GENETIC ANALYSIS ON YIELD, OIL CONTENT AND QUALITY CHARACTERISTICS OF SELECTED *Brassica rapa* L. GENOTYPES

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BY

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CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC ANALYSIS ON YIELD, OIL CONTENT AND QUALITY CHARACTERISTICS OF SELECTED *Brassica rapa* L. GENOTYPES"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING,** embodies the result of a piece of *bona fide* research work carried out by **NASRAT JAHAN SHELLY**, bearing Registration No. **03-01074** under my supervision and guidance. No part of the thesis has been submitted anywhere 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 been duly acknowledged by her.

Dated: December 2021
Place : Dhaka, Bangladesh

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

Dedicated

to

My Beloved Parents, Husband and Children

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ABSTRACT

The investigation was carried out at the experimental field and in the Biochemistry and Agricultural Chemistry and Environmental Science laboratory of Sher-e-Bangla Agricultural University, Dhaka during Nov/2017 to Dec/2021 with seven selected *Brassica rapa* genotypes to develop elite breeding lines with high yield potential, short duration and high oil content with better quality. BARI Sar-6 had the highest yield (8.41 g plant^{-1}) but had very long duration (110 days), while Tori-7 had the lowest yield (4.25 g plant^{-1}) with short duration (81.66 days), on the other hand Brown Special matured early (80.66 days) with moderate yield (5.88 g plant^{-1}). Most of the F_1s were intermediate type between their parents for morphological characteristics and performed better than their both parents for most of the quantitative traits. Tori-7 × Brown Special matured early in 80 days, while the highest yield (27.67 g plant^{-1}) had recorded in Tori-7 × Yellow special. The highly significant and the highest negative heterosis for maturity had recorded in BARI Sar-6 × Brown Special over the better parent (-23.33%) and in BARI Sar-6 × BARI Sar-17 over the mid parent (-13.22%). For yield plant^{-1}, Yellow Special × Tori-7 showed the highly significant and the highest positive heterosis over both the parents (352.37% and 245.01% respectively). Considering the highest positive (except earliness) and the highly significant GCA effects, Brown Special was the best general combiner for earliness and yield plant^{-1}, while based on SCA effects, the cross BARI Sar-6 × Brown Special was the best for earliness and BARI Sar-15 × Brown Special was the best for yield plant^{-1}. Therefore, these genotypes might be used for further improvement of these traits. Generation mean analysis revealed that, F_1s were superior over their both parents but F_2s means indicated inbreeding depression in most cases. BC_2 performed better than BC_1 in most of the crosses for yield plant^{-1}. The significant scaling tests for most of the traits across the crosses indicated the presence of epistasis but insignificant $\chi 2$ values in most cases indicated the absence of epistasis and thus, six-parameter model (Hayman, 1958) had suggested to explain the nature of gene actions. Significant negative additive gene effects for most of the traits across the crosses indicated non-additive gene action and selection might be ineffective but in those cases significant positive additive gene effects had found selection might be effective. While heterosis breeding could be explored for significant positive dominance gene effects in most other cases. However, where, both additive and dominance gene effects were significant and positive, reciprocal recurrent selection might be suggested. For oil content, the parent - Yellow Special, F_1 - Brown Special × Yellow Special, F_2 - BARI Sar-14 × Yellow Special and in both BC_1 and BC_2 - Tori-7 × BARI Sar-14 contained the highest amount of oil, 45.05%, 39.04%, 37.71%, 38.98% and 38.57 % respectively. Among the parents - Tori-7, in all F_1, F_2 and BC_1 - Tori-7 × Yellow Special and among BC_2 - Yellow Special × BARI Sar-6 contained the highest amount of poly unsaturated fatty acid, 16.98%, 19.27%, 21.54%, 21.57% and 16.47 % respectively. Among the parent - Tori-7, in all F_1, F_2 and BC_1-Tori-7 × Yellow Special and among BC_2- Yellow Special × BARI Sar-6, contained the lowest amount of erucic acid, 44.97%, 45.37%, 45.42%, 45.49% and 46.67 % respectively. So, these genotypes might be used for further development of these traits.

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LIST OF ABBREVIATIONS OF TECHNICAL SYMBOLS AND TERMS

FULL WORDS	ABBREVIATIONS
Agro-Ecological Zone	AEZ
Analysis of variance	ANOVA
And others / Co-workers	*et al.*
Bangladesh Agricultural Research Institute	BARI
Back Cross	BC
Better Parent	BP
Coefficient of variance	CV
Centimeter	cm
Degrees of freedom	df
Exempli gratia (by way of example)	e.g.
Food and Agriculture Organization	FAO
First filial generation (The first generation of a cross between two dissimilar homozygous parents)	F_1
The second generation of a cross between two dissimilar homozygous parents	F_2
Fatty Acid Methyl Ester	FAME
General Combining Ability	GCA
Gram	g
Hectare	ha
Heterosis Over Better Parent	HBP
Heterosis Over Mid Parent	HMP
Least Significant Difference	LSD
Mono Unsaturated Fatty Acid	MUSFA
Mid Parent	MP
Poly Unsaturated Fatty Acid	PUSFA
Percentage	%
Randomized complete block design	RCBD
Sher-e-Bangla Agricultural University	SAU
Specific Combining Ability	SCA
Standard Error	SE
Saturated Fatty Acid	SFA
Triple Super Phosphate	TSP
Unsaturated Fatty Acid	USFA

CHAPTER I

INTRODUCTION

Brassica is a genus of plants in the mustard family (*Brassicaceae*). The members of the genus are informally known as cruciferous vegetables, cabbages, or mustard plants. Crops from this genus are sometimes called *cole crops* derived from the Latin *caulis*, denoting the stem or stalk of a plant. The *Brassicaceae* family contains many economically important plant crops. More than 170 million tons of cultivated vegetables and oilseeds produced worldwide each year (FAO, 2019). This family contains about 3500 species and 350 genera and is one of the economically most important plant families (Quijada *et al*., 2007). The family of *Brassicaceae* is an important source of edible roots, stems, leaves, buds and inflorescences as well as of edible or industrial oils, condiments and forage. One intensively cultivated diploid species of this family is *Brassica rapa* L. (2n = 20, AA), which has a long history of domestication. It is cultivated for livestock and human consumption and includes many well-known varieties, such as rapeseed, cabbage, cauliflower, broccoli, brussels sprouts, turnip, various mustards and weeds (Warwick, 2011). *Brassica rapa* and *Brassica campestris* were first described as two species by Linnaeus, with *Brassica rapa* being the turnip form and *Brassica campestris* the wild weedy form. Later on it was shown that these were the same species so the taxa were combined under the name *Brassica rapa* (Toxopeus *et al*., 1984). The primary center of origin for *Brassica campestris* recently known as *Brassica rapa* is near the Himalayan region and the secondary center of origin is located in the European-Mediterranean area and Asia (Downey and Robbelen, 1989).

