation (GCV)	7.98	8.30	3.32	7.68	9.22	183.60	27.57	9.77	16.36	21.08	7.09	15.56
Phenotypic coefficient of variation (PCV)	8.48	8.53	3.55	8.32	10.24	183.91	28.05	11.81	20.76	22.08	7.99	17.69
Heritability (Broad sense- h^2b)	88.55	94.70	87.70	85.17	81.08	99.66	96.59	68.35	62.13	91.08	78.71	77.31
Genetic advance (%)	4.62	5.54	5.36	15.06	0.95	2.90	56.35	0.83	0.35	7.76	0.40	1.55
Genetic advance as percentage of mean	15.46	16.64	6.41	14.60	17.11	377.56	55.81	16.63	26.56	41.43	12.96	28.18

DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousands seed weight (g), YPP= Yield per plant (g).

The outcome showed that this trait's expression is influenced by environmental factors. Plant height showed the greatest genotypic, phenotypic, and environmental variances, according to Khan *et al.* (2013). For this trait, in the present study, the phenotypic and genotypic coefficients of variation were recorded lower 8.32 and 7.68, respectively (Table 6). The findings are in conformity with the genotypic and phenotypic coefficient of variations (5.84 and 8.36, respectively) found by Lakra *et al.* (2020). High heritability (85.17%) with the moderate value of genetic advance (15.06) and moderate genetic advance as percentage of mean (14.60) were observed for plant height. Patel *et al.* (2019) reported resembling results where plant height was exhibited high heritability (89.72%) with moderate type of genetic advance as percent of mean (14.62%). High heritability associated with moderate genetic advance as percent of mean indicated that inheritance of plant height was controlled by additive type of genetic action, hence, selection for this trait may be effective to get short stature plant of *B. rapa*.

4.1.5 Number of primary branches per plant

Based on the number of primary branches per plant, the genotypes showed highly significant variation, as indicated by the mean sum square of 0.84 (Table 4). The range of primary branches were 4.60 to 6.57 (Table 5). The maximum number of primary branches holding plant was found in V17 (6.57) followed by V19 (6.43), P5 (6.33) and P4 (6.20). However, the minimum number of primary branches per plant were observed in case of V3 (4.60) (Table 5). The genotypic variance and phenotypic variance were observed 0.26 and 0.32, respectively. Moderate genotypic coefficient of variation (9.22) and phenotypic coefficient of variation (10.24) was observed for this trait indicating considerable variation was present among the genotypes (Table 6). The minimal environmental effects were attributed to the expression of this trait, as indicated by the lowest differences between the genotypic and phenotypic coefficient of variation. Selection for the trait may be successful because of the high heritability (81.08%), minor genetic advance (0.95), and moderate genetic advance as a percentage of mean (17.11). These results suggested that heritability was caused by additive genetic action. Evangelin *et al.* (2023) estimated high heritability with high genetic advance as percent of mean for this trait.

4.1.6 Number of secondary branches per plant

Highly significant mean sum of square (5.96) was observed for number of secondary branches per plant (Table 4) and the ranges of number of secondary branches 0.00 to 5.23 (Table 5). P5 (5.23) exhibited the maximum number of secondary branches per plant which was followed by P6 (4.76). The lowest number of secondary branches per plant was observed in P7, V3, V10, V11and V21, where no secondary branches were found (0.00) (Table 5). The genotypic and phenotypic variance was recorded as 1.98 and 1.99, respectively. High genotypic coefficient of variation (183.60) and phenotypic coefficient of variation (183.91) was found for the trait (Table 6). The negligible differences between GCV and PCV indicated that there exist very low environmental effects. Evangelin *et al.* (2023) estimated high genotypic and phenotypic coefficient of variations (23.01 and 24.23) for secondary branches. High heritability (99.66%) with lower genetic advance (2.90) and high genetic advance as percent of mean (377.56) indicating that genes responsible for the expression of the trait was controlled by the additive genetic action. The obtained value indicated that the selection pressure was high and the traits can be selected for had a high heritability. Evangelin *et al.* (2023) reported high heritability (90.18) and high genetic advance as percent of mean (45.01) in case of number of secondary branches per plant.

4.1.7 Number of siliquae per plant

According to Table 4, there was a highly significant variation in the mean sum of squares for the number of siliquae per plant, which was 2352.82. The highest number of siliquae was observed in P5 (173.87) whereas the lowest number of siliquae was found in V7 (68.03) followed by V12 (68.13), V3 (68.20) and P3 (68.30) (Table 5). The phenotypic variance (802.14) and genotypic variance (774.78) was higher with a large environmental variance (27.37) was found for the trait. However, the higher genotypic coefficient of variance (27.57) and phenotypic coefficient of variance (28.05) was recorded (Table 6). The heritability estimated for this trait was higher (96.59%) along with higher genetic advance (56.35) and a higher genetic advance as percentage of mean (55.81) (Table 6). Similar findings were made by Mandal *et al.* (2022) who reported high heritability (80.61%) and moderate genetic advance (14.36%). Thus, the selection process could take advantage of this characteristic to further improve it.

According to estimates from Mekonnem *et al.* (2014) and Alam (2010), siliqua per plant had a moderately high GCV, high heritability, and genetic advance per plant.

4.1.8 Siliqua length (cm)

The mean sum square for siliqua length was demonstrated 0.82 (Table 4) that were highly significant. Siliqua length of among the genotypes ranged from 3.83 cm to 6.13 cm (Table 5). V10 (6.13 cm) exhibited the longest siliqua which is followed by V7 (5.94 cm) and P2 (5.61 cm) whereas the shortest siliqua was reported in V1 (3.83 cm). Lower estimates of genotypic variance (0.24) and phenotypic variance (0.35) was observed for siliqua length whereas the environmental variance was insignificant (Table 6). Low to moderate estimates of genotypic coefficient of variation (9.77) and phenotypic coefficient of variation (11.81) was demonstrated for the traits. Lakra *et al.* (2020) reported low GCV and PCV for the concerned characters. High heritability (68.35%) was estimated with low genetic advance (0.83) and a moderate genetic advance as percentage of mean (16.63) for the trait (Table 6). Yadava *et al.* (2011) found high heritability (88.50%) with moderate genetic advance as percent of mean (17.71%) for siliqua length. Characters with high heritability associated with moderate genetic advance as percent of mean provide an assumption on the entity of additive gene effects on the inheritance of this trait.

4.1.9 Beak length (cm)

The mean sum square for beak length was observed was 0.16 (Table 4) that are highly significant. Beak length of the genotypes ranged from 0.97 cm to 1.79 cm (Table 5). The longest beak length was observed in V20 (1.79 cm) followed by V10 (1.62 cm) and V7 (1.55 cm) whereas the shorter beak length was found in V3 (0.97 cm) and V5 (0.97cm). Lower value of genotypic variance (0.05) and phenotypic variance (0.07) was observed for beak length whereas the environmental variance was negligible (Table 6). It also exhibited moderate genotypic coefficient of variation (16.36) as well as phenotypic coefficient of variation (20.76). High heritability (62.13%) was estimated with low genetic advance (0.35) and a high genetic advance as percentage of mean (26.56) for the trait (Table 6). High heritability coupled with high genetic advance as percent of mean given an assumption on the existence of additive gene effects on the expression of this trait.

4.1.10 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant differences (48.21) among the genotypes where it ranged from 13.93 to 29.13 (Table 5). The maximum number of seeds per siliqua was found in P3 (29.13) which is followed by V15 (25.67) while the lowest number of seeds were reported in P6 (13.93). The genotypic and phenotypic variance for the trait was 15.56 and 17.08, respectively with an environmental variance 1.52 (Table 6). Higher value of genotypic coefficient of variance (21.08) and phenotypic coefficient of variance (22.08) was observed for the trait. Higher heritability (91.08%) besides low genetic advance (7.76) and higher genetic advance as percentage of mean (41.43) indicating, the character was governed by additive gene actions.

4.1.11 Thousand seeds weight (g)

Highly significant variation was found for the character with the mean sum of square was 0.16 (Table 4). Thousand seed weight extended from 2.60 g to 3.73 g. The highest value was observed in P4 (3.73 g) followed by V1 (3.52 g), V12 (3.43g), V13 (3.37g) and V7 (3.23 g) while V10 (2.60 g) was recorded as the minimum seed weight (Table 5). The least value of phenotypic variance and genotypic variance for the selected character was recorded as 0.06 and 0.05, respectively with the environmental variance of (0.01). Table 6 displays a low recorded genotypic coefficient of variation (7.09) and phenotypic coefficient of variation (7.99). Amsalu (2020) made comparable observations, recorded low GCV and PCV (0.062 and 0.131, respectively) for 1000 seed weight. All of these indications pointed to the environment as having a significant influence on this character's expression. While the estimated heritability (78.71%) was higher with low genetic advance (0.40) as well as moderate genetic advance as percentage of mean (12.96) suggested that character was governed by additive gene actions. Therefore, for this trait, improving the lines through the selection process may be beneficial. Comparable results were found with Patel *et al.* (2019), who reported moderate genetic advance as a percentage of mean (18.61%) and high heritability (96.65%).

Plate 9. Variation among siliqua length of 21 F_1 hybrids and their seven parents

4.1.12 Yield per plant (g)

Highly significant variation was observed among the genotypes for yield per plant and the mean sum of square was 2.41 (Table 4). The analyzed result revealed that yield per plant was varied from 3.51 g to 6.95 g (Table 5). The highest value was observed in P5 (6.95 g) which was statistically similar with V4 (6.83 g) and V13 (6.68 g). However, genotypes V7 (3.51) was recorded for the lowest yield per plant value. Yield per plant exhibited the lowest value for genotypic (0.73) and phenotypic variance (0.95) whereas

the environmental variance was negligible (0.22). The estimated phenotypic coefficient of variance (17.69) and genotypic coefficient of variance (15.56) was moderate (Table 6), indicating considerable variations were exhibited by yield per plant that could be beneficial for selecting the segregating lines in next. The high heritability (77.31%) was recorded for this character along with low genetic advance (1.15) and high genetic advance as percentage of mean (28.18%). Therefore, direct selection by selecting these traits may be effective for yield improvement because traits are highly heritable and less affected by environment. Selection for few generations will be sufficient for improvement of such traits. Patel *et al.* (2019) found moderate phenotypic coefficient of variation of seed yield per plant (16.42) and total number of branches per plant (11.58).

4.2 Correlation analysis among the variables of both parents and their crosses

To estimate the correlation of yield with related characters, one must have a thorough understanding of the various characters with the target trait as well as among the various characters themselves. There are two types of correlation: positive and negative. Positive correlation denotes that the two traits are changing in the same direction (either increasing or decreasing), while negative correlation denotes that the first trait is increasing along with a decrease in the second (or vice versa). Positive correlation in linkage is attributed to the coupling phase, while negative correlation is linked to the repulsion phase. When the respective genes are situated far apart on the same chromosome or on different chromosomes, it indicated no correlation.

Correlated characters are of interest to find out the genetic causes of correlation through the pleiotropic action of genes, to know the level of selection for one character that will cause simultaneous change in other characters and find out correlation between characters and their fitness. The strength of the correlation is not dependent on the direction or sign. Thus, the same value bearing either positive or negative sign are equal in the degree of association of the measured variable. Different yield attributing traits very often exhibit variable direct and/or indirect associations among themselves that create a complex situation making the selection process for breeder strenuous. In Table 7 the results obtained from correlation analysis of twelve characters are presented.

Table 7: Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients among twelve yield and yield contributing characters for all seven parents and their crosses

Parameters	DFF	D 50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
DFF	1**	0.832**	0.599**	0.009ns	0.009ns	-0.351**	-0.436**	-0.067ns	-0.021ns	0.553**	0.193ns	0.168ns
D50%F	0.880**	1**	0.805**	0.050ns	0.031ns	-0.280**	-0.334**	-0.077ns	-0.028ns	0.437**	0.323**	0.167ns
DM	0.676**	0.868**	1**	0.174ns	0.138ns	0.063ns	0.001ns	0.164ns	0.203ns	0.203ns	0.259*	0.195ns
PH	0.038ns	0.061ns	0.157ns	1**	0.233*	0.184 ns	0.237*	-0.163ns	-0.041ns	0.083ns	0.273*	0.529**
NPB	-0.029ns	0.012ns	0.150ns	0.270ns	1**	0.466**	0.466**	-0.037ns	0.036ns	-0.333**	-0.010ns	0.296**
NSB	-0.374*	-0.289ns	0.066ns	0.197ns	0.520**	1**	0.784 **	0.170ns	0.288**	-0.427**	-0.341**	0.314**
NSP	-0.492**	-0.358ns	-0.001ns	0.252ns	0.506**	0.800**	1**	0.125ns	0.156ns	-0.630**	-0.262*	0.459**
SL	-0.031ns	-0.075ns	0.197ns	-0.260ns	0.029ns	0.206ns	0.175ns	1**	0.614**	-0.184ns	-0.209ns	-0.172ns
BL	-0.038ns	-0.031ns	0.282ns	-0.030ns	0.018ns	0.363ns	0.205ns	0.828**	1**	-0.210ns	-0.096ns	-0.125ns
NSS	0.621**	0.456*	0.232ns	0.135ns	-0.436*	-0.447*	-0.670**	-0.233ns	-0.246ns	1**	-0.027ns	0.231*
TSW	0.226ns	0.405 *	0.301ns	0.306ns	-0.048ns	-0.383*	-0.319ns	-0.280ns	-0.068ns	-0.028ns	1**	0.092ns
YPP	0.152ns	0.157ns	0.256ns	0.687**	0.274ns	0.358ns	0.470*	-0.210ns	-0.102ns	0.181ns	0.005ns	1**

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, ns= non-significant.

Here, DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousands seed weight (g), YPP= Yield per plant (g).

4.2.1 Days to first flowering

Days to first flowering showed positive and highly significant association with days to 50% flowering (0.880, 0.832), days to maturity (0.676, 0.599) and number of seed per siliqua (0.621, 0.553) at both genotypic and phenotypic level (Table 7). Positive but non-significant association was found with plant height (0.038, 0.009), thousand seed weight (0.226, 0.193) and yield per plant (0.152, 0.168) at both genotypic and phenotypic level whereas primary branches per plant (0.009) showed positive but non-significant association only at phenotypic level. Significant negative association was reported with number of secondary branches per plant (-0.374, -0.351) and number of siliqua per plant (-0.492, -0.436) at both genotypic and phenotypic level whereas negative and non-significant association was noticed with siliqua length (-0.031, -0.067) and (-0.038, -0.021) at both level. Days to first flowering showed a highly significant and positive correlation with plant height, siliqua per plant, days to 50% flowering, and seed yield, according to Maurya *et al*. (2012) and Tadesse and Alemu (2019). However, they reported a negative association with secondary branches per plant.

4.2.2 Days to 50% flowering

Days to 50% flowering showed positive and significant association with days to maturity (0.868, 0.805), number of seeds per siliqua (0.456, 0.437) and thousand seed weight (0.405, 0.329) at both genotypic and phenotypic level (Table 7). Positive but non-significant association was found with plant height (0.061, 0.050), number of primary branches per plant (0.012, 0.031) and yield per plant (0.157, 0.167) at both genotypic and phenotypic level. Highly significant negative association of days to 50% flowering was reported with number of secondary branches per plant (-0.280) and number of siliquae per plant (-0.334) at only phenotypic level whereas negative and non-significant association was noticed with siliqua length (-0.075, -0.077) and beak length (-0.031, -0.028) at both level. At the same time negative and non-significant association was estimated for number of secondary branches per plant (-0.289) and number of siliquae per plant (-0.358) at only genotypic level. In addition, Tadesse and Alemu (2019) found a negative correlation between the number of secondary branches per plant and the days to 50% flowering, but they also found a highly significant and

positive correlation between the days to first flowering and plant height, siliqua per plant, and seed yield.