After cereals, oilseeds are the 2nd food sources throughout the world (Siavash *et al*., 2005). Rapeseed and mustard oil is the most useful of all cooking oils and it contains a significant amount of ω-3 and ω-6 fatty acids. This oil has a high nutritional quality due to its lowest levels of saturated fatty acids, balanced amount of unsaturated fatty acids and being free from cholesterol (Gunstone *et al*., 1994; Hui & Bailey's, 1996). It has 38-40% protein with a complete profile of amino acids including lysine, methionine and cysteine (Rashid, 2013). It is not only a high energy food but also a carrier for fat soluble vitamins (A, D, E and K) in the body. It also serves as important source of raw material for different industrial uses such as in making soaps, paints, hair oils, lubricants, textile

auxiliaries, pharmaceuticals etc. oil cakes and meals are used as animal feeds and manures. The advantageous chemical composition and relatively low price offer it as a valuable seed in human foods as additive and to feed animals (Gadei *et al*., 2012).

Brassica rapa also has the high medicinal values. Various plant parts of different sub-species of *Brassica rapa* are full of some important anticancer and antioxidant compounds including glucosinolates, carotenoids, flavonoids, ketones, aldehydes, vitamin C, selenium, etc. (Jan *et al*., 2018). Oil contains a high amount of selenium and magnesium, which gives anti-inflammatory properties. It also helps in stimulating sweat glands and thus helps in lowering body temperature. Besides the medicinal value, it is also used to relieve the pain related with arthritis, muscle sprains and strains. Seed and leaf paste is said to heal cattle wounds (Sood *et al.,* 2010).

Therefore, mustard and rapeseed have become the major oilseed crops and the leading source of edible oil occupied the 3rd most important position among the oilseed crop in the world and the world area harvested under mustard and rapeseed is 38,509,853 MT and production is 75,711,806 MT (FAOSTAT, 2020). Bangladesh has also suitable climate and soil conditions for the production of oilseed species all the year round. However, the production of oilseed cannot meet up its annual demand because since her independence to current date there is continuous decline in both acreage and total production of oilseeds except some exceptional years (Chowdhury *et al*., 2014). It also happened due to low yield potential of the traditional oilseed crops varieties, high infestation of diseases and pests, instability of yield due to micro-climatic fluctuation and more profitable crops are available in place of oilseeds in the cropping patterns. Usually, farmers do not allocate their good piece of land and do not follow modern cultural practices for oil crops, thus their yields are low and the oil production in Bangladesh is decreasing while oil crop area are replaced by HYV Boro rice and high population pressure (Amin, 2009). Bangladesh has been facing acute shortage of edible oil for the last several decades as the consumption of edible oils continues to grow in Bangladesh in pace with population growth and economic development so the import of the commodity also increases gradually and steadily.

In Bangladesh total cultivated area under rapeseed and mustard cultivation is 0.589 million hectares which produces 1.34 ton ha^{-1} in 2020-21 (AIS, 2022). *Brassica rapa* is

the main oil yielding species in Bangladesh and occupies the 1st position in respect of area and production (Naznin *et al.,* 2015). Other two major local cultivars*, Brassica juncea* and *Brassica napus* are high yielding but not short durable so comparatively low yielding *Brassica rapa* is widely grown in the country for their short duration and fulfills our requirement approximately 50% (Islam, 2015). Although short durable, low yielding and pest susceptible variety Tori-7 of *Brassica rapa* is popular in Bangladesh but still there is lack of improved short durable varieties with higher yield.

Moreover, many farmers showed negative attitudes towards oilseed cultivation for scarcity of chemical fertilizers with high price, unavailability HYV seed, lack of technical know-how and frequent natural calamities which are the barriers of oilseed crops expansion in Bangladesh (Miah and Mondal, 2017). Therefore, a big gap has been prevailing between supply and demand of edible oils. Our internal production can meet only about 21% of our consumption. The rest 79 % is met from the import. Presently, on an average, 2.3 to 2.4 million MT of edible oils, both in oil form and in seeds form, are imported in the country (BBS, 2020). Consumption of oils and fats in Bangladesh shows an increasing trend, which is the highest among the developing countries (Alam, 2020). In 2019, total consumption of oils and fats was 3.04 million MT which is about 2.97 % higher compared to 2018 and the average per capita consumption of oils and fats is seen approaching 18.7 kgs (Alam, 2020). Hence, it is extremely needed to increase the total production of edible oils by fitting the oilseed crops in existing cropping patterns by replacing the low yielding varieties by short duration HYVs, appropriate necessary management practices and expanding the area of cultivation where-ever possible. The traditional varieties can be replaced by the short duration (75-80 days) yellow seeded variety, having yield capacity of 1.50-1.65 ton per hectare and can easily be grown in the T. Aman-Mustard-Boro cropping system with 2-3% increased oil content for yellow seed without hampering existing Boro cultivation (Biswas *et al.,* 2019). Therefore, oilseed research should be directed towards the minimization of yield gap through the development of the high yielding short duration varieties to fit into the profitable cropping patterns with higher adaptability and stability which will ultimately increase the oil production in the country.

On the other hand, oil quality is determined by both the nutritional and functional aspects,

which in turn, primarily determined by the fatty acid profile of the oil including palmitic, stearic, oleic, linoleic, linolenic, eicosenoic and erucic acids which is highly variable on variety types (Nasr *et al*., 2006; Javidfar *et al.,* 2007). Though *Brassica species* provide many advantageous properties but it also contains toxic erucic acid and glucosinolate (Rashid, 2013) thus used in limited quantities. Erucic acid damages cardiac muscle of animals, and glucosinolates, made it less nutritious in animal feed (O'Brien, 2008). Rapeseed-mustard oil contains up to 54% erucic acid (Sahasrabudhe, 1977). *Brassica rapa* had oil and erucic acid content 31% and 41 %, respectively (Yousef *et al*., 2015) while food-grade canola oil (rapeseed 00 oil) has been generally recognized as safe by the United States Food and Drug Administration (CFR, 2010). Therefore, one of the main breeding objective regarding rapeseed and mustard should be the development of varieties with superior oil quality besides the oil quantity (Azizi *et al.,* 1999).

Though the crop has the high nutritional values and has occupied a vast area in our country, but its low production indicates that the crop has received very little attention for its improvement. Increased yield and improved quality are generally confronted with laborious analyses and long term breeding programs. The major activities of plant breeding are building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Zayaet *et al.,* 2008). Hybridization is a common practice for combining the desirable characters of two or more lines or varieties into a single variety. The yield, duration and fatty acid composition of *Brassica* oils has been extensively modified to desirable extent by using conventional plant breeding and biotechnology-based techniques to create unique and improved varieties (Peter *et al*., 2002). New *Brassica* cultivars with high yield potential and wide range of edible oil qualities have been developed in many countries of the world and commercialized in recent years. World vegetable oil markets are highly competitive, so the steady improvement in oil quantity and quality of the *Brassica* oilseeds is essential to maintain or to increase market share, and/or to create new niche markets. However, the cross-incompatibility occurring in wide hybridization might hamper the possibility of obtaining hybrid progenies. For that reason, the crossability study is also essential and may give an insight into the cross-compatibility relationship among the species, the direction of success of crossing, and the crossability barriers of some combinations, if any.

Development of high yielding cultivars also requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations (Shukla *et al.,* 2006). The choice of selection of breeding methods for genetic improvement of any crops is mainly dependent on the knowledge of type and relative amount of genetic component and the presence of epistatic interaction for different traits in the plant materials under investigations. Information on the type of gene action involved in the inheritance of a character is helpful in deciding the breeding procedures to be followed for crop improvement. Thus the study was under taken to know the nature of gene action governing the studied characters. The present study will help to know about the nature of gene action for analyzing the genetic makeup of a crop and its magnitude for quantitative characters for deciding effective breeding methods for improvement of yield and related traits.

In our country limited works has been carried out for the development of *Brassica rapa* varieties in terms of higher yield, short duration, better oil quality and content. Crossing among selected *Brassica rapa* genotypes with desirable genetic composition may produce a desirable genotype. Therefore, considering this situation the experiment was carried out with a suitable crossing program among the selected *Brassica rapa* genotypes to fulfill the following objectives.

1. To develop the short duration *B. rapa* genotypes with high yield potential.
2. To isolate the segregants with higher oil content and good oil quality from different generations (F_1, F_2, BC_1 and BC_2) of *B. rapa.*
3. To study the gene actions controlling the traits in different generations.

CHAPTER II

REVIEW OF LITERATURE

In Bangladesh *Brassica rapa* is the major edible oil producing crop. There are many studies related to the present topics on *Brassica* spp. have been carried out in the world. The review of literature concerning the studies are presented under the following heads:

2.1 Characterization for morphological traits

2.2 Heterosis analysis

2.3 Combining ability analysis

2.4 Gene action study

2.5 Genotypic and phenotypic variability

2.6 Heritability and genetic advance

2.7 Fatty acid content

2.1 Characterization for morphological traits

Muthoni *et al.* (2010) evaluated 47 lines of Ethiopian mustard to study the agro-morphological traits for characterization. Significant differences observed in most of the quantitative traits with 88% of the accessions flowering after 84 days from sowing. Among the qualitative traits, great variation was seen in leaf number plant^{-1}, leaf bloom and leaf blade blistering.

Malek *et al.* (2012) synthesized a *Brassica napus* genotype by hybridization between its diploid progenitor species *Brassica rapa* and *Brassica oleracea* followed by chromosome doubling. Synthetic *Brassica napus* (AACC, 2n = 38) was identified with bigger petals, fertile pollens and seed setting and had increased growth over parents and exhibited wider ranges with higher coefficients of variations than parents for morphological and yield contributing characters, and yield plant^{-1}. Siliqua length and beak length was longer, number of seeds siliqua^{-1}, 1000-seed weight and seed yield plant^{-1} were higher in synthetic *Brassica napus* than the parents. Although flowering time in synthetic *Brassica napus* was earlier than both parents, however the days to maturity was little higher over early maturing *Brassica rapa* parent. The synthesized *Brassica napus* has great potential to produce higher seed yield.

Yadav *et al.* (2013) carried out morphological characterization of Indian mustard. 78 genotypes were grouped for several morphological descriptors. Number of lobes varies from

low to medium. Stem colour varies from light green to dark green. Wide diversity has been observed for leaf length (40.2 to 63cm) and leaf breadth (18 to 27cm) also. No variability was observed for leaf division, petiole enlargement, petiole section, petiole color, flower color and siliqua surface outline. In majority of cases, leaf angle was prostrate type, leaf blade shape was spathulate, leaf division dentate, lyrate type, leaf apex and leaf blistering was intermediate, leaf tip and lamina attitude was straight, sparse hairs were present. Petiole length, width and thickness were intermediate type. Similar, findings were also observed for petal length, breadth, siliqua angle, length and width and also for pedicel and beak length. Seed color of all the genotype was black except RH 401Y (yellow). Maximum genotypes were of medium size (3-5g 1000 seed weight^{-1}) except RH 270 (>5g 1000 seed weight^{-1}).

Aktar *et al.* (2019) conducted an experiment to evaluate 18 *Brassica* genotypes for various morphological characters for yield and yield contributing traits. The genotypes differed significantly for all the traits. Considering two most important traits like early maturity and yield plant^{-1}, BD-7114 performed best among the studied genotypes.