4.2.3 Days to maturity

Days to maturity exhibited positive and significant association with thousand seed weight (0.259) at only phenotypic level (Table 7). Positive but non-significant association was found with plant height (0.157, 0.174), number of primary branches per plant (0.150, 0.138), number of secondary branches per plant (0.066, 0.063), siliqua length (0.197, 0.164), beak length (0.282, 0.203), number of seeds per siliqua (0.232, 0.203) and yield per plant (0.256, 0.195) at both genotypic and phenotypic level whereas number of siliquae per plant (0.001) showed negative and non-significant association only at genotypic level. Meena *et al.*, (2020) reported positive association with plant height (0.353), number of primary branches per plant (0.083), siliqua length (0.288), thousand seed weight (0.248) and yield per plant (0.356) at genotypic level.

4.2.4 Plant height (cm)

Plant height showed positive and highly significant association with yield per plant (0.687, 0.529) at both genotypic and phenotypic level. As this trait exhibited strong correlation with yield per plant, it can be used for selection for increasing yield. At phenotypic level plant height showed positive and significant association with number of primary branches per plant (0.233), number of siliquae per plant (0.237) and thousand seed weight (0.273) (Table 7). Positive but non-significant association was found with number of secondary branches per plant (0.197, 0.184) and number of seeds per siliqua (0.135, 0.083) at both genotypic and phenotypic level whereas primary branches per plant (0.270) and 1000-seed weight (0.306) showed positive but non-significant association only at genotypic level. Negative association was reported with siliqua length (-0.260, -0.163), beak length (-0.030, -0.041) at both genotypic and phenotypic level. Lakra *et al.*, (2020) reported positive correlation of plant height with yield at both genotypic and phenotypic level.

4.2.5 Number of primary branches per plant

Number of primary branches per plant showed positive and highly significant association with number of secondary branches per plant (0.520, 0.466) and number of

siliquae per plant (0.506, 0.466) at both genotypic and phenotypic level whereas with yield per plant (0.296) at only phenotypic level (Table 7). Positive but non-significant association was found with beak length (0.036) at phenotypic level, at the same time siliqua length (0.029), beak length (0.018) and yield per plant (0.274) at genotypic level. Significant negative association was reported with number of seeds per siliqua (-0.436, -0.330) at both genotypic and phenotypic level whereas negative and non-significant association was noticed with 1000-seed weight (-0.048, -0.010) at both level and siliqua length (-0.037) at phenotypic level. Meena *et al*. (2020) found that at the genotypic and phenotypic levels, there was a highly significant and positive correlation between the number of primary branches per plant and the number of secondary branches per plant.

4.2.6 Number of secondary branches per plant

Number of secondary branches per plant showed positive and highly significant association with number of siliquae per plant (0.800, 0.784) at both genotypic and phenotypic level (Table 7) whereas siliqua length (0.288) and yield per plant (0.314) showed positive and significant association at phenotypic level, that means the character can be used for selection for increasing seed yield. Positive but non-significant association was found with siliqua length (0.206, 0.170) at both genotypic and phenotypic level, at the same time number of secondary branches per plant is positively correlated with beak length (0.363) and yield per plant (0.358) at genotypic level. Significant negative association was reported with number of seeds per siliqua (-0.477, -0.427) and thousand seed weight (-0.383, -0.341) at both genotypic and phenotypic level. According to studies by Malek *et al*. (2000) and Mekonnen *et al*. (2014), the number of secondary branches and days to flower completion, day to maturity, siliqua length, seeds per siliqua, and thousand seed weight were found to be negatively correlated and not statistically significant at either the genotypic or phenotypic levels.

4.2.7 Number of siliquae per plant

Number of siliquae per plant showed positive and highly significant correlation with yield per plant (0.470, 0.459) at both genotypic and phenotypic level (Table 7). Thus, selection practiced for improving these traits individually or simultaneously, is likely to bring improvement in other traits due to correlated response. Positive but non-

significant association was found with siliqua length (0.175, 0.125) and beak length (0.205, 156) at both genotypic and phenotypic level. Highly significant negative association was reported with number of seeds per siliqua (-0.670, -0.630) at both genotypic and phenotypic level and thousand seeds weight -0.262 at phenotypic level. Ray *et al.* (2019) reported significant positive correlation of number of siliqua per plant with seed yield per plant.

4.2.8 Siliqua length (cm)

Siliqua length showed positive and highly significant association with beak length (0.828, 0.614) at both genotypic and phenotypic level (Table 7). Negative and non-significant association was noticed with number of seeds per siliqua (-0.233, -0.184), thousand seed weight (-0.280, -0.209) and seed yield per plant (-0.210, -0.172) at both level. Additionally, according to Rashid et al. (2015), siliqua length positively and marginally affected seed yield. In line with the research findings, Jamali et al. (2016) found a negative correlation between siliqua length and the number of primary branches per plant, days to flowering, days to maturity, and number of siliquae per plant.

4.2.9 Beak length (cm)

Beak length showed non-significant negative association with number of seeds per siliqua (-0.246, -0.210), thousand seed weight (-0.068, -0.096) and seed yield per plant (-0.102, -0.125) at both genotypic and phenotypic level (Table 7). Negative correlation indicates an inverse relationship between beak length and yield, which means an increase of beak length would show a decrease of yield.

4.2.10 Number of seeds per siliqua

Number of seeds per siliqua showed positive and non-significant correlation with yield per plant (0.181, 0.092) at both genotypic and phenotypic level (Table 7). Negative and non-significant association was found with thousand seeds weight (-0.028, -0.027) at both genotypic and phenotypic level.

4.2.11 Thousand seeds weight (g)

Correlation between thousand seed weight and yield was illustrated in (Table 7). At the genotypic and phenotypic levels, the weight of a thousand seeds exhibited a non-

significant positive correlation with the yield per plant (0.005, 0.092). This demonstrated that a rise in thousand seed weight would result in a rise in yield. This results are in conformity with Meena *et al.* (2020) where they found thousand seed weight had significant positive correlation with yield.

4.3 Path coefficient analysis

A technique for separating the observed correlation coefficient into the direct and indirect effects of yield-attributing components on yield is path coefficient analysis. Path analysis helps create an effective selection strategy by giving a clear picture of character associations. In contrast to simple correlation, which measures only the mutual association and ignores causation, path coefficient analysis identifies the causes and their relative importance (Ray *et al*., 2019).

Simple correlation is insufficient to determine complex relationships between the different traits associated with the dependent variable. The linear relationship between variables is shown by correlation coefficients. However, when a causal relationship between variables is required, describing these relationships alone is insufficient. The most popular statistical technique was suggested to be path coefficient analysis in order to determine the direct or indirect effects of yield contributing characters on seed yield per plant and to quantify the relative significance of each component on seed yield per plant.

The dependent variable in this case is seed yield per plant; the independent variables are various yield attributes, which include the number of primary branches, secondary branches, siliqua length, number of seeds per siliqua, days to first flowering, days to 50% flowering, days to 80% maturity, plant height, and so on. Table 8 provides an example of path coefficient analysis used to estimate the direct and indirect effects of yield contributing characters on seed yield per plant.

4.3.1 Days to first flowering

Days until first flowering had a positive direct effect (0.049) on yield per plant, according to path coefficient analysis. Days to 50% flowering (0.657), number of secondary branches per plant (0.097), number of seeds per siliqua (1.078), and thousand seed weight (0.185) were the positive indirect effects of the trait on seed yield per plant.

Days to maturity (-0.787), plant height (-0.009), number of primary branches per plant (-0.009), number of siliquae per plant (-1.096), length of siliqua (-0.001), and beak length (-0.013) were the negative indirect effects. Lastly, there was a non-significant positive genotypic correlation between the trait and seed yield per plant (0.152).

4.3.2 Days to 50% flowering:

Days to 50% flowering showed positive direct effect (0.745) towards seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to first flowering (0.043), number of primary branches per plant (0.004), number of secondary branches per plant (0.075), number of seeds per siliqua (0.792) and thousand seed weight (0.332). The trait showed negative indirect effect on seed yield per plant via days to maturity (-1.010), plant height (-0.015), number of siliquae per plant (-0.797), siliqua length (-0.002) and beak length (-0.011). Finally, the trait showed non-significant positive genotypic correlation with seed yield per plant (0.157). In order to improve yield, direct selection for this trait will be fruitful since its direct effect is positive and greater than the genotypic correlation coefficient, indicating a genuine relationship between them. The result was in conformity with Meena *et al.* (2020) where days to 50% flowering has direct positive effect on yield. Ray *et al.* (2019) also reported similar results.

4.3.3 Days to maturity

Seed yield per plant was negatively impacted by days to maturity, with a direct effect of -1.163. A similar finding was reported by Naznin *et al*. (2015) regarding the negative direct effect of days to maturity on yield per plant. Akter (2020) showed the similar result. The trait showed positive indirect effect on seed yield per plant via days to first flowering (0.043), days to 50% flowering (0.647), number of primary branches per plant (0.046), siliqua length (0.004), beak length (0.096), number of seeds per silique (0.404) and thousand seed weight (0.247). The trait showed negative indirect effect on seed yield per plant via plant height (-0.038), number of secondary branches per plant (-0.017) and number of siliquae per plant (-0.004). The trait had positive non-significant genotypic association with seed yield per plant (0.256).

Table 8: Direct and indirect effects of 12 characters on seed yield per plant of seven parents and their crosses of *Brassica rapa*

Parameters	DFF	D50%F	D80%M	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	Genotypic correlation with yield
DFF	**0.049**	0.657	-0.787	-0.009	-0.009	0.097	-1.096	-0.001	-0.013	1.078	0.185	0.152ns
D50%F	0.043	**0.745**	-1.010	-0.015	0.004	0.075	-0.797	-0.002	-0.011	0.792	0.332	0.157ns
D80%M	0.033	0.647	**-1.163**	-0.038	0.046	-0.017	-0.004	0.004	0.096	0.404	0.247	0.256ns
PH	0.002	0.046	-0.184	**-0.240**	0.083	-0.051	0.562	-0.006	-0.010	0.234	0.252	0.678**
NPB	-0.001	0.009	-0.175	-0.065	**0.305**	-0.135	1.126	0.001	0.006	-0.758	-0.040	0.274ns
NSB	-0.018	-0.216	-0.078	-0.047	0.159	**-0.259**	1.780	0.005	0.124	-0.776	-0.315	0.358ns
NSP	-0.024	-0.267	0.002	-0.061	0.155	-0.207	**2.224**	0.004	0.070	-1.163	-0.263	0.470*
SL	-0.002	-0.056	-0.229	0.063	0.009	-0.054	0.390	**0.022**	0.283	-0.406	-0.230	-0.210ns
BL	-0.002	-0.023	-0.328	0.007	0.006	-0.094	0.456	0.018	**0.342**	-0.427	-0.056	-0.102ns
NSS	0.031	0.340	-0.271	-0.032	-0.133	0.116	-1.491	-0.005	-0.084	**1.734**	-0.023	0.181ns
TSW	0.011	0.302	-0.350	-0.074	-0.015	0.099	-0.711	-0.006	-0.023	-0.049	**0.821**	0.005ns

Residual effects (R) = 0.0226

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, ns= non-significant.

Here,

DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousands seed weight (g), YPP= Yield per plant (g).

4.3.4 Plant height (cm)

The direct effect of plant height on seed yield per plant was negative (-0.240). Plant height had a direct negative impact on yield per plant, as shown by Uddin *et al*. (2013), supporting the outcome. The aforementioned parameter showed positive but indirect effect on seed yield per plant via days to first flowering (0.002), days to 50% flowering (0.046), number of primary branches per plant (0.083), number of siliquae per plant (0.562), number of seeds per silique (0.234) and thousand seed weight (0.252). The trait showed negative indirect effect on seed yield per plant via days to maturity (-0.184), number of secondary branches per plant (-0.051), length of siliquae (-0.006) and beak length (-0.010). Plant height had positive genotypic as well as significant association with seed yield per plant (0.687). Rathod *et al*. (2013) reported plant height has negative direct contributions towards yield.

4.3.5 Number of primary branches per plant

Number of primary branches per plant showed positive direct effect (0.305) towards seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 50% flowering (0.009), number of siliquae per plant (1.126), length of siliqua (0.001) and beak length (0.006). The trait showed negative indirect effect on seed yield per plant via days to first flowering (-0.001), days to 80% maturity (-0.175), plant height (-0.065), number of secondary branches per plant (-0.135), number of seeds per siliqua (-0.758) and thousand seed weight (-0.040). Akter (2020) reported the same findings. The trait had non-significant positive genotypic association with seed yield per plant (0.274). Chaubey *et al.* (2022) reported number of primary branches per plant nullified lower magnitude of positive direct effect with yield.

4.3.6 Number of secondary branches per plant

Number of secondary branches per plant showed negative direct effect (-0.259) towards seed yield per plant. The trait showed positive indirect effect on seed yield per plant via number of primary branches per plant (0.159), number of siliquae per plant (1.780), length of siliquae (0.005) and beak length (0.124). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.018), days to 50% flowering (-0.216), days to maturity (-0.078), plant height (-0.047), number of seeds per siliqua (-

0.776) and thousand seed weight (-0.315). The trait had positive non-significant genotypic association with seed yield per plant (0.358).

4.3.7 Number of siliquae per plant

Number of siliquae per plant exhibited highest positive direct effect (2.224) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to maturity (0.002), number of primary branches per plant (0.155), length of siliqua (0.004) and beak length (0.070). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.024), days to 50% flowering (-0.267), plant height (-0.061), number of secondary branches per plant (-0.207), number of seeds per siliqua (-1.163) and thousand seed weight (-0.263). The trait had significant positive genotypic association with seed yield per plant (0.470). Direct effect (2.224) is positive and higher than the genotypic correlation coefficient (0.470) which exhibited true relationship between them and direct selection for this trait will be effective for yield improvement. The results were in conformity with Chaubey *et al.* (2022) where they reported positive direct effects of number of siliquae per plant towards yield at both genotypic and phenotypic level (0.121, 0.088), respectively.

4.3.8 Siliqua length (cm)

Length of siliqua showed positive direct effect (0.022) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via plant height (0.063), number of primary branches per plant (0.009), number of siliquae per plant (0.390) and beak length (0.283). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.002), days to 50% flowering (-0.056), days to maturity (-0.229), number of secondary branches per plant (-0.054), number of seeds per siliqua (-0.406) and thousand seed weight (-0.230). The trait had non-significant negative genotypic association with seed yield per plant (-0.210). Meena *et al.* (2020) investigation are in conformity with the results where they reported siliqua length had positive direct contribution towards yield.

4.3.9 Beak length (cm)

Beak length showed positive direct effect (0.342) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via plant height (0.007), number of primary branches per plant (0.006), number of siliquae per plant (0.456) and siliqua length (0.018). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.002), days to 50% flowering (-0.023), days to maturity (-0.328), number of secondary branches per plant (-0.094), number of seeds per siliqua (-0.427) and thousand seed weight (-0.056). The trait had non-significant negative genotypic association with seed yield per plant (-0.102).

4.3.10 Number of seeds per siliqua

Number of seeds per siliqua showed positive direct effect (1.734) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 1st flowering (0.031), days to 50% flowering (0.340) and number of secondary branches per plant (0.116). The trait showed negative indirect effect on seed yield per plant via, days to maturity (-0.271), plant height (-0.032), number of primary branches per plant (-0.133), number of siliquae per plant (-1.491), siliqua length (-0.005), beak length (-0.084) and thousand seeds weight (-0.023). The trait had positive non-significant genotypic association with seed yield per plant (0.181).