2.2 Heterosis

Heterosis breeding approach is one of the most successful technological options being employed for the improvement of brassica variety for quality and quantity of seed yield and other yield related parameters. Crosses between parents of presumably different origins gave greater heterosis than crosses between parents that were presumably more closely related (Allard, 1960). Rapeseed breeding programs are focused mainly on improving seed yield. One of the ways to improve seed yield in oilseed rape is heterosis breeding. The review of literature concerning the studies are presented below:

Das *et al.* (2010) studied 12 F_1 crosses for some yield contributing traits. Heterosis was calculated over the mid parent and the better parent. The hybrids RLM-514 × M-91, M-261 × Sampad, RLM-514× Sampad, RLM-514 × M-91, M-7 × Sampad, M-261 Dholi and RLM-514 × M-91 were excellent for days to flowering, pollen sterility percentage, plant height, secondary branches and number of siliqua plant^{-1}and seed yield on the basis of heterosis value.

Gupta *et al.* (2010) carried out half diallel analysis of eight parents to estimate heterosis and heterobeltiosis in *Brassica juncea*. The highest heterosis and heterobeltiosis were observed in seed yield 100 siliqua^{-1} and days to 50% flowering in cross IC-199715 × IC-199714, EC-289602 × Prakash in the number of primary branches plant^{-1} and harvest index, Agra Local

× Pusa Bahar in main axis length, Poorbijaya × Agra Local in number of siliqua on main axis and EC-289602 × Pusa Bahar in the biological yield and seed yield plant^{-1}. Different cross showed the maximum value of the better and the mid-parent heterosis for the remaining traits.

Sabaghnia *et al*. (2010a) developed 36 hybrids through diallel cross and measured heterosis. The significant heterosis was observed for all the traits it implies that the utilization of the heterosis could be effective for genetic improvement of oil contents and other traits.

Cuthbert *et al.* (2011) studied heterosis for seed quality traits with the high erucic acid in rapeseed. The high parent heterosis and the commercial heterosis for seed oil content up to 9 % and up to 14 %, respectively, was observed with hybrids displaying seed oil content as high as 533 g kg^{-1}. Erucic acid concentration displayed commercial heterosis.

Mohammed (2011) estimated heterosis in seven parental lines and their 21 F_1 of *Brassica carinata*. Standard heterosis ranged from -8.22% for harvest index to 191.57% for number of pods plant^{-1}, while for seed yield plant^{-1} it ranged from -16.64 to 66.09%.

Dar *et al.* (2012) estimated heterosis among 45 F_1 hybrids for seed yield and related traits. The most desirable cross combination viz., CR-1485 × CR-1607 for seed yield plant^{-1} also showed desirable mid and better parent heterosis for 1000-seed weight and primary branches plant^{-1}. The cross combinations CR-1485 × CR-1607 (primary branches plant^{-1}), CR1630 × KS-101 (secondary branches plant^{-1}), CR-2638 × KOS-1 (number of siliqua on main raceme), CR-1630 × CR-2871 (number of siliqua plant^{-1}), CR-1607 × KOS-1 (days to maturity) and KOS-1 × KS-101 (oil content) showed the highest mid and better parent heterosis.

Sincik *et al.* (2014) studied heterosis in *Brassica rapa* L. with five diverse genotypes in a 5 × 5 full diallel crosses including the reciprocals to determine the heterotic performance of the crosses for seed yield and yield components. The significant positive mid-parent and high-parent heterosis were obtained in several crosses in important yield components.

Ali *et al.* (2015) estimated heterosis in *Brassica juncea* L. out of 56 crosses, 34 crosses for oil content, 32 crosses for protein content showed the significant heterosis. 16 crosses for glucosinolate content, 32 crosses for erucic acid content and 32 crosses for linolenic acid content showed the significant negative heterosis. For oleic acid content, 49 crosses revealed the positive values, with the significant positive heterosis in 17 crosses. The significant

positive heterobeltiosis was recorded in 26 crosses for glucosinolate, 27 crosses for protein and eight crosses for oleic acid content. The significant negative heterobeltiosis was recorded in seven crosses for glucosinolate, 21 crosses for erucic acid, 11 crosses for linolenic acid content while 41 crosses showed the positive heterobeltiosis for oleic acid content and 22 crosses showed the negative heterobeltiosis for linolenic acid content.

Chaudhari *et al.* (2015) studied heterosis in nine parents, their 36 hybrids and one standard check (Benoy) of rapeseed following half diallel analysis. The promising crosses based on standard heterosis were PS 66 × YSB 2001, GS 1 × YSB 2001 and GS 1 × YSB 4-2005. The hybrids PS 66 × NDYS 53-1 and SSK 9203 × AA14 were found promising based on the high SCA and heterosis for oil content and erucic acid content.

Rahman *et al.* (2016) demonstrated allelic diversity of *Brassica napus* L. The mid-parent heterosis (MPH) showed a negative correlation with seed yield of the inbred lines in all three populations; however, a positive correlation existed between seed yield of the inbred lines and heterosis over Hi-Q (HiQH) (or, inbred vs. hybrid yield). On average, the level of MPH in hybrid of the inbred lines derived from *Brassica napus* × *Brassica oleracea* cross was twice greater than the level of heterosis found for the inbred lines derived from spring × spring or winter × spring *Brassica napus* crosses. The inbred population derived from winter × spring cross gave the highest seed yield, and this population also gave the highest HiQH.

Barupal *et al.* (2017) studied heterosis in ten lines, five testers and their 50 F_1s of Indian mustard. GM-3 × RGN-145, RGN-48 × Kranti and Gm-3 × Kranti had the highest negative and the significant heterosis and heterobeltiosis for days to flowering. Five hybrids showed the negative and the significant heterosis and heterobeltiosis, in which RGN-48 × RGN-145 and RGN-48 × Geeta were earliest in maturity. The most heterotic cross was RGN-48 × Kranti for days to flowering and maturity, plant height, number of branches and seed yield plant^{-1}.

Rai *et al.* (2017) studied heterotic performance for yield and yield related traits. The best threehybrids showing heterosis and heterobeltiosis were PM-21 × RSPR-01, PM-21 × Varuna and Pusa karishma × kranti. The parents PM-21 (23.47) and varuna (22.60) respectively showed the highest seed yield plant^{-1}. The highest seed yield plant^{-1} were found in Pusa karishma × varuna (27.43) and PM-21 × RSPR-01(22.47).

Singh *et al.* (2017) assessed the heterosis among six intra-specific crosses in yellow sarson with six parental genotypes, 12 F_1 and F_2 populations for the quantitative traits. In all cross

combinations, the hybrids performed better than their respective parents and significant positive standard and better parent heterosis was observed for the trait seed yield plant^{-1}.

Bharti *et al.* (2018) measured the extent of heterosis in diallel cross in Indian mustard. 21 F_1 crosses with seven diverse parents were evaluated for 12 characters, Heterosis ranged from 3.41 (PM-21 x PM-24) to 101.34 percent (PM-22 x Pusa-Karishma) for yield plant^{-1}. The crosses PM-21 ×PM-22, PM-21 × Pusa-Karishma, PM-22 × PM-24, PM-22 × Pusa-Karishma and PM24 × Pusa-Karishma had the high postive heterosis for seed yield plant^{-1}.

Kaur *et al.* (2019) studied Line × Tester effect showing the positive significant heterosis for all the traits except plant height, siliqua length, days to maturity and test weight. The cross, IC597879 × IC-571648 was found to be the most significant for yield plant^{-1}. On the basis of per se performance and estimates of heterosis, the cross IC-597879 × IC-571648 found to be the most promising followed by IC-597919 × IC-335852 and IC-589669 × IC-338586 for seed yield plant^{-1}. So these could be used in hybridization and heterosis breeding respectively.

Rameeh (2019) evaluated heterobeltiosis of eight genotypes of *Brassica napus* in half diallel crosses. Most of the crosses showed the significant positive high parent heterosis for seed yield with the significant heterotic effects for siliqua plant^{-1}. L41 × LF2 and L31 × L401 with the high significant heterobeltiosis of grain yield were the superior combinations for breeding.

Wolko *et al.* (2019) estimated heterosis of *Brassica napus*. 60 doubled haploid (DH) lines and two generations of hybrids were evaluated. For the first group, for plant height, silique length, and the number of seeds siliqua^{-1} a large number of hybrids showed the significant positive heterosis. For the second group, for number of branches and siliqua plant^{-1} and 1000 seed weight, hybrids exhibited both the positive and the negative significant heterosis.

2.3 Combining ability analysis

For the characters studied, both significant and insignificant results were noted in the literatures discussed in this chapter.

Aghao *et al.* (2010) estimated the GCA and SCA of ten parents and 45 crosses of Indian mustard. The GCA and SCA effects showed the significant variation in yield contributing traits, On the basis of significant GCA effects two parents were identified as the best combiner for days to flowering and maturity, plant height, number of pods plant^{-1}, 1000-seed weight. Among the hybrids Varuna × Seeta was identified as the best cross.

Ali *et al*. (2010) conducted an experiment on *Brassica napus* L. (Canola) and indicated the highly significant differences among the parents and their hybrids for days to flowering and maturity, number of primary and secondary branches, number of pods and yield plant^{-1}, number of seeds pod^{-1} which were controlled by partial-dominance type gene action but plant height and 1000 seed weight reflected nearly complete dominance type gene action.

Gupta *et al.* (2010) estimated GCA and SCA in *Brassica juncea* L. GCA and SCA variances were significant in all characters. The higher variance of GCA (σ2g) was for 50% flowering and maturity, plant height and 1000-seed weight, whereas the higher variance of SCA (σ^2s) was in seed yield and other remaining parameters.

Rameeh (2010) evaluated 15 F_2 progenies and six parents of *Brassica napus* and revealed that the significant GCA and SCA effects for all the studied traits which indicated both additive and non-additive gene action was present but degree of dominance less than unity observed for length of pod and 1000-seed weight indicating effects of additive gene action.

Sabaghnia *et al.* (2010b) estimated the GCA and SCA effects in some rapeseed genotypes and reported SCA variances were greater than GCA variances which showed the non-additive gene action in these traits. SCA × year interactions were significant for all the traits but GCA × year interactions were significant only for seeds pod^{-1} and oil percent.

Singh *et al*. (2010b) studied combining ability in a diallel analysis of ten Indian mustard genotypes. Predominance of non-additive gene effects were found for plant height, primary branches and seed yield plant^{-1} while rest of the traits were inherited by additive gene effects. Significant GCA effects were observed for seed yield, oil content, earliness and dwarfness. SCA effects were also significant for seed yield, oil content and other yield attributing traits.

Turi *et al.* (2010) studied combining ability in *Brassica juncea* L. GCA effects were highly significant for oil percentage and glucosinolates while SCA effects were highly significant for all traits except for oleic acids. The magnitude of GCA effects were greater than SCA effects for glucosinolate, erucic acid and protein content. Both additive and non-additive gene effects suggesting the integrated breeding program to utilize both gene effects.

Yadav *et al.* (2010) in a line × tester analysis with fourteen lines and five tester revealed that both additive and non-additive gene actions were involved in controlling yield contributing traits. The significant positive SCA effects were observed for seed yield,

1000-seed weight and number of pods in the main shoot, number of primary and secondary branches and the negative significant SCA effects for plant height.

Azizinia (2011) performed complete diallel analysis with eight genotypes. The significant variance were observed for plant height, number of lateral branches, number of pods in the main raceme, number of seeds pod^{-1}, 1000-seed weight, seed yield and oil contents. 1000-seed weight, oil contents and seed yield exhibited significant GCA and SCA effects.

Dar *et al.* (2011) studied combining abilities of *Brassica rapa* and showed that the variance due to dominance gene effects were much higher than the additive variance for number of primary and secondary branches, pods plant^{-1}, number of seeds pod^{-1}, 1000-seed weight and oil contents. The ratio of GCA to SCA was less than unity for all the traits, GCA of parents alone would not be advisable to select materials in segregating generations, but a combination involving both GCA and SCA of the parents and their crosses would be useful.