4.3.11 Thousand seeds weight (g)

Thousand seed weight showed positive direct effect (0.821) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 1st flowering (0.011), days to 50% flowering (0.302) and number of secondary branches per plant (0.099). The trait showed negative indirect effect on seed yield per plant via, days to maturity (-0.350), plant height (-0.074), number of primary branches per plant (-0.015), number of siliquae per plant (-0.711), siliqua length (-0.006), beak length (-0.023) and number of seeds per siliqua (-0.049). The trait had positive non-significant genotypic association with seed yield per plant (0.005).

The residual effect of path analysis revealed that a few characters of really important to the contribution to the yield which are not taken in the study but also consider in future. Some residual effects was also observed this experiment (R= 0.0226). It was suggested

that during selection, these characters may be given due to emphasis for developing high yielding varieties. Hence, emphasis should be given to select these traits for yield enhancement of *Brassica*.

4.4 Combining ability analysis:

The analysis of variance for combining ability studies revealed that variances due to GCA and SCA were significant for all the characters under study. The results represented that additive as well as non-additive gene action played significant role for the inheritance of these characters (Table 9). Similar results were reported by Adhikari *et al.*, 2018. De *et al.* (2009) reported that estimated mean square due to GCA and SCA effects were significant for plant height, 25-pod weight, 100 seed weight and seed number per pod while only SCA effects were significant for the remaining characters like number of branches per plant, number of seed per 15 pods and seed yield per plant that indicated presence of both additive and non-additive genetic variances were played important role for the inheritance of the aforementioned characters. Nasim *et al.* (2014) reported that the GCA mean square was significant for pods on main raceme only where the SCA variances was significant for all the characters like primary branches per plant, pod length, 100-seed weight and seed yield per plant that means only non-additive gene actions involved for the inheritance of the aforementioned characters.

The SCA variance component were observed to be higher than respective GCA variances component (σ^2GCA/ σ^2SCA ratio <1) for all the characters, which indicates the preponderance of non-additive gene action for the inheritance of this characters (Table 10). De *et al.* (2009) as well as Ram *et al.* (1976) reported the higher effect of non-additive gene action than additive gene action for yield and most of its yield contributing characters. Niranjana *et al.* (2014) found preponderance of non-additive gene actions for the inheritance of all the yield and yield contributing characters.

Table 9. Analysis of variances (Mean Square) of GCA and SCA value for twelve characters of *Brassica rapa*

Source	d.f	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
GCA	6	13.12**	16.19**	8.64**	124.61**	0.45*	5.16**	2335.23**	0.53**	0.13**	42.65**	0.10**	1.98**
SCA	21	3.86**	5.39**	7.92**	49.77**	0.23**	1.08**	341.14**	0.20*	0.03	8.47**	0.04**	0.47*
Error	54	0.73	0.43	1.08	10.93	0.06	0.01	27.43	0.11	0.03	1.52	0.01	0.22

* = Significant at 5% level of probability, ** = Significant at 1% level of probability

DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousands seed weight (g), YPP= Yield per plant (g).

Table 10. Estimation of genetic components of variance due to general combining ability, specific combining ability and σ^2gca/ σ^2sca ratio

Variance component	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
σ^2gca	1.03	1.20	0.08	8.32	0.02	0.45	221.57	0.04	0.01	3.80	0.01	0.17
σ^2sca	3.13	4.96	6.84	38.84	0.17	1.07	313.71	0.09	0.01	6.95	0.03	0.25
σ^2gca/ σ^2sca	0.33	0.24	0.01	0.21	0.12	0.42	0.71	0.44	1.00	0.55	0.33	0.68

Here, DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliqua per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousand seeds weight (g), YPP= Yield per plant (g).

4.4.1 Analysis of general combining ability (GCA) effects

4.4.1.1 Days to first flowering

Negative GCA effects was expected for days to first flowering. It helped to develop early maturing varieties. Among the selected parents P6 (-1.70) exhibited the highest negative significant GCA effects, considered as the best general combiner for early flowering followed by P5 (-1.03) and P2 (-0.96). On the contrary, P1 (1.33) followed by P3 (1.01) had the highest positive value in case of days to first flowering (Table 12). In his study, Singh *et al*. (2019) identified two of the six lines as good general combiners for days to first flowering. Chaurasiya *et al.* (2018) reported out of 7 parental lines, three lines exhibited negative GCA value where two lines were highly significant for the concerned characters.

4.4.1.2 Days to 50% flowering

In case of days to 50% flowering also negative GCA effects was desirable. Three parents showed negative GCA effects, among them P6 (-1.62) was reported the best combiner line as it had the highest significant negative value followed by P5 (-1.21) and P2 (-1.06) whereas P4 (1.83) had the highest positive significant value for days to 50% flowering (Table 12). Singh *et al.* (2010) and Nasrin *et al.* (2011) reported negative significant GCA effects for days to maturity.

4.4.1.3 Days to maturity

If days to maturity exhibited significant negative GCA effects, it will be desirable for outcoming early matured plants. Among the seven parental material, five parents showed negative GCA effects however, only P6(-1.04) showed the desired negative GCA effects with strong significance and considered as best general combiner for days to maturity (Table 12) while the maximum positive and highly significant value was observed in P4 (1.96). Niranjana *et al.* (2014) reported HYOLA 401 parents of *B. juncea* was good general combiner for earliness as it expressed significant negative GCA estimates for days to 50% flowering and days to maturity.

Table 11. General Combining Ability (GCA) of twelve characters of 7 parents in mustard (*Brassica rapa*)

Parents	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
P1	1.33**	1.38**	-0.22	-0.50	0.08	-0.43**	-5.97**	-0.47**	-0.26**	1.51**	0.01	0.25
P2	-0.96**	-1.06**	-0.52	-5.54**	-0.23**	-0.29**	-0.46	0.29**	0.05	-1.43**	-0.04	-0.73**
P3	1.01**	0.57**	0.52	-0.08	-0.22*	-0.52**	-13.74**	0.01	-0.01	3.04**	0.04	0.19
P4	0.97**	1.83**	1.96**	5.00**	0.06	-0.45**	-8.69**	0.11	0.08	0.28	0.18**	0.02
P5	-1.03**	-1.21**	-0.33	4.09**	0.23**	1.29**	28.66**	0.09	0.08	-2.55**	-0.01	0.76**
P6	-1.70**	-1.62**	-1.04**	-3.20**	0.29**	0.90**	14.85**	0.09	0.05	-2.41**	-0.17**	-0.26*
P7	0.38	0.12	-0.37	0.21	-0.22*	-0.48**	-14.64**	-0.12	0.01	1.57**	-0.01	-0.22
Max	1.33	1.83	1.96	5.00	0.29	1.29	28.66	0.29	0.08	3.04	0.18	0.76
Min	-1.70	-1.62	-1.04	-5.54	-0.23	-0.48	-14.64	-0.47	-0.26	-2.55	-0.17	-0.73
SE (gi)	0.21	0.16	0.26	0.82	0.06	0.02	1.29	0.08	0.04	0.31	0.03	0.11
SE (sij)	0.53	0.40	0.64	2.03	0.15	0.06	3.21	0.20	0.10	0.76	0.07	0.29

* = Significant at 5% level of probability, ** = Significant at 1% level of probability

Here, DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousands seed weight (g), YPP= Yield per plant (g)

4.4.1.4 Plant height (cm)

Plant height is one of the important traits for development of dwarf plant. As lodging is a problem in case of mustard. Hence, for plant height negative GCA effects was desirable. Strong significance and negative effects were found in P2(- 5.54) and P6 (-3.20). On the contrary, P4 (5.00) and P5 (4.09) revealed the highest positive value with strong significance (Table 11). These parental lines can be produce tallest plant through hybridization. Negative GCA effects for plant height were also reported by Niranjana *et al.* (2014).

4.4.1.5 Number of primary branches per plant

In case of number of primary branches per plant, positive GCA effects of parent was desirable to get more number of branches per plant in their hybrid combinations which may ultimately increase yield of *Brassica*. P6 (0.29) was considered as the best general combiner as it possessed the highest positive and significant value followed by P5 (0.23), while, P2 (-0.23) parent showed highest significant negative value for primary branches per plant followed by P7 (-0.22) (Table 11). Chaurasiya *et al.* (2018) found among 7 parents, 2 parents showed positive and significant GCA for number of primary branches per plant.

4.4.1.6 Number of secondary branches per plant

In considering to get the best general combiner for number of secondary branches per plant, the parent P5 (1.29) showed the strong significance with positive direction which was followed by P6 (0.90) while P7 (-0.48) was regarded as poor general combiner. Kaur *et al.* (2019) worked on 8 parents, among them 2 showed positive and significant GCA effects for number of secondary branches per plant.

4.4.1.7 Number of siliquae per plant

Number of siliquae per plant is one of the important traits for increasing yield. Positive and significant general combining effects are desirable for number of siliquae per plant. Parental materials P5 (28.66) showed highest positive and significant GCA effects, hence it was reported as the best combiner which is followed by P6 (14.85). On the contrary P7 (-14.64) was poor combiner because it exhibited maximum undesirable effects for number of siliquae which was followed by P3(-13.74) (Table 11). Nasim *et*

al. (2014) reported out of 5 parental lines, 2 lines namely- G-902 (3.01) and G-909 (7.37) exhibited desirable positive GCA effects.

4.4.1.8 Siliqua length (cm)

In case of siliqua length parental line P2 (0.29) was considered as the best general combiner as only it possessed the highest positive and significant value, while, P1 (-0.47) parent showed highest negative and significant value for this character (Table 11). Kaur *et al.* (2019) found among the parental lines, only 1 parent showed positive and significant GCA for siliqua length. Niranjana *et al.* (2014) reported singificant positive heterosis of two parental lines for siliqua length.

4.4.1.9 Beak length (cm)

In case of beak length negative GCA effects of parent was desirable. P1 (-0.26) was considered as the best general combiner as it possessed the highest negative and significant value, while, P4 (0.08) and P5 (0.08) parent showed highest positive value for beak length (Table 11).

4.4.1.10 Number of seeds per siliqua

In case of number of seeds per siliqua, positive GCA effects of parent was desirable to get more yield. For number of seeds per siliqua, the parental lines P3 (3.04) was considered as the best general combiner as it possessed the highest positive and significant value followed by P1 (1.51), while, P5 (-2.55) parent showed highest negative and significant value for number of seeds per siliqua followed by P6 (-2.41) (Table 11). Adhikari *et al.* (2018) found among 10 parents, only 1 parent showed positive and significant GCA for number seeds per siliqua and considered as good general combiner for this traits.

4.4.1.11 Thousand seeds weight (g)

Positive GCA effects for thousand seed weight is desirable, because heavier the seed higher will be the yield. The analyzed result revealed that parental line P4 (0.18) exhibiting positive significance of GCA and positive but non significance result obtained by P3 and P1 (Table 11) indicating the tendency of the parental lines to boost the yield. However, negative and significant GCA effects were also observed in

parental line P6 (-0.17). In case of 1000 seed weight, Gul *et al.* (2019) and Maurya *et al.* (2014) observed most of the varieties had negative and significant GCA effects.

4.4.1.12 Yield per plant (g)

A promising general combiner will be chosen from parents with a positive GCA based on yield per plant. P5 (0.76) had the highest positive significant values among the chosen parents, making it the superior combiner for high yielding cultivars, followed by P1 (0.25). Table 11 indicates that P2 (-0.73) and P6 (-0.26) did not exhibit good combiners for improving this trait, as they demonstrated significant but negative GCA effects. Four of the eight varieties' seed yields per plant showed a positive effect, according to Inayat *et al.* (2019).

The parents having high general combining ability and fixable type of gene action, (Additive and additive × additive) types of epistasis, these could be successfully exploited by developing homozygous line have used for improved character for which improvement was desired (Chaurasia *et al.*, 2018). These parental lines might be utilized for producing the intermating populations in order to get desirable recombinants in *Brassica rapa*.

4.4.2 Analysis of specific combining ability (SCA) effects

Analysis of specific combining ability is important parameter for judging the specific combinations for exploiting it through heterosis breeding programme. The good specific combinination are selected based on their SCA effects. The effects of SCA are due to three types of gene actions: dominance, additive x dominance, and dominance x dominance. These gene actions produce high performance in specific cross combinations. The magnitude and direction of the noteworthy effects for the chosen parents, considering relevant comparisons and providing insight for the upcoming breeding program. Table 12 represented the estimated specific combining ability effects for each of the twelve characters of the seven parental lines.

4.4.2.1 Days to first flowering

Negative amplitude of SCA value were preferred to obtain plants with early maturity in case of days to first flowering. Among the 21 F_1s derived from the half diallel mating, 12 lines had negative SCA effects in which V3 (-2.84) was noted for the highest value followed by V15 (-2.58), V13 (-2.51), V5(-2.18), V2(-1.89) V14(-1.84) and V1(-1.58). V13 was obtained from a high general combiner × low general combiner, and V5 was obtained from a high general combiner × poor general combiner. Hybrids V3 and V15 were created by combining two poor general combiners.

4.4.2.2 Days to 50% flowering

Days to 50% flowering exhibited negative estimates of SCA effects which was useful to obtain early mature plants. Among the 21 F_1s derived from the diallel mating, 16 lines had negative SCA effects in which V15 (-3.34) was noted for the highest negative value followed by V18 (-2.60), V13 (-2.34), V2 (-1.94), V3 (-1.86), V17 (-1.53) and V12 (-1.38). Hybrid V15 was the good specific combiner which was obtained through the combination of two poor general combiners, which reflected non-additive gene action, that is nonfixable in nature and could be exploited only through heterosis breeding for further improvement. Adhikari *et al.* (2018) reported 3 crosses which had significant negative SCA for flowering, among them two crosses derived from poor general combiner × poor general combiner.

4.4.2.3 Days to maturity

One useful metric for choosing early-maturing plants is the number of days to maturity. Negative estimates of SCA effects were preferable in the case of days to maturity in order to obtain plants with earliness. Among the 21 F_1s derived from the diallel mating, 19 lines had negative SCA effects in which V15 (-2.82) was noted for the good specific combiner followed by V14 (-2.48), V3 (-2.41), V2 (-2.30), V13 (-2.19). Singh *et al.* (2022) provided support for it by observing that three F_1 lines had significant negative SCA effects.

Table 12. Estimation of specific combining ability (SCA) of twelve character's of 21 F_1's derived from 7 ×7 half diallel cross in mustard (*Brassica rapa*)

Crosses	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
V1 (P1×P2)	-1.58**	-1.30**	-1.93**	-1.63	-0.15	0.24**	-0.85	-0.98**	0.01	-3.43**	0.47**	-0.21
V2 (P1×P3)	-1.89**	-1.94**	-2.30**	2.79	0.02	0.29**	11.59**	0.08	-0.02	1.27	-0.18*	0.84**
V3 (P1×P4)	-2.84**	-1.86**	-2.41**	-1.83	-1.07**	0.12	-18.09**	-0.26	-0.16	1.79*	-0.20*	-1.10**
V4 (P1×P5)	1.49**	1.51**	0.89	9.95**	0.13	-0.59**	11.16**	-0.32	-0.12	-1.51	0.06	0.32
V5 (P1×P6)	-2.18**	-1.08*	-1.74*	-1.28	0.23	-0.89**	-16.97**	-0.45*	-0.13	1.75*	0.12	-0.01
V6 (P1×P7)	0.08	-1.16**	-0.07	1.30	0.28	0.29**	4.26	0.18	-0.01	1.27	-0.01	0.37
V7 (P2×P3)	0.08	0.51	-0.67	-7.30**	0.49**	0.48**	-18.71**	0.64**	0.22*	-4.42**	0.15*	-1.46**
V8 (P2×P4)	1.45	-0.75	-1.44*	-2.45	-0.09	0.11	-8.80*	-0.23	-0.08	2.07*	-0.19*	-0.10
V9 (P2×P5)	1.12*	-0.05	-0.82	0.13	0.20	-1.40**	-26.76**	-0.39	-0.20	2.53**	0.04	-0.10
V10 (P2×P6)	1.12*	0.03	-1.11	-7.77**	-0.96**	-1.37**	-20.82**	0.76**	0.22*	5.13**	-0.27**	0.42
V11 (P2×P7)	0.71	-0.71	-0.78	-7.95**	0.26	0.01	0.28	0.11	-0.20	-2.92**	-0.07	-0.49
V12(P3×P4)	-0.18	-1.38**	-0.82	0.42	-0.50**	0.35**	-10.39**	0.17	0.10	0.23	-0.13	-0.38
V13 (P3×P5)	-2.51**	-2.34**	-2.19**	0.97	-0.50**	-1.53**	6.59	0.03	-0.23*	-3.00**	-0.25**	0.23
V14 (P3×P6)	-1.84**	-1.27**	-2.48**	-4.37*	0.14	-0.84**	18.67**	-0.21	-0.22*	-4.68**	0.01	-0.17
V15 (P3×P7)	-2.58**	-3.34**	-2.82**	16.15**	0.05	0.44**	2.63	-0.44*	-0.24*	1.94*	0.05	0.44
V16 (P4×P5)	0.86	0.73	-0.96	-6.88**	-0.39*	-0.67**	-8.59*	0.20	0.04	1.39	-0.08	0.06
V17 (P4×P6)	0.86	-1.53**	-1.93**	3.91	0.69**	-0.98**	-8.99*	0.25	0.10	-1.42	-0.06	-084**
V18 (P4×P7)	-0.88	-2.60**	-1.93**	4.50*	0.27	0.54**	19.85**	-0.24	-0.02	-0.07	-0.19*	0.69*
V19 (P5×P6)	-0.14	-1.16**	-1.63*	6.93**	0.38*	0.89**	-15.37**	0.11	0.08	2.31**	0.10	0.22
V20 (P5×P7)	-0.55	-0.90*	-1.30	-1.82	-0.51**	-0.50**	1.83	0.07	0.40**	-3.20**	-0.05	-0.61*
V21 (P6×P7)	-0.21	1.84**	2.07**	-7.43**	-0.33*	-1.18**	19.17**	-0.50*	-0.20	-2.11*	0.27**	-0.93**

Table 12 (Cont'd)

Crosses	DFF	D50%F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
SE(gi-gj)	0.32	0.25	0.39	1.25	0.09	0.04	1.97	0.13	0.06	0.47	0.04	0.18
SE(Sij-Sik)	0.79	0.61	0.96	3.06	0.23	0.09	4.84	0.31	0.15	1.14	0.10	0.43
SE (Sij-Skl))	0.78	0.60	0.95	3.02	0.23	0.09	4.78	0.31	0.15	1.13	0.10	0.42
SE(rij-rkl)	0.86	0.65	1.04	3.31	0.25	0.10	5.23	0.33	0.17	1.23	0.11	0.46

DFF= Days to 1st flowering, D50%F= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliquae per plant, SL= Siliqua length (cm), BL= Beak length (cm), NSS= Number of seeds per siliqua, TSW= Thousands seed weight (g), YPP= Yield per plant (g). * = Significant at 5% level of probability, ** = Significant at 1% level of probability

4.4.2.4 Plant height (cm)

Negative estimates of SCA effects were also preferred in the case of plant height to produce dwarf plants. Among the 21 F_1's derived from the diallel mating, 11 lines exhibited negative estimate of SCA effects in which V11 (-7.95) was noted for the best specific combiner followed by V10 (-7.77), V21 (-7.43), V7 (-7.30), V16 (-6.88), V14 (-4.37) and V8 (-2.45). Hybrid V11 was the good specific combiner which was obtained through the combination of good general combiner × poor general combiner, V10 developed from good general combiner × good general combiner, V21 from good general combiner × poor general combiner and V7 obtained from the combinations of good general combiner × average general combiner, which indicated additive type og gene action in controlling the expression of this trait. These cross combinations would give rise to transgressive segregants in later generations. Adhikari *et al.* (2018) reported 3 crosses which had significant negative SCA for plant height. Inayat *et al.* (2019) reported 24 cross combinations exhibited desired negative SCA effects for plant height among the crosses derived from 8×8 diallel crosses.

4.4.2.5 Number of primary branches per plant

Twelve crossings between the F_1 progenies showed the positive specific combining ability effects required to optimize siliqua production in a plant. As a result, they were identified as the best specific combiner for selection. Of the combinations, V17 (0.69), V7 (0.49), and V19 (0.38) showed the highest positive and significant SCA effects. The combinations of high general combiner and average general combiner produced the high SCA effects found in V17. On the other hand, high general combiner and high general combiner produced V19 and low general combiner and low general combiner produced the results of V7. Conversely, as shown in Table 12, negative SCA effects were noted in V3 (-1.07), V10 (-0.96), and so forth. While Chowdhury *et al.* (2004) and Singh *et al.* (2000) reported that the majority of the lines showed positive SCA effects for primary branches, Maurya *et al.* (2014) reported that out of 28 crossings, 13 crossings had positive SCA effects.

4.4.2.6 Number of secondary branches per plant

A total of 11 crosses reported the positive specific combining ability effects among the 21F_1 hybrids, which was desirable to produce maximum siliqua in a plant. Within the

combinations, V19(0.89), V18(0.54), V7(0.48) and V15(0.44) found as the highest positive and significant SCA effects, therefore, reported as the best specific combiner for selection. Good general combiner × good general combiner produced high SCA effects in V19, indicating additive gene action in controlling the expression of this trait. These cross combinations would result in transgressive segregants in subsequent generations, while V18, V7, and V15 derived from poor general combiner × poor general combiner combinations. On the other hand, negative SCA effects was observed in V13 (-1.53), V9 (-1.40), V10 (-1.37) and so on (Table 12). Akabari *et al.* (2014) reported out of 28 crossings, 15 crosses had positive SCA effects.

4.4.2.7 Number of siliquae per plant

In case of number of siliquae per plant, positive findings of SCA effects were useful to get high yielding genotype. Among the 21 F_1s produced from the diallel mating, 10 combinations exhibited positive SCA effects in which V18 (19.85) was reported for the best specific combiner followed by V21(19.17), V14(18.67), V2(11.59), V4(11.16), V13(6.59) and V6(4.26). Hybrid V18 was the good specific combiner which was obtained through the combination of poor general combiner × poor general combiner, V21 derived from good general combiner × poor general combiner and V14 obtained from the combinations of poor general combiner × good general combiner. Akabari *et al.* (2014) reported 8 crosses which had highly significant positive SCA for this trait.

4.4.2.8 Siliqua length (cm)

Siliqua length is an important yield contributing parameters, for which positive estimates of SCA is rewarding. In the present study, there were 2 crosses that revealed positive significant SCA effects for siliqua length (Table 12). The highest significant positive SCA value was illustrated by the cross combination V10 (0.76) followed by V7 (0.64) and reported as the best specific combiner for the related trait. Among the hybrid combinations, V10 and V7 was produced due to the combination of high general combiner × average general combiner, which indicated presence of additive gene action in controlling the expression of this trait and these cross combinations would give rise to transgressive segregants in subsequent generations. Therefore, in a future breeding program, these cross combinations could be chosen to produce a desirable hybrid with longer siliqua. However, negative but significant SCA effects for the aforementioned

traits was observed in 4 cross combinations. Significant siliqua length was also reported by Inayat *et al*. (2019) and Singh *et al*. (2019), who discovered that the majority of cross combinations had positive and significant SCA effects.

4.4.2.9 Beak length (cm)

Three of the twenty-one cross combinations had significant negative SCA effects on beak length (Table 12). Highest significant negative SCA effects was illustrated by the cross combination V15 (-0.24) followed by V13 (-0.23).

4.4.2.10 Number of seeds per siliqua

There were 7 crosses that had positive significant SCA effects for number of seeds per siliqua (Table 12). The highest significant positive SCA value was reported by the cross combination V10 (5.13) which was followed by V9 (2.53), V19 (2.31) and V8 (2.07). Among the combinations, V10 and V9 was produced through the combination of poor general combiner × poor general combiner, which indicated present of non-additive gene action in controlling the expression of this trait. However, negative and significant SCA effects for number of seeds per siliqua was observed in 7 cross combinations. According to Inayat *et al*. (2019) and Singh *et al*. (2019), there were negative SCA effects for seeds per siliqua in half of the crossing lines.

4.4.2.11 Thousand seeds weight (g)

Three crosses had positive significant SCA effects for thousand seeds weight out of twenty-one cross combinations (Table 12). Considered the best specific combiner for the trait in question, cross combination V1 (0.47) produced the highest significant positive SCA effects, followed by V21 (0.27). Combining of average general combiner with poor general combiner and poor general combiner with poor general combiner resulted in the combinations V1 and V21, respectively. However, six cross combinations showed significant and negative SCA effects for 1000-seed weight. Additionally, Gul *et al.* (2019) calculated adverse effects for the majority of the lines.

4.4.2.12 Yield per plant (g)

Nine of the twenty-one hybrids had favorable SCA effects for yield per plant (Table 12). V2 (0.84) showed the highest SCA effects, followed by V18 (0.69). The combinations of poor general combiner × poor general combiner and average general combiner × average general combiner produced the high SCA effects of V18 and V2, respectively. As a result, these crosses can be assessed to produce heterotic hybrid combinations and recognized as an improved specific combiner for yield. The best lines in F_1 populations had positive, significant effects on yield per plant, according to studies by Gul *et al*. (2019) and Maurya *et al.* (2014), while Inayat *et al*. (2019) found non-significant SCA effects on yield per plant.

4.5 Heterosis analysis

Heterosis is an appropriate tool for predicting the hybrid performance. Heterotic investigations can provide basis for exploitation of valuable hybrid combinations in further breeding procedure (Nassimi *et al.*, 2006b). Exploitation of heterotic effects for yield and yield contributing characters provides an additional opportunity to improve and develop hybrids offspring for yield component. Standard heterosis/ economic heterosis is used to determine the amplitude of superior lines (F_1) over a variety which is commercially popular. In this investigation, BARI sharisha-14 was utilized as a check variety to report the F_1 populations for the observation. Heterotic value of the F_1 hybrids for different characters were measured over mid parent (MP), better parent (BP) and standard check (s) and represented Table 13.

4.5.1 Days to first flowering

For days to first flowering, significant negative heterosis is desirable. A significant along with high amplitude of heterosis was illustrated for days to first flowering in comparison to the mid parent, better parent and commercial variety. For the aforementioned characters significant negative heterosis over mid parent was observed in 13 hybrids ranging from -4.43% to -16.49%. Highest negative heterosis over mid parent was observed in V15 (16.49%) which is followed by V2 (-16.15%), V13 and V14 (-14.59%) and V3 (-14.56%). All the crosses showed negative heterosis over better parent except V9 and V10. Highest significant negative value was recorded in V13 (-24.77%) and V14 (-24.77%). All the 21 crosses exhibited negative heterosis over

commercial variety, where the highest negative heterosis was observed in V19 (-16.49%) which is followed by V5 (-15.47%), V13 (-15.47%) and V14 (-15.47%). Liton *et al.* (2017) reported significant negative heterosis over mid parent and better parent. Significant negative heterosis is desirable for the selection of hybrid in short duration. Additionally, the hybrids performing significant negative heterosis over both mid parent, better parent as well as commercial variety might be useful for developing early maturing varieties.

4.5.2 Days to 50% flowering

In case of days to 50% flowering, significant negative heterosis is useful for earliness. Among the 21 crosses, 20 crosses exhibited significant negative mid parent heterosis where the crosses V15 (-19.64%) showed highest negative heterosis followed by V18 (-15.87%), V13 (-14.96%), V2 (-14.89%) and V12 (-14.18%). All the 21 crosses exhibited significant negative heterosis over better parent, where the crosses V13 (-22.88%) revealed the highest negative heterosis over BP followed by V15 (-22.02%), V17 (-21.32%), V14 (-21.18%) and V18 (19.67%). Over commercial variety all the 21 crosses showed significant negative heterosis, the cross combination V19 (-20.73%) exhibited highest negative heterosis followed by V13 (-18.03%), V15 (-17.12%), V10 (-17.11%) and V14 (-16.22%). Kaur *et al.* (2019) reported significant negative heterosis over better parent and standard check for the concerned traits, where they reported highest negative heterosis over better parent and standard check was -13.19% and -13.66% respectively.

4.5.3 Days to maturity

In case of days maturity significant negative heterosis is desirable for the development of short durated crop variety. Among the 21 crosses, most of the crosses exhibited significant negative heterosis over mid parent value except V21, where the crosses V14 (-7.98%) showed highest negative heterosis followed by V2 (-7.89.87%), V15 (-7.78%), V3 (-7.43%) and V13 (-7.37%). Similarly, 20 crosses exhibited significant negative heterosis over better parent, where the crosses V14 (-10.69%) revealed the highest negative heterosis over BP followed by V17 (-10.46%), V15 (-10.33%), V3 (-10.10%) and V18 (-9.75%). Over commercial variety, the cross combination V5 (-5.46%), V14 (-5.46%), V19 (-5.46%) exhibited highest negative heterosis. For the

majority of the crosses of the relevant traits, Kaur *et al*. (2019) reported significant negative standard heterosis where the highest negative heterosis over standard check was reported -8.58%.

4.5.4 Plant height

For plant height, significant negative heterosis was desirable for development of plant having short stature. At the same time positive significant heterosis also desirable for plant height in order to get maximum yield. Out of 21 cross combinations, highest negative significant heterosis over mid parent, better parent and check variety was observed in V10 (-16.41%, -17.91% and -14.28%, respectively), whereas highest positive significant heterosis was recorded in V15 and the ranges over mid parent, better parent and check variety was 19.51%, 18.01% and 18.01% respectively. That indicated the cross combination V10 can be selected for dwarfness and V15 can be selected for maximize the yield of *B. rapa.* Gain (2021) reported significant negative heterosis for plant height in *B. juncea*.

4.5.5 Number of primary branches per plant

In case of number of primary branches per plant significant positive heterosis is useful for getting higher yield. Among the 21 crosses, 7 crosses exhibited positive heterosis over mid parent value where the crosses V7 (6.81%) and V17 (7.35%) showed significant positive heterosis. 2 crosses exhibited highly significant positive heterosis over better parent. Over commercial variety 11 crosses showed significant positive heterosis, the cross combination V17 (29.33%) exhibited highest significant positive heterosis followed by V19 (26.57%) and V5 (20.67%). Kaur *et al.* (2019) reported four cross combinations exhibited significant positive heterobeltiosis for the concerned traits ranging from 31.25% to 38.89%, whereas seven cross showed highest positive useful heterosis ranging from 33.33% to 66.67% over the commercial check. Similar results were reported by Patel *et al.* (2010) and Meena *et al.* (2014).