Gupta *et al.* (2011) estimated GCA and SCA effects in eight lines of *Brassica juncea* and their crosses. The significant GCA and SCA effects were observed among parents and hybrids for most of the traits. The GCA variance was higher than SCA variance for days to 50% flowering and 80% maturity, plant height and 1000-seed weight whereas SCA variance was higher for seed yield, number of primary and secondary branches and yield 100 pods^{-1}.

Nasrin *et al.* (2011) studied GCA and SCA of seven Indian mustard genotypes. The significant GCA effects were found for days to flowering and maturity, primary branches and seed yield plant^{-1}, 1000 seed weight, seeds pod^{-1}. Number of primary and secondary branches, number of pods and seed yield plant^{-1} and 1000 seed weight showed significant SCA effects in different hybrids. The GCA variances were higher than the SCA variances for plant height, days to maturity, pod length, number of seeds pod^{-1} and 1000 seed weight.

Parmar *et al.* (2011) estimated GCA and SCA effects in some rapeseed genotypes and revealed that both the additive and the non-additive genetic variance were important for controlling the studied traits. The ratio of variance of GCA over SCA revealed non additive gene action for all the traits except days to maturity.

Rameeh (2011a) determined combining abilities of *Brassica napus* L. The significant ratio of GCA to SCA effects was observed for 1000 seed weight indicated additive gene effects controlling this trait. The SCA effects for siliqua plant^{-1} had main role for seed yield.

However, most of the crosses having the significant positive SCA effects for seed yield had at least 1% with significant positive GCA effect for yield components.

Rameeh (2011b) studied combining abilities of quantitative and qualitative traits in 21 genotypes at two different nitrogen levels and revealed significant GCA and SCA effects for all the traits. The nitrogen × GCA mean square was not significant for all studied traits indicated stability of additive genetic effects in different conditions. The significant nitrogen × SCA mean squares for days to flowering and maturity and oil content. Significant positive and negative SCA effects were found for most crosses at zero nitrogen. Rameeh (2011c) studied the combining abilities of some winter and spring rapeseed genotypes using line × tester analysis. Non-additive gene effects for plant height and grain yield were indicated by significant mean square of line × tester. Significant SCA for plant height and grain yield was observed in few crosses. The mean square of Line × tester was also significant for seeds pod^{-1}, 1000-seed weight and seed yield.

Rameeh (2011d) performed line × tester analysis to estimate GCA and SCA effects for yield and its components. The significant positive GCA effects for seed yield and number of pods plant^{-1} were observed and almost all crosses showed the significant positive SCA effects for pods plant^{-1} and seed yield. Non-additive gene effects were significant for plant height and grain yield as indicated by significant value of mean square Line × tester.

Sincik *et al.* (2011) estimated the combining abilities using diallel crosses of four rapeseed (*Brassica napus* L.) genotypes. Analysis revealed that GCA effects were highly significant for plant height and pods main raceme^{-1}. While SCA effects were significant for plant height, number of pods main raceme^{-1}, number of seeds pod^{-1} and seed plant^{-1}.

Turi *et al.* (2011) studied GCA and SCA effects for yield and yield components in *Brassica juncea* L. The GCA effects were highly significant for yield plant^{-1} and 1000-seed weight, while non-significant for number of pods plant^{-1}, pod length and seeds pod^{-1}. The SCA effects were highly significant for all the traits except seeds pod^{-1}. Both additive and the non-additive genetic effects were revealed suggesting the use of integrated breeding strategies.

Vaghela *et al.* (2011) crossed six parents in a half diallel fashion of Indian mustard (*Brassica juncea* L.) to determine the combining ability. The significant GCA and SCA

effects for all the characters except oleic acid was observed. The GCA to SCA ratio was less than unity and only few crosses showed significant SCA effects for seed yield.

Verma *et al*. (2011) studied combining ability of twelve diverse female and three male parents and found non-additive gene effects had greater importance for all the characters. Three parents behaved as the best general combiners for seed yield plant^{-1}. The SCA effects were also significant for yield and its contributing traits in some crosses.

Azizinia (2012) determined the combining abilities of eight parents using diallel cross. 1000 seed weight, oil content and seed yield showed significant GCA and SCA effects. There were significant positive effects for yield and yield components.

Arifullah *et al.* (2012) crossed eight genotypes in 8×8 diallel system for combining ability analysis and revealed significant GCA effects for most of the traits except plant height and siliqua length. UCD-8/4, KJ-119 and BRS-2 were good general combiners for yield related traits. A cross BRS-2 × UCD-8/4 showed the best desired SCA for number of primary branches and siliqua plant^{-1}. S-9 × Canola Raya for siliqua length, Canola Raya × UCD-8/4 for number of seeds siliqua^{-1}, KJ119 × BRS-2, BARD-1 × NIFA Raya for 1000 seed weight while cross BRS-2 × UCD-8/4 for seed yield showed good positive SCA effects, involving at least one of the promising general combiner parents.

Rameeh (2012) studied GCA and SCA effects of six lines and two testers of spring rapeseed (*Brassica napus* L.) in a Line × tester analysis and reported that non-additive genetic effects controlled the number of pods plant^{-1} and seed yield. Most of the crosses showed the negative SCA effects which indicated that at least one parent have significant negative GCA effects.

Sincik *et al.* (2014) estimated combining ability in five *Brassica rapa* L. genotypes in 5 × 5 full diallel crosses including the reciprocals. The mean squares of the GCA, SCA and RCA were statistically significant for all the traits studied. The parent Malvira was a good general combiner because this parent had the highest significant positive GCA effects for all the traits. Lenox proved to be a good general combiner for plant height. The parents exhibited positive GCA effects for seed yield so, they could be used for further breeding studies.

Chaudhari *et al.* (2015) studied combining ability in nine parents and 36 hybrids and one standard check of rapeseed in half diallel analysis. The ratio of $ó^2_{gca}/ó^2_{sca}$ suggested predominance of non- additive gene effects for all the characters except days to maturity.

Based on GCA effects the parents GS 1 and PS 66 were selected as good general combiners for seed yield plant^{-1} and component traits. While parents SPAN, AA 14 and SSK 9203 proved to be good general combiners for quality traits viz., oil content, erucic acid. The cross NDYS 53-1 × AA 14, YSB 2001 × SSK 9203 and SPAN × SSK 9203 exhibited significant SCA effects for seed yield plant^{-1} and its associated traits.