Table 13: Estimation of heterosis over mid parent (MPH), heterobeltiosis over better parent (BPH) and standard heterosis (SH) over the check varieties in 21 F_1's hybrids

Cross combinations	Days to first flowering			Days to 50% flowering			Days to maturity		
	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)
V1 (P1×P2)	-8.98**	-20.36**	-12.77**	-9.35**	-17.10**	-12.62**	-6.36**	-6.90**	-5.07**
V2 (P1×P3)	-16.15**	-16.52**	-6.19**	-14.89**	-15.26**	-9.92**	-7.89**	-9.59**	-4.29**
V3 (P1×P4)	-14.56**	-18.53**	-9.27**	-12.95**	-14.75**	-6.30**	-7.43**	-10.10**	-2.73**
V4 (P1×P5)	-0.52ns	-12.03**	-2.04ns	-1.41ns	-10.26**	-5.41**	-2.89**	-3.45**	-1.56**
V5 (P1×P6)	-14.15**	-24.08**	-15.47**	-9.43**	-17.95**	-13.51**	-6.20**	-7.28**	-5.46**
V6 (P1×P7)	-8.00**	-12.03**	-2.04ns	-11.39**	-13.67**	-9.00**	-3.67**	-4.60**	-2.73**
V7 (P2×P3)	-5.26**	-17.42**	-7.21**	-6.98**	-15.26**	-9.92**	-5.86**	-8.11**	-2.73**
V8 (P2×P4)	1.65ns	-7.16**	-6.19**	-8.68**	-18.05**	-9.92**	-6.16**	-7.37**	-1.95**
V9 (P2×P5)	6.09**	4.88**	-10.30**	-3.62**	-4.11**	-16.22**	-4.65**	-4.65**	-3.90**
V10 (P2×P6)	3.64*	2.39ns	-12.37**	-4.16**	-5.13**	-17.11**	-5.26**	-5.81**	-5.07**
V11 (P2×P7)	1.13ns	-7.21**	-7.21**	-8.64**	-14.40**	-14.40**	-4.28**	-5.74**	-3.90**
V12 (P3×P4)	-8.20**	-12.83**	-2.04ns	-14.18**	-15.59**	-7.22**	-6.57**	-7.58**	0.00
V13 (P3×P5)	-14.59**	-24.77**	-15.47**	-14.96**	-22.88**	-18.03**	-7.37**	-9.59**	-4.29**
V14 (P3×P6)	-14.59**	-24.77**	-15.47**	-12.68**	-21.18**	-16.22**	-7.98**	-10.69**	-5.46**
V15 (P3×P7)	-16.49**	-21.08**	-11.32**	-19.64**	-22.02**	-17.12**	-7.78**	-10.33**	-5.07**
V16 (P4×P5)	1.66ns	-6.12**	-5.13**	-4.58**	-14.75**	-6.30**	-5.42**	-8.66**	-1.17ns
V17 (P4×P6)	-0.56ns	-8.17**	-7.21**	-11.53**	-21.32**	-13.51**	-6.76**	-10.46**	-3.12**
V18 (P4×P7)	-6.68**	-7.16**	-6.19**	-15.87**	-19.67**	-11.70**	-6.19**	-9.75**	-2.34**
V19 (P5×P6)	-2.42ns	-2.42ns	-16.49**	-7.86**	-8.84**	-20.73**	-5.65**	-6.20**	-5.46**
V20 (P5×P7)	-4.43**	-11.33**	-11.33**	-9.19**	-15.32**	-15.32**	-4.66**	-5.03**	-4.29**
V21 (P6×P7)	-5.57**	-12.37**	-12.37**	-1.93ns	-9.00**	-9.00**	-0.98ns	-1.17ns	-1.17ns

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, ns= non-significant.

Table 13 (Cont'd)

Cross combinations	Plant height (cm)			Number of primary branches per plant			Number of secondary branches per plant	
	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)
V1 (P1×P2)	-5.70**	-9.53**	-5.64**	-6.36**	-12.40**	2.95ns	-57.58**	-75.65**
V2 (P1×P3)	7.42**	6.79**	4.12*	-3.57ns	-9.55**	6.30*	-45.95**	50.00**
V3 (P1×P4)	-0.07ns	-7.42**	4.58**	-24.40**	-25.80**	-9.45**	-100.00**	-100.00**
V4 (P1×P5)	14.30**	9.37**	15.31**	-2.93ns	-5.69**	17.52**	-61.85**	-80.31**
V5 (P1×P6)	-1.46ns	-3.53*	2.99ns	0.42ns	1.49ns	20.67**	-86.61**	-93.07**
V6 (P1×P7)	4.22**	2.93ns	2.93ns	2.62ns	-5.03*	11.61**	52.94ns	-23.53ns
V7 (P2×P3)	-11.62**	-14.50**	-10.83**	6.81**	6.50*	9.65**	-36.30**	-62.61**
V8 (P2×P4)	-8.88**	-12.38**	-1.01ns	-7.54**	-15.00**	3.74ns	-79.53**	-88.69**
V9 (P2×P5)	-4.03*	-4.55**	0.63ns	-0.61ns	-9.48**	12.80**	-88.40**	-92.33**
V10 (P2×P6)	-16.41**	-17.91**	-14.38**	-17.62**	-23.34**	-8.86**	-100.00**	-100.00**
V11 (P2×P7)	-13.06**	-14.58**	-11.19**	3.70ns	2.50ns	4.92ns	-100.00*	-100.00**
V12 (P3×P4)	1.88ns	-5.10**	7.21**	-14.79**	-21.45**	-4.13ns	-18.75ns	-35.00ns
V13 (P3×P5)	5.31**	1.34ns	6.86**	-12.98**	-18.87**	-0.98ns	-100.00**	-100.00**
V14 (P3×P6)	-4.70**	-6.15**	-6.15**	1.37ns	-5.13*	12.80**	-89.11**	-93.33**
V15 (P3×P7)	19.51**	18.01**	18.01**	-0.48ns	-1.91ns	0.98ns	100.00ns	0.00
V16 (P4×P5)	-4.65**	-7.83**	4.12*	-13.33**	-14.22**	6.89**	-65.23**	-82.22**
V17 (P4×P6)	0.76ns	-4.78**	7.58**	7.35**	5.97**	29.33**	-90.57**	-95.16**
V18 (P4×P7)	4.74**	-1.28ns	11.53**	-0.18ns	-9.19**	10.83**	516.67**	208.33**
V19 (P5×P6)	6.46**	4.00*	9.65**	3.96ns	1.58ns	26.57**	-23.32**	-26.77**
V20 (P5×P7)	1.63ns	-0.99ns	4.39**	-11.83**	-20.54**	-0.98ns	-59.08**	-79.55**
V21 (P6×P7)	-8.61**	-8.86**	-8.36**	-5.22**	-12.75**	3.74ns	-100.00**	-100.00**

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, ns= non-significant.

Table 13 (Cont'd)

Cross combinations	Number of siliquae per plant			Siliqua length (cm)			Beak length (cm)		
	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)
V1 (P1×P2)	-18.83**	-31.90**	38.69**	-27.18**	-31.73**	-25.78**	-7.88ns	-21.28**	-23.97**
V2 (P1×P3)	14.77**	-0.68ns	38.78**	-5.73ns	-6.10ns	-10.66**	-17.41*	-30.61**	-30.14**
V3 (P1×P4)	-29.89**	-32.52**	1.90ns	-14.15**	-17.08**	-15.13**	-21.77**	-34.46**	-33.56**
V4 (P1×P5)	1.07ns	-22.47**	101.40**	-16.13**	-17.97**	-16.86**	-18.22**	-31.29**	-30.82**
V5 (P1×P6)	-27.29**	-42.67**	38.76**	-17.62**	-19.85**	-19.38**	-21.77**	-34.46**	-33.56**
V6 (P1×P7)	5.49ns	-9.49**	26.40**	-9.24**	-11.43**	-11.43**	-14.63*	-28.08**	-28.08**
V7 (P2×P3)	-34.00**	-50.66**	1.64ns	13.36**	5.88ns	15.12**	7.64ns	5.44ns	6.16ns
V8 (P2×P4)	-30.53**	-39.80**	24.01**	-5.15ns	-8.02**	0.00	-6.57ns	-8.78ns	-7.53ns
V9 (P2×P5)	-34.03**	-40.86**	53.64**	-8.69**	-11.05**	-3.29ns	-14.58**	-16.33**	-15.75*
V10 (P2×P6)	-36.95**	-41.64**	43.17**	13.52**	9.27**	18.80**	12.11ns	9.46ns	10.96ns
V11 (P2×P7)	-15.89**	-37.53**	28.69**	-2.14ns	-6.06*	2.13ns	-18.47**	-19.86**	-19.86**
V12 (P3×P4)	-19.55**	-50.58**	1.79ns	4.14ns	0.19ns	2.33ns	-0.34ns	-0.68ns	0.68ns
V13 (P3×P5)	1.11ns	-29.59**	82.92**	0.69ns	-2.66ns	-0.58ns	-22.45**	-22.45**	-21.92**
V14 (P3×P6)	4.85ns	-25.47**	80.38**	-2.78ns	-5.78ns	-5.23ns	-23.39**	-23.65**	-15.95**
V15 (P3×P7)	11.44**	10.10*	12.36**	-11.27**	-13.76**	-13.76**	-27.65**	-27.89**	-27.39**
V16 (P4×P5)	-18.29**	-35.39**	67.83**	1.79ns	1.32ns	4.46ns	1.69ns	1.35ns	2.74ns
V17 (P4×P6)	-25.40**	-39.42**	46.62**	4.21ns	3.42ns	5.62ns	4.05ns	4.05ns	5.47ns
V18 (P4×P7)	16.04**	-3.57ns	45.63**	-9.11**	-10.06**	-8.14**	-6.80ns	-7.43ns	-6.16ns
V19 (P5×P6)	-23.12**	-25.75**	92.88**	0.48ns	-0.75ns	2.33ns	3.05ns	2.70ns	4.11ns
V20 (P5×P7)	-3.16ns	-32.94**	74.21**	-4.00ns	-5.45ns	-2.52ns	22.18**	21.77**	22.60**
V21 (P6×P7)	-28.36**	-49.38**	22.52**	-13.62**	-13.87**	-12.37**	-20.40**	-20.95**	-19.86**

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, ns= non-significant.

Table 13 (Cont'd)

Cross combinations	Number of seeds per siliqua			Thousand seeds weight (g)			Yield per plant (g)		
	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)
V1 (P1×P2)	-18.17**	-27.44**	-38.39**	19.32**	18.92**	13.55**	-11.74**	-18.47**	-9.76*
V2 (P1×P3)	-0.13ns	-16.48**	-1.60ns	-1.34ns	-2.32ns	-4.84**	12.62**	10.60**	27.20**
V3 (P1×P4)	15.99**	5.54ns	-10.55**	-8.36**	-17.69**	-0.97ns	-24.10**	-26.84**	-12.57**
V4 (P1×P5)	-9.00*	-23.62**	-35.14**	7.17**	5.74**	0.97ns	6.22ns	-1.73ns	28.14**
V5 (P1×P6)	11.51**	-7.56*	-21.50**	7.45**	2.36ns	-2.26ns	-4.85ns	-6.94ns	3.00ns
V6 (P1×P7)	0.09ns	-7.46*	-7.46**	1.32ns	-0.97ns	-0.97ns	4.98ns	0.00	10.69*
V7 (P2×P3)	-30.11**	-45.41**	-36.22**	8.39**	6.95**	4.19*	-36.98**	-42.74**	-34.15**
V8 (P2×P4)	16.64**	13.59**	-21.26**	-9.00**	-18.77**	-2.26ns	-17.28**	-26.37**	-12.00**
V9 (P2×P5)	12.36**	5.49ns	-30.73**	5.50**	4.78**	-0.97ns	-9.36*	-22.01**	1.69ns
V10 (P2×P6)	32.01**	22.17**	-19.78**	-7.14**	-11.26**	-16.13**	-7.33ns	-12.59**	-7.50**
V11 (P2×P7)	-22.85**	-36.10**	-36.10**	-1.66ns	-4.19*	-4.19*	-21.28**	-23.64**	-23.64**
V12 (P3×P4)	-4.05ns	-23.55**	-10.67**	1.48ns	-8.04**	10.65**	-14.72**	-16.33**	0.00
V13 (P3×P5)	-25.52**	-44.39**	-35.02**	14.23**	11.59**	8.71**	2.14ns	-3.88ns	25.33**
V14 (P3×P6)	-31.86**	-49.64**	-41.16**	4.21**	-1.66ns	-4.19*	-10.53*	-14.02**	-1.13ns
V15 (P3×P7)	-5.03*	-11.88**	2.97ns	0.33ns	-0.97ns	-0.97ns	3.32ns	-3.43ns	11.07*
V16 (P4×P5)	12.63**	3.18ns	-28.48**	-4.22**	-15.01**	2.26ns	-4.80ns	-8.77**	18.95**
V17 (P4×P6)	-2.82ns	-12.21**	-39.15**	-5.31**	-18.77**	-2.26ns	-26.46**	-30.61**	-17.07**
V18 (P4×P7)	-2.89ns	-17.77**	-17.77**	-10.53**	-17.96**	-1.29ns	2.39ns	-5.96ns	12.38**
V19 (P5×P6)	13.57**	11.83**	-35.54**	7.91**	4.17*	-3.22ns	-1.26ns	-10.50**	16.70**
V20 (P5×P7)	-26.06**	-41.72**	-41.72**	2.68ns	-0.97ns	-0.97ns	-11.56**	-21.87**	1.88ns
V21 (P6×P7)	-18.84**	-36.74**	-36.74**	2.26ns	2.26ns	2.26ns	-25.31**	-27.30**	-23.08**

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, ns= non-significant.

4.5.6 Number of secondary branches per plant

Number of secondary branches per plant is an important yield contributing characters for which significant positive heterosis is desirable. Out of 21 crosses, only one cross exhibited significant positive heterosis for secondary branches per plant. But most of the crosses showed significant negative heterosis over mid parent and better parent. The utmost negative heterosis over mid parent and better parent was observed in V3, V10, V11, V13 and V21 and the numerical value was -100% for the both cases and all the 5 genotypes. The highest positive value over mid parent and better parent was observed in V18 (516.67%, 208.33%). This cross combination can be selected for further improvement of the traits. In case of number of secondary branches per plant, standard heterosis over check variety was not mentioned in the Table 12, because there wasn't any secondary branches in the check variety (P7).

4.5.7 Number of siliquae per plant

In case of number siliquae per plant, significant positive heterosis is useful for getting higher yield. Among the 21 crosses, 3 crosses exhibited significant positive heterosis over mid parent value where the crosses V2 (14.77%) showed highest positive heterosis followed by V18 (16.04%) and V5 (11.44%). Out of 21 crosses only one cross V15 (10.10%) exhibited significant positive heterosis over better parent. Over commercial variety 18 crosses showed highly significant positive heterosis, the cross combination V4 (101.40%) exhibited highest positive heterosis followed by V14 (92.88%), V13 (82.92%) and V14 (80.38%). Liton *et al.* (2017) reported four cross combinations exhibited significant positive heterosis over mid parent and better parent for the concerned.

4.5.8 Siliqua length (cm)

Among the 21 crosses, 2 crosses exhibited significant positive heterosis over mid parent value where the crosses V10 (13.52%) showed highest positive heterosis followed by V7 (13.36%) whereas crosses V10 (9.27%) exhibited highly significant positive heterosis over better parent. Over commercial variety, 2 crosses showed significant positive heterosis, the cross combination V10 (18.80%) exhibited highest positive heterosis for siliqua length followed by V7 (15.12%). Liton *et al.* (2017) reported out of 15 crosses, only 3 crosses exhibited positive significant heterosis over mid-parent

whereas only two crosses revealed significant positive heterosis over better-parent. Rameah *et al.* (2003) reported both significant positive and negative heterosis over mid-parent and better-parent for siliqua length.

4.5.9 Beak length (cm)

Out of the 21 crosses, 12 crosses exhibited significant heterosis over mid parent and 13 crosses over better parent, among them only two crosses exhibited positive significant heterosis over mid-parent, better parent and commercial variety.

4.5.10 Number of seeds per siliqua

In case of number of seeds per siliqua, significant positive heterosis is useful for getting higher yield. Data persuation for heterosis revealed that 7 hybrids had positive and significant mid parent heterosis ranged V5 (11.51%) to V10 (32.01%) whereas 3 hybrids had significant positive heterobeltiosis ranged from V19 (11.83%) to V10 (22.17%). Among the 21 crosses, none of the hybrids showed significant positive heterosis over commercial variety. Liton *et al.* (2017) reported four cross combination exhibited significant positive heterobeltiosis and mid parent heterosis for the concerned traits.

4.5.11 Thousand seed weight (g)

Thousands seed weight is one of the emergent parameters to get higher yielding *Brassica* variety. For this context, significant heterosis with positive value is preferable for this observation. Significant positive heterosis over commercial check was observed in V1 (13.55%) preceded by V12 (10.65%) and V13 (8.71%) where, V4 (0.97%) showed the lowest value without significance (Table 13). Positive heterosis over mid parent was also observed in V1 (19.32%) indicating the highest value which was followed by V13(14.23%) and V7 (8.39%). Out of 21 crosses, 6 crosses exhibited positive heterosis over better parent. Hybrid V1 (18.92%) exhibited highest positive heterosis over better parent where hybrid V21 (2.26%) was reported as for the lowest heterobeltiosis (Table 13). Meena *et al.* (2014) reported, except one all the cross combinations showed negative better parent heterosis, on the other hand, Gupta *et al.* (2010) and Kumar *et al.* (2017) found among 50 crosses, majority of the crosses had positive heterobeltiosis for 1000 seed weight.

4.5.12 Yield per plant (g)

In case of yield per plant, 6 crosses showed positive heterosis value for mid parent, where the crosses V2 (12.62%) exhibited highly significant positive heterosis over mid parent. Among the combinations, only V2 (10.60%) manifested significant positive heterosis over better parent. 11 crosses manifested positive heterosis over check variety, where V4 (28.14%) showed highest value followed by V2 (27.20%), V13 (25.33%) and V16 (18.95%) manifested better heterotic effects over the check and V9 (1.69%) was recorded for its minimum value (Table 13). Liton *et al.* (2017) reported out of 15 crosses, only single hybrid CC14 (35.99%) showed significantly positive heterosis over mid and better parent heterosis.

4.6 Components of variation and genetic parameter

Genetic variance components, including D, H_1, H_2, F, h^2, E, $(H_1/D)^{0.5}$, $H_2/4H_1$, and heritability in the narrow sense (h^2n), were calculated using Hayman's (1954) diallel cross method and are displayed in Table 14.

4.6.1 Days to first flowering:

From the analysis of variance component, it was found that both additive (D) and dominance variance (H_1 and h^2) are all significant for this character. The obtained value revealed the possibility of presence of both additive and dominant gene action for controlling this trait. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For days to first flowering, the value of $(H_1/D)^{0.5}$ was 1.02, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. Mean covariance of additive and dominant variance is another important genetic parameter, which is expressed as F. Here F value was 17.25 that is more than 0 with positive sign, indicated dominant alleles are more frequent than recessive alleles. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects was -186.47 which is far away to 0.25, indicated asymmetry of positive and negative alleles in the parental gene pool. The value of narrow sense heritability (h^2n) was reported low (0.99) which indicated much effects of environmental influence.

4.6.2 Days to 50% flowering:

From the analysis of variance component, it was recorded that both additive (D) and dominance variance (H_1 and h^2) are all significant for this character. The obtained value revealed the possibility of presence of both additive and dominant gene action for controlling this trait. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For days to 50% flowering, the value of $(H_1/D)^{0.5}$ was 1.08, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. Mean covariance of additive and dominant variance is another important genetic parameter, which is expressed as F. Here F value was 12.77 that is more than 0 with positive sign, indicated dominant alleles are more frequent than recessive alleles.

Table 14: Components of genetic variance for 12 traits in 7×7 half diallel cross of *Brassica rapa*

Genetic parameter	DFF	D 50% F	DM	PH	NPB	NSB	NSP	SL	BL	NSS	TSW	YPP
D	15.64**	15.05**	7.48**	29.71**	0.26**	5.35**	1883.59**	0.02**	0.02**	32.49**	0.11**	0.36**
F	17.25**	12.77**	6.16**	25.18**	0.13**	4.84**	1449.55**	-0.13**	-0.03**	23.10**	0.12**	-0.45**
H_1	16.42**	17.65**	21.03**	231.39**	0.88**	4.36**	1454.93**	0.78**	0.11**	36.32**	0.17**	1.73**
H_2	-12249.73**	-15200.35**	-96230.57**	-146791.56**	-419.35**	-4.08**	-137916.46**	-342.11**	-23.25**	-4790.86**	-130.95**	-413.92**
h^2	-57.36**	-67.90**	-158.65**	-180.67**	-10.27**	-4.89**	-232.63**	-9.38**	-2.61**	-35.22**	-5.13**	-11.07**
E	0.23**	0.13**	0.36**	3.47**	0.02**	0.002*	8.78**	0.04**	0.01**	0.48**	0.004**	0.07**
$(H_1/D)^{0.5}$	1.02	1.08	1.68	2.79	1.84	0.90	0.88	5.60	2.28	1.06	1.26	2.19
$H_2/4H_1$	-186.47	-215.30	-1144.06	-158.60	-118.67	-0.23	-23.70	-110.03	-50.63	-32.97	-191.95	-59.98
h^2n (%)	0.99	0.74	0.31	0.12	0.24	1.10	0.98	0.02	0.11	0.68	0.60	0.13

Here,

*=Significant at 5% level, **=Significant at 1% level, D= Additive variance, H_1=Dominance variance, H_2=Proportions of positive and negative genes in the parents, F=Relative frequency of dominant and recessive alleles in the parents, h^2=Dominance effect over all loci in heterozygous phase, E=Environmental variance, $(H_1/D)^{0.5}$=Mean degree of dominance, h^2n (%) = Percentage of narrow sense heritability

$H_2/4H_1$ is a measure of proportion of genes with positive and negative effects was -215.30 which is far away to 0.25, indicated asymmetry of positive and negative alleles in the parental gene pool. The value of narrow sense heritability (h^2n) was reported low (0.74) which indicated much effects of environmental influence.

4.6.3 Days to maturity:

For days to maturity, both additive (D) and non-additive components (H_1 and h^2) were found significant (Table 14). The obtained value revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant, which suggested unequal distribution of dominant and recessive genes in the parents. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For days maturity, the ratio $(H_1/D)^{0.5}$ was 1.68, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was far away to 0.25, indicated dominance genes having increasing and decreasing effects on this trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported low (0.31) which indicated much effects of environmental influence.

4.6.4 Plant height:

For the observation plant height, both additive (D) and non-additive components (H_1 and h^2) were found significant (Table 14) which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant, which suggested unequal distribution of dominant and recessive genes in the parents. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For plant height, the ratio $(H_1/D)^{0.5}$ was 2.79, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was far away to 0.25, indicated genes having increasing and decreasing effects on this

trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported low (0.12) which indicated much effects of environmental influence.

4.6.5 Number of primary branches per plant:

Additive (D) and dominance components (H_1 and h^2) were found significant (Table 14) for number of primary branches per plant in numerical analysis which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant, which suggested unequal distribution of dominant and recessive genes in the parents. Importantly, H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For number of primary branches per plant, the ratio $(H_1/D)^{0.5}$ was 1.84, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was -118.67 which was far away to 0.25, indicated genes having increasing and decreasing effects on this trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported low (0.24) which indicated much effects of environmental influence.

4.6.6 Number of secondary branches per plant:

Additive (D) and dominance components (H_1 and h^2) were found significant (Table 14) for number of secondary branches per plant in numerical analysis which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant, which suggested unequal distribution of dominant and recessive genes in the parents. Importantly, H_1 value is more than H_2 value with negative sign reported unequal distribution of positive and negative alleles of parents. For number of secondary branches per plant, the ratio $(H_1/D)^{0.5}$ was 0.90, which indicated partial dominance present. The environmental component (E) was 0.002 for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was -0.23 near to 0.25, ascertained equal distribution of positive and negative alleles among the parents. The value of narrow sense heritability (h^2n) was reported (1.10).

4.6.7 Number of siliquae per plant:

From the analysis of variance component, it was found that both additive (D) and dominance variance (H_1 and h^2) are all significant for this character. The obtained value revealed the possibility of presence of both additive and dominant gene action for controlling this trait. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For number of siliquae per plant, the value of $(H_1/D)^{0.5}$ was 0.88, which indicated partial dominance in all the loci. The environmental component (E) was significant for this character and the value was 8.78. Mean covariance of additive and dominant variance is another important genetic parameter, which is expressed as F. Here F value was 1449.55 that is more than 0 with positive sign, indicated dominant alleles are more frequent than recessive alleles. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects was -23.70 which is far away to 0.25, indicated asymmetry of positive and negative alleles in the parental gene pool. The value of narrow sense heritability (h^2n) was reported (0.98).

4.6.8 Siliqua length:

From the analysis of variance component, it was found that both additive (D) and dominance variance (H_1 and h^2) are all significant for this character. The obtained value revealed the possibility of presence of both additive and dominant gene action for controlling this trait. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For siliqua length, the value of $(H_1/D)^{0.5}$ was 5.60, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. Mean covariance of additive and dominant variance is another important genetic parameter, which is expressed as F. Here F value was -0.13 which indicated recessive alleles are more frequent than dominant alleles. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects was -110.03 which is far away to 0.25, indicated asymmetry of positive and negative alleles in the parental gene pool. The value of narrow sense heritability (h^2n) was reported low (0.02) which indicated much effects of environmental influence.

4.6.9 Beak length:

For the observation beak length, both additive (D) and non-additive components (H_1 and h^2) were found significant (Table 14) which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant with negative sign, which suggested recessive alleles are more frequent than dominant alleles in the parents. H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For beak length, the ratio $(H_1/D)^{0.5}$ was 2.28, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for beak length the value was far away to 0.25, indicated genes having increasing and decreasing effects on this trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported low (0.11) which indicated much effects of environmental influence.

4.6.10 Number of seeds per siliqua:

Additive (D) and dominance components (H_1 and h^2) were found significant (Table 14) for number of seeds per siliqua in numerical analysis which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant, which suggested unequal distribution of dominant and recessive genes in the parents. Importantly, H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For number of seeds per siliqua, the ratio $(H_1/D)^{0.5}$ was 1.06, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was -32.97 which was far away to 0.25, indicated genes having increasing and decreasing effects on this trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported (0.68).

4.6.11 Thousand seed weight:

Additive (D) and dominance components (H_1 and h^2) were found significant (Table 14) for number of primary branches per plant in numerical analysis which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant, which suggested unequal distribution of dominant and recessive genes in the parents. Importantly, H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For thousand seeds weight, the ratio $(H_1/D)^{0.5}$ was 1.26, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was -191.95 which was far away to 0.25, indicated genes having increasing and decreasing effects on this trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported low (0.60) which indicated much effects of environmental influence.

4.5.12 Yield per plant:

Additive (D) and dominance components (H_1 and h^2) were found significant (Table 14) for seed yield per plant in numerical analysis which revealed the possibility of presence of both additive and dominant gene action for controlling this trait. F value represented mean covariance of additive and dominant variance, here F value found significant with negative sign, which suggested recessive alleles are more prevalent than dominant alleles in the parents. Importantly, H_2 value is more than H_1 value with negative sign reported that distribution of dominant and recessive alleles are unbalanced with negative effects of parents. For yield per plant, the ratio $(H_1/D)^{0.5}$ was 2.19, which indicated over dominance in all the loci. The environmental component (E) was significant for this character. $H_2/4H_1$ is a measure of proportion of genes with positive and negative effects, for days to maturity the value was -59.98 which was far away to 0.25, indicated genes having increasing and decreasing effects on this trait and irregularly distributed in the parents. The value of narrow sense heritability (h^2n) was reported (0.13).

4.7 Vr-Wr graph:

On the basis of parental variance (Vr) and parent offspring co-variance (Wr) a two dimensional depiction were made which was known as Vr- Wr graph. The nature (+/-) and magnitude of 'a' (the Y intercept) depicted average level of degree of dominance. When the regression line passed Wr axis above the point of origin suggesting partial dominance for controlling the trait. If the regression line intersected Wr axis below the point of origin touching the limiting parabola suggested over dominance for controlling the trait. The array point distribution indicated parental order of dominance which is provided by (Wr+Vr) values. For any trait, the parents which are more closer to the point of origin contained maximum frequency of dominant alleles and observed lower value of (Wr+Vr) while, parent with maximum frequency of recessive alleles will fall far from the origin.

4.7.1 Days to first flowering:

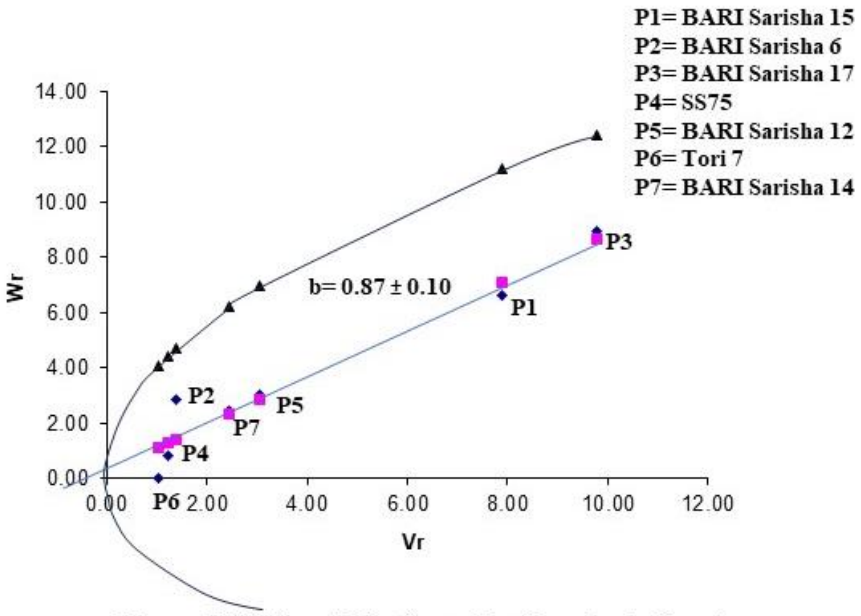

Figure 1. Vr-Wr graph for days to first flowering in *Brassica rapa*

The regression line intercepted Wr axis above the point of origin suggested partial dominance for controlling the traits (Figure 1). Parents P4 and P6 were closer to the point of origin indicated that, they contained maximum number of dominant alleles. Parents P1and P3 fell far away from the point of origin indicating maximum number of recessive alleles. Shrimali *et al* (2017) also recorded partial dominance for days to flowering.

4.7.2 Days to 50% flowering:

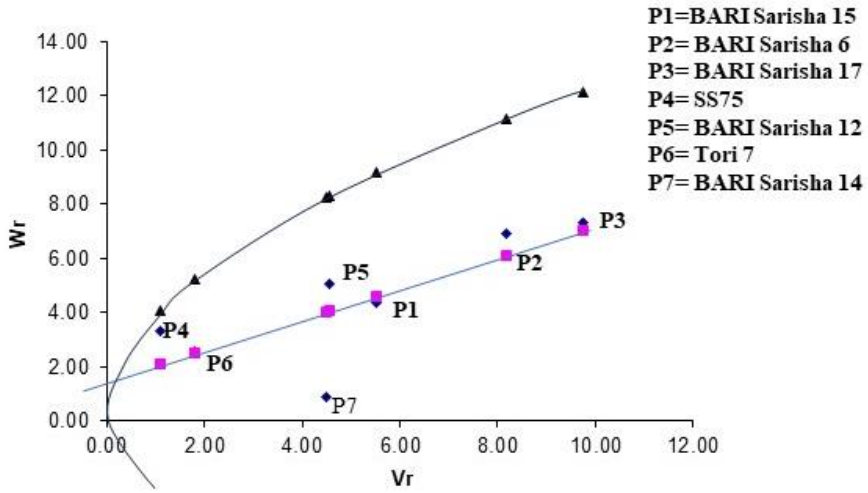

Figure 2. Vr-Wr graph for days to 50% flowering in *Brassica rapa*

The above figure depicted that the regression line intersected Wr axis on positive side and above the point of origin, represented partial dominance for controlling the traits. The parents P4 and P6 occupied the closest position to the point of origin hence revealing the dominant alleles for this trait. Parents P3 and P2 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. The remaining parents exhibited equal frequency of dominant and recessive alleles as their position remaining in the middle position of graph.