Atikunnaher, *et al.* (2017) evaluated combining ability in 21 rapeseed materials in a diallel analysis. The highly significant GCA and SCA effects were found for the studied traits. Based on GCA effects, the best general combiners were Nap-9908 for number of siliqua and seed yield plant^{-1} and seeds siliqua^{-1}. The GCA variance was higher than SCA variance for all the studied traits except days to 50% flowering and number of secondary branches plant^{-1}. Similarly, based on SCA effects the best combiners were Nap-9905×Nap-205 for number of primary branches and seed yield plant^{-1}, Nap-9901×Nap-205 for secondary branches, siliqua length and seeds siliqua^{-1} and Nap-9908×Nap-9901 for number of siliqua plant^{-1}. So, these could be utilize in future rapeseed breeding program.

Rai *et al.* (2017) studied the GCA and SCA effects for yield and related traits by Line × tester design. Results revealed that none of the parents showed significant GCA effect in the desired direction for all the traits. Pusa karishma was found to be the best general combiner for most of the traits, followed by PM-21 and varuna. The parents PM-21 (23.47) and varuna (22.60), respectively showed the highest seed yield plant^{-1}. The crosses showing the highest seed yield plant^{-1} were Pusa karishma × varuna (27.43) and PM-21 × RSPR-01(22.47).

Channa *et al.* (2018) crossed fourteen accessions and four testers of *Brassica napus* L. in line × tester mating to estimate GCA and SCA effects for seed yield, yield components and oil content in four environments. The highly significant differences were detected among the parents and hybrids for all the traits across environments. Plant height, setting position of first primary branch and length of terminal raceme were controlled by additive genes, whereas primary branches, siliqua and seed yield plant^{-1}, seeds siliqua^{-1}, 1000 seed weight, oil content, and seed yield were controlled by non-additive gene action. The accessions SP-Armada, 9E49, and CZ25 and the tester Zhong9 were good general combiners for seed yield. Among the 56 F_1 hybrids, four hybrids Zhong9 × CZ25, GZ1R × 9E38, Zhong7 × 9E38, and Zhong7 × CZ49 showed the higher yield than the control and were the

outstanding combinations for seed yield. These hybrids were recommended to be included in future breeding programs.

Inayat *et al.* (2019) studied combining ability in eight mustard genotypes and their 56 combinations in F_2 population in a complete diallel fashion. All the traits showed the significant GCA effects. All the traits also gave significant SCA effects except seed yield plant^{-1}. The genotypes NUMYT-103 and NUMYT-123 were the best general combiner among all the cultivars for showing desirable positive GCA effects for pods main raceme^{-1} and pod length and desirable negative GCA effect for plant height. F_2 specific cross combination, NUMYT-103 × NUMYT-117 showed the highest desirable positive SCA effects for seed yield plant^{-1}. The best reciprocal cross for pod length was NUMYT-117 × NUMYT-103.

Kaur *et al.* (2019) studied Line × Tester effect and found the positive significant effects for all the traits except plant height, siliqua length, days to maturity and test weight. The significant differences were observed for both GCA and SCA effects. IC-597919 was found to be good general combiner for most of the traits. The cross combinations namely, IC597879 × IC-571648 was found to be the most significant for yield plant^{-1}.

Rameeh (2019) conducted a half diallel crosses of eight spring genotypes of *Brassica napus* L. Significant GCA and SCA effects were estimated for all the traits except 1000 seed weight indicating prominence of additive and non-additive gene effects for mentioned traits.

Singh *et al.* (2019) evaluated 5×5 diallel crosses of Indian mustard along with their parents to estimate GCA and SCA effects of parents and crosses, respectively. The significant differences were observed for both GCA and SCA for almost all the traits. The high magnitude of GCA and SCA effects indicated the presence of both additive and non-additive gene interactions for the inheritance of different traits. Parents, IC-571663 and IC-317528 were exhibited to be good general combiners for seed yield plant^{-1}, based on SCA effects, the high ranking crosses for yield and its component traits were IC-571649 × IC-571663, IC-571649 × IC-317528, IC-571649 × IC-338586 and IC-599679 × IC-338586.

2.4 Gene action study

Checa *et al.* (2007) reported that *Phaseolus vulgaris* L. genotypes have the highest yield potential of all accessions found in the species to determine the inheritance of climbing capacity traits in three crosses made within and between gene pools (Andean × Andean [BRB32 × MAC47], Meso-american × Mesoamerican [T$_1$́o Canela × G2333], and

Mesoamerican × Andean [G2333 × G19839]) using generation means analysis. Six generations (P_1, P_2, F_1, F_2, BC1 and BC2) were evaluated at two growth stages (40 and 70 days after planting). Results showed the importance of additive compared with the dominant–additive portion of the genetic model. Broad-sense heritabilities for the traits varied from 62.3% to 85.6% for PH and from 66.5% to 83.7% for IL. The generation means analysis and heritability suggested that the inheritance of PH and IL in climbing beans is relatively simple.

Sharmila *et al.* (2007) studied the nature and magnitude of gene effects for yield and its components in *Sesamum indicum* L. by generation mean analysis using four crosses of different sesame cultivars: VS 9510 × Co1; NIC 7907 × TMV 3; Cianno 13/10 × VRI 1; and Si 1115/1 × TMV 3. The P_1, P_2, F_1, F_2, BC1 and BC2 generations were studied for seven quantitative traits. The analysis showed the presence of additive, dominance and epistatic gene interactions. The additive dominance model was adequate for plant height in the NIC 7907 × TMV3 and Si1115/1 × TMV 3 crosses and for capsule length in the VS 9510 × Co1, NIC 7907 × TMV 3 and Si 1115/1 × TMV three crosses. An epistatic digenic model was assumed for the remaining crosses. Duplicate-type epistasis played a greater role than complementary epistasis. The study revealed the importance of both additive and non-additive types of gene action for all the traits studied.