4.7.3 Days to maturity:

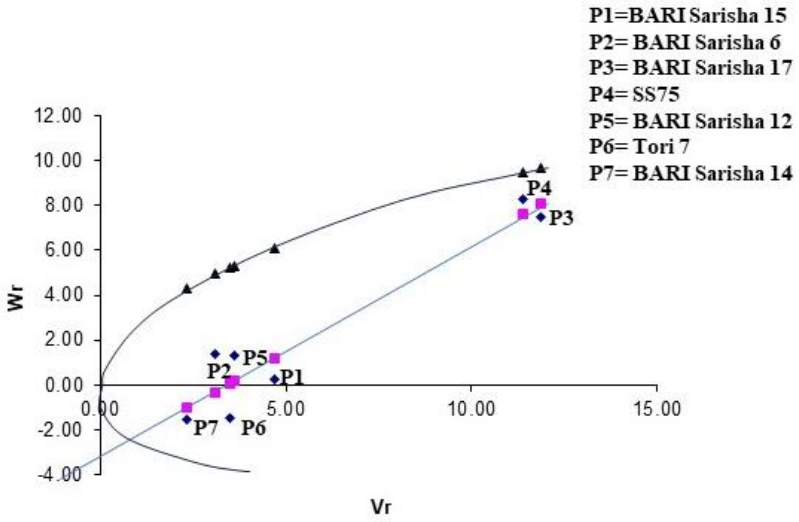

Figure 3. Vr-Wr graph for days to maturity in *Brassica rapa*

For graphical analysis, regression line intersected Wr axis below the point of origin, represented over-dominance for controlling the traits (Figure 3). The parent P7, P6, P2, P5 and P1 occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parents P3 and P4 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. Shrimali *et al* (2017) also reported over dominance for controlling the traits days to maturity.

4.7.4 Plant height:

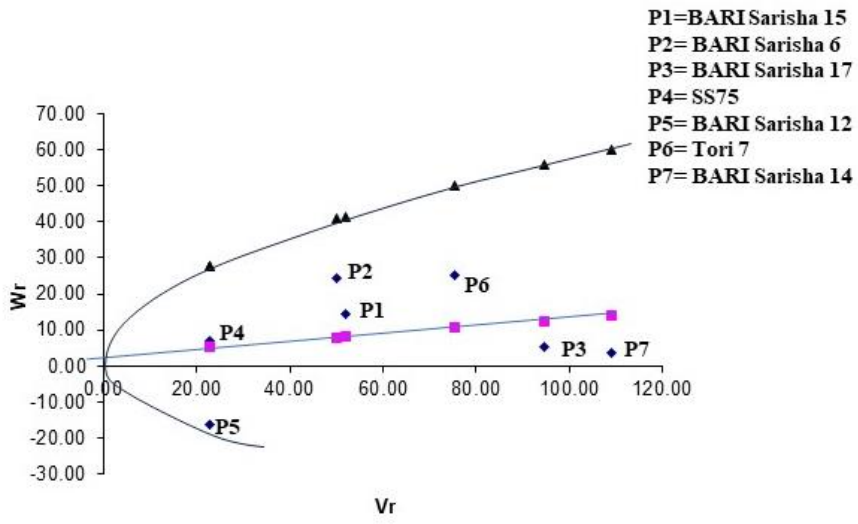

Figure 4. Vr-Wr graph for plant height in *Brassica rapa*

The above figure depicted that the regression line intersected Wr axis on positive side and above the point of origin, represented partial dominance for controlling the traits. Considerable gene differences were present among the parental lines for plant height as the array points of parents are too much scattered. The parents P4 and P5 occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parents P3 and P7 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. The remaining parents exhibited equal frequency of dominant and recessive alleles as their position remaining in the middle position of graph. Shrimali *et al* (2017) reported over dominance for controlling the traits plant height.

4.7.5 Number of primary branches per plant:

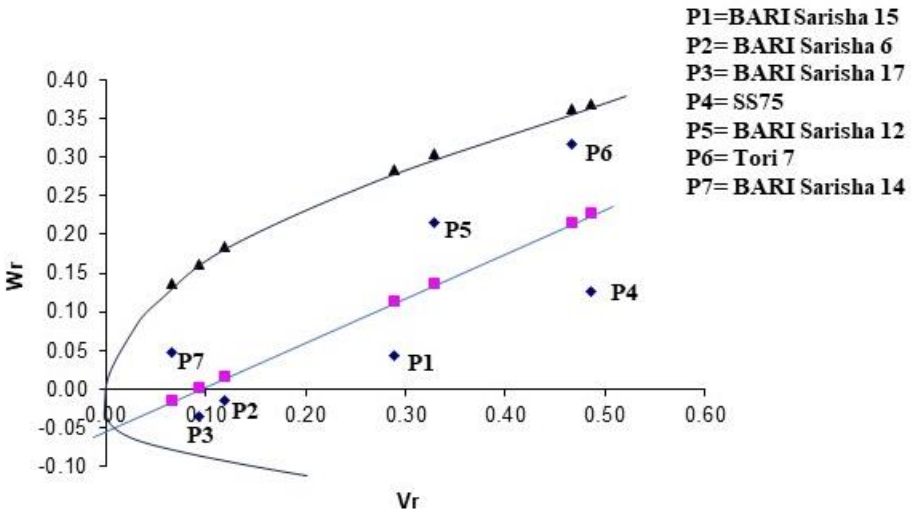

Figure 5. Vr-Wr graph for number of primary branches per plant in *Brassica rapa*

For graphical analysis, regression line intersected Wr axis below the point of origin, represented over-dominance for controlling the traits (Figure 5). Considerable gene differences were present among the parental lines for number of primary branches per plant as the array points of parents are too much scattered. The parents P1, P7 and P2 occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parents P6 and P4 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. The parents P1 and P5 exhibited equal frequency of dominant and recessive alleles as their position remaining in the

middle position of graph. Noshin *et al* (2003) reported partial dominance for number of primary branches per plant.

4.7.6 Number of secondary branches per plant:

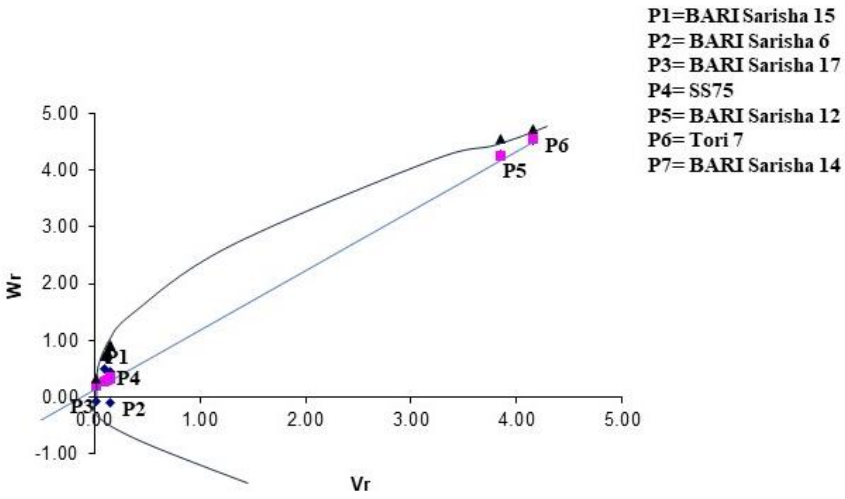

Figure 6. Vr-Wr graph for number of secondary branches per plant in *Brassica rapa*

The above figure depicted that the regression line intersected Wr axis on positive side and above the point of origin, represented partial dominance for controlling the traits. Most of the parents contained dominant alleles for this trait as they occupied the closer position to the point of origin. Parents P5 and P6 possess maximum number of recessive alleles as they occupied farthest position from the point of origin.

4.7.7 Number of siliquae per plant:

For graphical analysis, regression line intersected Wr axis above the point of origin, represented partial dominance for controlling the traits (Figure 7). Considerable gene differences were present among the parental lines for number of siliquae per plant as the array points of parents are too much scattered. The parents P7 and P4 occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parents P6 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. The parents P2, P5 and P3 exhibited equal frequency of dominant and recessive alleles as their position remaining in the middle position of graph. The results were in conformity with Noshin *et al* (2003), where they reported partial dominance for siliquae per main inflorescence.

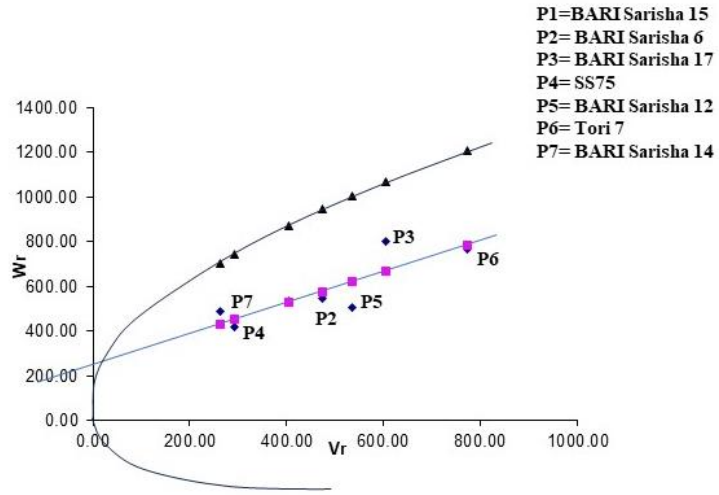

Figure 7. Vr-Wr graph for number of siliqua per plant in *Brassica rapa*

4.7.8 Siliqua length:

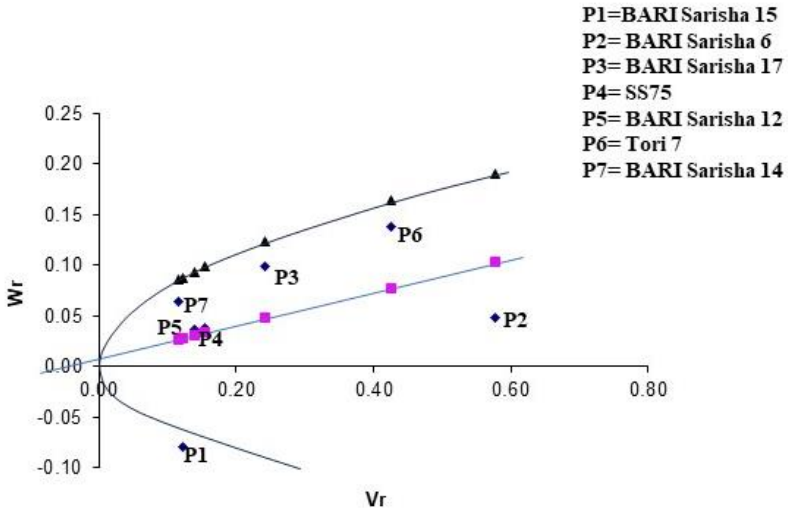

Figure 8. Vr-Wr graph for siliqua length in *Brassica rapa*

For graphical analysis, regression line intersected Wr axis above the point of origin, represented partial dominance for controlling the traits (Figure 7). Considerable gene differences were present among the parental lines for siliqua length as the array points of parents are too much scattered. Parents P2 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. Most of the parents occupied the closer position to the point of origin hence revealing the dominant alleles for this trait.

4.7.9 Beak length:

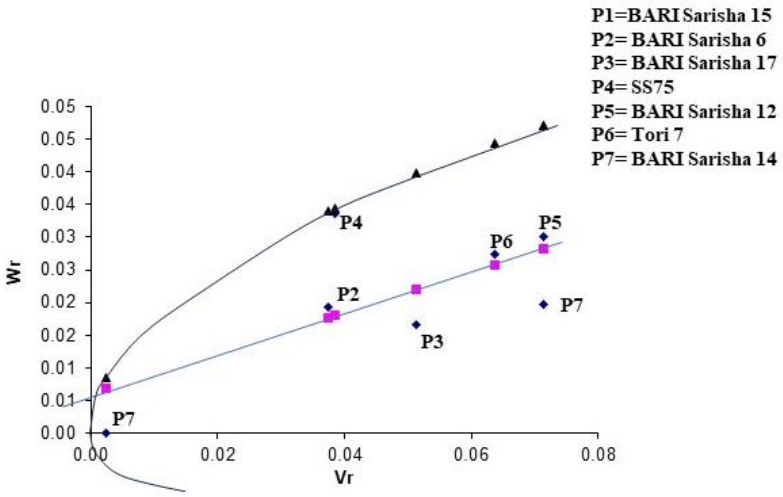

Figure 9. Vr-Wr graph for beak length in *Brassica rapa*

For graphical analysis, regression line intersected Wr axis above the point of origin, represented partial dominance for controlling the traits (Figure 9). Considerable gene differences were present among the parental lines for beak length as the array points of parents are too much scattered. The parents P7 occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parents P5, P6 and P7 possess maximum number of recessive alleles as they belonged farthest position from the point of origin. The parents P2, P4 and P3 exhibited equal proportion of dominant and recessive alleles as their position lying in the middle position of graph.

4.7.10 Number of seeds per siliqua:

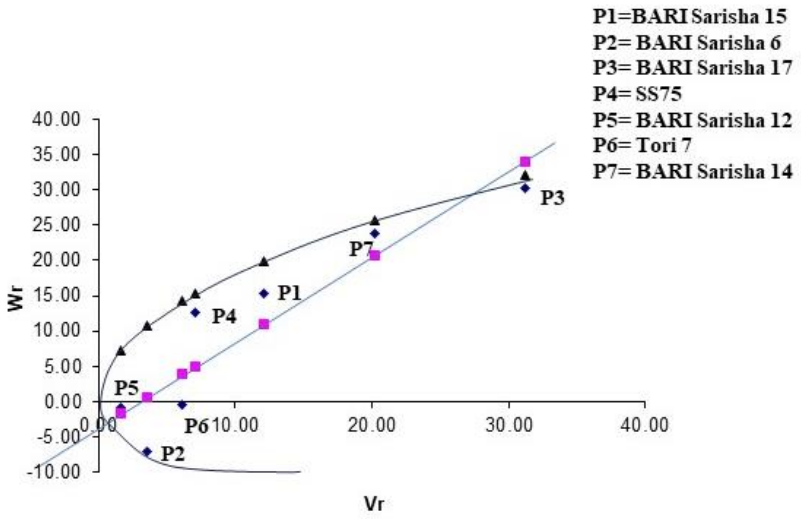

Figure 10. Vr-Wr graph for number of seeds per siliqua in *Brassica rapa*

For graphical analysis, regression line intercepted Wr axis below the point of origin, represented over-dominance for controlling the traits (Figure 10). Considerable gene differences were present among the parental lines for number of seeds per siliqua as the array points of parents are too much scattered. From the array points position on regression line it was evident that most of the parents occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parent P3 possess maximum frequency of recessive alleles as they hold farthest position from the point of origin. Shrimali *et al* (2017) also recorded over dominance for number of seeds per siliqua.

4.7.11 Thousand seed weight:

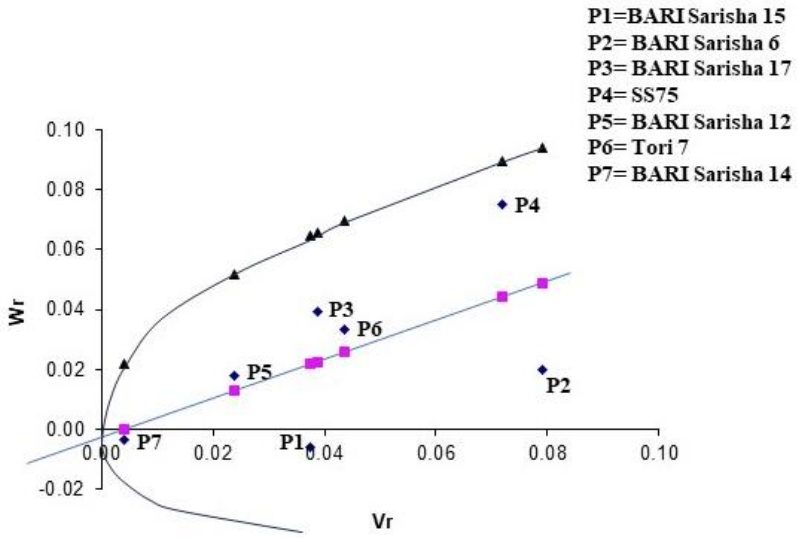

Figure 11. Vr-Wr graph for thousand seeds weight in *Brassica rapa*

The regression line of thousand seeds weight passed Wr axis below the point of origin, suggested over-dominance for controlling the traits (Figure 11). Considerable gene differences were present among the parental lines for thousand seeds weight as the array points of parents are widely scattered. From the array points position on regression line it was evident that P7 occupied the closer position to the point of origin hence revealing the dominant alleles for this trait. Parents P4 and P2 possess maximum number of recessive alleles as they occupied farthest position from the point of origin. The remaining parents contained equal frequency of dominant and recessive alleles as their position remaining in the middle position of graph. Shrimali *et al* (2017) also recorded over dominance for thousand seed weight.

4.7.12 Yield per plant:

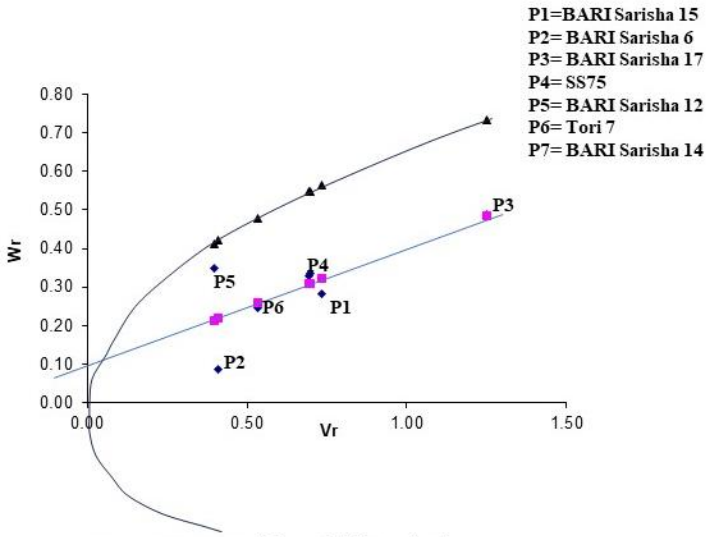

Figure 12. Vr-Wr graph for seed yield per plant in *Brassica rapa*

The regression line intercepted Wr axis above the point of origin suggesting partial dominance for controlling the traits (Figure 12). Most of the parents were closer to the point of origin indicated that, they contained maximum number of dominant alleles. Parents P3 fell far away from the point of origin indicating maximum number of recessive alleles. The results were in conformity with Noshin *et al* (2003), where they reported partial dominance for yield per plant.

CHAPTER V

SUMMARY AND CONCLUSION

The present study was carried out on seven parents of *B. rapa* with their 21 F_1 hybrids to evaluate them for different yield and yield contributing parameters. The experiment was entitled "Gene Action and Heterosis for Quantitative Traits in *Brassica rapa* L.". The present investigation was designed to access heritability of the traits, genetic advance, association between traits, direct and indirect effects of the traits towards yield, general combining ability effects of the parents and specific combining ability of the hybrids as well as heterotic effects of the hybrids in order to identify potential parents and promising cross-breeding partners in developing varieties with desirable traits. The present experiment was carried out with seven parents and their 21 F_1's developed from 7×7 half diallel procedure for 12 quantitative characters at research field of Sher-e-Bangla Agricultural University using Randomized Complete Block Design with three replications during two consecutive season, 2021-2022 (Rabi) and 2022-2023 (Rabi).

For every observation made during this study, the phenotypic variance was found to be greater than the genotypic variance. The high phenotypic and genotypic coefficient of variations was observed for number of secondary branches per plant (183.91, 183.60), number of siliquae per plant (28.08, 27.57) and number of seeds per siliqua (22.08, 21.08). Siliqua length (11.81, 9.77), beak length (20.76, 16.36) and yield per plant (17.69, 15.56) were exhibited moderate value for phenotypic and genotypic coefficient of variations, while the rest of observation exhibited low value for the concerned study. All the observations exhibited higher heritability value. In terms of the number of secondary branches per plant (99.66 and 377.56), siliquae per plant (96.59 and 55.81), beak length (62.13 and 26.56), number of seeds per siliqua (91.08, 41.43), and yield per plant (77.31 and 28.18), high heritability in conjunction with high genetic advance as a percentage of mean was reported.

Correlation coefficient analysis revealed that yield per plant was significantly and positively correlated with plant height (0.529), number of primary branches per plant (0.296), number of secondary branches per plant (0.314), number of siliquae per plant (0.459) and number of seeds per siliqua (0.231) at phenotypic level. Yield per plant was significantly and positively associated with plant height (0.678) and number of siliquae

per plant (0.470) at genotypic level. However positive association was also observed for all the observations except siliqua length and beak length at genotypic level. This positive correlation revealed increasing the concerned characters was highly leading to improvement of yield.

The genotypic path coefficient was carried out considering yield per plant as dependent characters whereas other yield components as independent characters. The path coefficient value represented that seed yield per plant exhibited positive direct effect with days to first flowering (0.049), days to 50% flowering (0.745), number of primary branches per plant (0.305), number of siliquae per plant (2.224), siliqua length (0.022), beak length (0.342), number of seeds per siliqua (1.734) and thousand seed weight (0.821). The highest direct positive effects exhibited by number of siliquae per plant (2.224). Negative direct effects are observed by days to maturity (-1.163), plant height (-0.240) and secondary branches per plant (-0.259).

In the present investigation highly significant value for GCA and SCA variances was recorded for all the characters. That means additive as well as nonadditive gene actions are prevailing for the inheritance of the characters under study. The SCA variance is higher than the GCA variances for all the characters under study, indicated the preponderance of non-additive type of gene action for the inheritance of the characters.

The general combining ability effects towards desirable direction among the seven parents revealed that P6 exhibited highest negative GCA for days to first flowering, days to 50% flowering and days to maturity, so it can be considered as good general combiner for the development of early maturing variety which is followed by P5 and P2. P2 and P6 exhibited highest significant negative GCA for plant height and it can be used for development of variety with short stature. P4 and P5 exhibited highest positive significant GCA value, so these two parents can be used for tall type plant. For number of primary branches per plant, secondary branches per plant, siliqua per plant, P5 and P6 considered as good combiner whereas P5 showed highest positive significant GCA value for yield per plant. P5 was considered as good general combiner for yield related attributes.

In the studied crosses, V15 (P3×P7), V3 (P1×P4) and V13 (P3×P5) exhibited maximum negative significant SCA effects for days to first flowering, days to 50% flowering and

days to maturity which were desirable for these characters for development of variety with earliness and V15 (P3×P7) exhibited highest positive significant SCA effect for plant height where V10 (P2×P6) showed highest negative SCA effect which can be used for dwarfness. Among twenty F_1 hybrids, two crosses, viz. V17 (P4×P6) and V7 (P2×P3) showed significant positive SCA effects for number of primary branches per plant and V19 (P5×P6), V18 (P4×P7) and V7 (P2×P3) showed positive significant SCA for number of secondary branches per plant. For number of siliquae per plant, five cross combinations out of twenty one showed positive significant SCA effect and the highest positive significant SCA effect showed in V18 (P4×P7). Out of twenty one tested F_1 hybrids, two crosses viz. V2 (P1×P3) and V18 (P4×P7) exhibited positive significant SCA effect for yield.

The hybrids V1, V2, V3, V5, V6, V7, V12, V13, V14, V15, V18, V20 and V21 showed the negative significant heterosis over mid parent and better parent for the character days to first flowering where the highest negative heterosis over mid parent and better parent was observed in V2 and (V13, V14), respectively. All the total 21 crosses showed significant negative heterosis over commercial variety for days to first flowering except V4 and V12 whereas the highest negative value was observed in V2. In case of days to 50% flowering, cross combination V15 showed the highest negative significant heterosis over MP, V13 over BP and V19 over check variety. In case of days to maturity, cross combination V14 showed the highest negative significant heterosis over MP, BP and check variety. For plant height, cross combination V15 showed the highest negative significant heterosis over MP, BP and check variety. Cross combination V7 showed the highest positive significant heterosis over MP, BP and check variety for number of primary branches per plant. Cross combination V18 showed the highest positive significant heterosis over MP and BP for the character of secondary branches per plant. For number of siliquae per plant, cross combination V18, V15 and V4 showed the highest positive significant heterosis over MP, BP and check variety respectively. For siliqua length, cross combination V10 showed the highest positive significant heterosis over MP, BP and check variety. For beak length, cross combination V20 showed the highest positive significant heterosis over MP, BP and check variety. Cross combinations V10 showed positive and significant heterosis over MP and BP for siliqua per plant, on the other hand none of the crosses exhibited significant positive heterosis over commercial variety. Cross combinations V1 showed

positive and significant heterosis over MP and BP and check variety for the character thousand seeds weight. For yield per plant only the crosses, V2 showed significant positive heterosis over MP, BP and check variety.

The components of genetic variance showed both additive and dominance variance are significant for all the studied characters. The value of mean degree of dominance indicated presence of overdominance in all the loci for all the characters except number of secondary branches per plant and number of siliquae per plant.

Vr-Wr graph showed over dominance for days to maturity, number of primary branches per plant, number of seeds per siliqua and thousand seed weight, and thus heterosis breeding is important to improve those traits.

Recommendations:

- Among the parents P5 and P6 can be used for future breeding programme
- Among the cross combination V1 (P1×P2), V2 (P1×P3), V10 (P2×P6), V13 (P3×P5), V14 (P3×P6), V15 (P3×P7), V18 (P4×P7) and V19 (P5×P6) can be used for future breeding programme

CHAPTER VI

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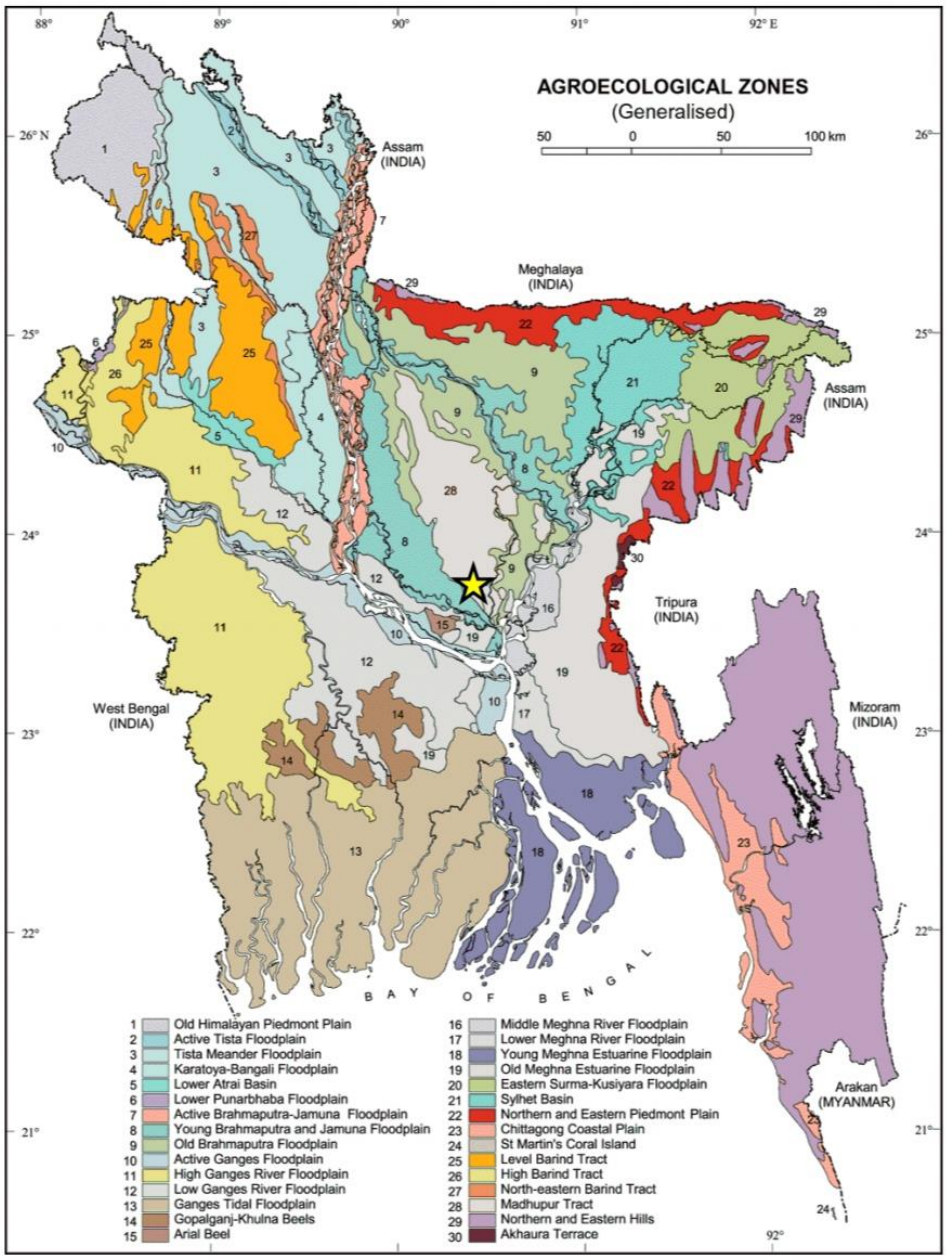
APPENDICES

Appendix 1. Map showing the experimental site of the study



★ The experimental site under study

Appendix 2. Morphological, mechanical and chemical characteristics of soil of the experimental site as observed prior to experimentation (0 -15 cm depth).

A. Morphological characteristics of the experimental field

Morphological features	**Characteristics**
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Mechanical composition

Particle size	**Constitution**
Texture	Loamy
Sand	40%
Silt	40%
Clay	20%

C. Chemical composition

Soil Characters	**Values**
Organic matter	1.44%
Potassium	0.15 meq/100 g soil
Calcium	1.00 meq/100 g soil
Magnesium	1.00 meq/100 g soil
Total nitrogen	0.072
Phosphorus	22.08 μ g/g soil
Sulphur	25.98 μ g/g soil
Boron	0.48 μ g/g soil
Copper	3.53 μ g/g soil
Iron	262.6 μ g/g soil
Manganese	164 μ g/g soi
Zinc	3.32 μ g/g soi

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

Appendix 3. Monthly records of air temperature, relative humidity and rainfall hours during the period from November 2021 to March 2022 and November 2022 to March 2023.

Month	Year	Monthly average air temperature (° C)			Average relative humidity (%)	Total rainfall (mm)
		Maximum	Minimum	Mean		
Nov.	2021	29.3	20.3	24.8	74	34.5
Dec.	2021	26.1	17.0	21.55	74	12.5
Jan.	2022	25.9	15.2	20.55	71	7.4
Feb.	2022	29.5	17.8	23.65	63	28.9
Mar.	2022	34.1	22.0	28.05	62	65.7
Nov.	2022	29.4	19.5	24.45	68	32.2
Dec.	2022	26.4	14.8	20.6	62	12.3
Jan.	2023	25.8	13.0	19.4	59	8.3
Feb.	2023	28.5	15.4	21.95	52	28.2
Mar.	2023	32.7	21.0	26.85	50	64.0

Source: Bangladesh Meteorological Department (Climate division), Agargaon, Dhaka