Naveed *et al.* (2009) carried out an experiments to assess the genetic potentiality for drought tolerance through breeding and selection in six generations of four crosses between pairs of genotypes with a degree of tolerance to drought in okra genotypes. Narrow sense heritability and genetic advance varied across crosses, traits and stress conditions. For fruit yield, narrow sense heritability and genetic advance were high under non-stress condition as compared to drought, which indicated that direct selection of fruit yield would only be feasible under non stress conditions. Among the agronomic traits, although number of pods plant^{-1} had shown good narrow sense heritability and genetic advance under drought, yet leaf water potential appeared to be the better indicator for selection criteria owning to the higher heritability under drought. Among the crosses, Sanam × Arka Anamika appeared elite in terms of narrow sense heritability and genetic gain compared with other crosses, with the highest fruit yield and pod number plant^{-1} under both conditions. Thus, chances to find stress tolerant breeding material in segregating populations of this cross are promising.

Khodambashi *et al.* (2012) estimated heritability and gene action for grain yield and its related traits in lentil, six basic generations were evaluated. Generation mean analysis using A, B, C and joint scaling tests indicated that additive [a], dominance [d] and at least one of the epistatic effect (additive × additive [aa], additive × dominance [ad] and dominance × dominance [dd]) were involved in the inheritance of the studied traits. However, simple additive-dominance model was sufficient only for pod length. Significant dominance [d] and dominance × dominance [dd] interactions with opposite sign indicated duplicate epistasis for all the traits except pod length. Narrow-sense heritability was low for seed yield plant^{-1}, pod length, number of seeds pod^{-1} and 1000-seed weight and moderate for other traits. Average dominance ratio was more than unity for seed yield plant^{-1}, number of primary and secondary branches, pod length, and 100-seed weight, which showed the high importance of dominance gene effect in control of these traits. Due to the presence of greater non-additive gene effects combined with low narrow-sense heritability, selection for almost all of the studied traits in this cross, especially in early generations, would be complex in conventional methods.

Jatothu *et al.* (2013) estimates gene effects through joint scaling test of three and six parameter and sequential fit model in five crosses for eleven characters. Simple additive dominance model exhibited lack of good fit for all the traits. So, sequential fit model was searched after eliminating the non-significant parameters of six parameter model. Five parameter sequential fit model was observed for number of primaries plant^{-1} (cross 1), number of seeds capsule^{-1} (cross 4), oil content (cross 2 and 3), seed yield plant^{-1} (cross 1) and chlorophyll content (cross 3). Best fit four parameter sequential model was observed for number of primaries plant^{-1} (cross 2) and 1000 seed weight (cross 1). The higher order interactions epistasis or linkage were observed for days to 50 % flowering (cross 1, 2, 3, 4, and 5), days to maturity (cross 1, 2, 3, and 4), plant height (cross 3, 4, and 5), number of effective primaries plant^{-1} (cross 3, 4, and 5), number of effective capsules plant^{-1} (cross 2, 3, 4, and 5), number of seeds capsule^{-1} (cross 1, 2, 3, and 5), 1000 seed weight (cross 4 and 5), seed yield plant^{-1} (cross 4 and 5), oil content (cross 1, 4, and 5) and chlorophyll content (cross 1, 2, 4, and 5). Differential model schemes for same trait in different crosses were noticed in the present investigation. It was due to different parents involved with variable gene frequency with opposing and reinforcing genetic effects. The magnitude of [d] was relatively small to that of other genetic effects. This indicated that, additive genes are playing a minor role in the inheritance of these traits.

Lal *et al.* (2013) performed genetic analyses for heat tolerance parameters. Three crosses namely Raj 3765 × PBW343, Raj 3765 × Raj 4037 and Raj 3765 × Raj 4083 of four parents were used. A, B, C and D scaling tests revealed that additive-dominance model was inadequate for all the crosses for days to maturity, two crosses for days to heading, and one cross for grain protein content, indicated presence of non-allelic interactions. However, all the three crosses showed adequacy of additive-dominance model for grain yield and its components. Among digenic interaction dominance × dominance (l) and additive × additive (i) were more important as compared to additive × dominance (j) for most of the characters. Duplicate type of epistasis was exhibited for days to maturity in two crosses viz. Raj 3765 × PBW 343 and Raj 3765 × Raj 4037, while for grain protein content in one cross Raj 3765 × Raj 4037.

Mulugeta *et al.* (2013) evaluated 36 genotypes (eight parents and 28 F_1 diallel crosses) to study the inheritance of two number of seeds pod^{-1} and 1000 seed weight. The significant difference was observed between the genotypes, parents, and crosses for these traits. Both the additive and the non- additive types of gene actions were important in the inheritance of number of seeds pod^{-1}. The significant b1 was obtained for this trait. The b2 and b3 however, were not significant, suggesting the absence of gene a symmetry. From Wr/Vr g raph, inheritance of seeds pod^{-1} was governed by partial dominance with additive gene action.

Divya et al. (2014) studied six generations viz., P_1, P_2, F_1, F_2, BC1 and BC2 of a cross between blast susceptible high-yielding rice cultivar ADT 43 and resistant near isogenic line (NIL) CT13432-3R, carrying four blast resistance genes Pi1, Pi2, Pi33 and Pi54 to study the nature and magnitude of gene action for disease resistance and yield attributes. The epistatic interaction model was adequate to explain the gene action in most of the traits. The interaction was complementary for number of productive tillers, economic yield, lesion number, infected leaf area and potential disease incidence but duplicate for the remaining traits. Among the genotypes tested under epiphytotic conditions, gene pyramid lines were highly resistant to blast compared to individuals with single genes indicating that the non-allelic genes have a complementary effect when present together.

Prajapati *et al.* (2014) studied the nature of gene interaction in the inheritance of thirteen yield and its components traits by deploying generation mean analysis following six parameter models for parents P_1 and P_2, F_1, F_2, and BC1 and BC2 generations of four

crosses of Indian mustard. The additive and non-additive gene action involve in seed yield plant^{-1} in all crosses, number of seeds siliqua^{-1} and number of siliqua plant^{-1} in the crosses GM1 × Vardan and IC 491446 × GM 2 with greater magnitude of non-additive gene action for inheritance of character. All 3 types of digenic interactions among the linked pairs of genes, additive × additive (i), additive ×dominance (j) and dominance × dominance (l), contributed significantly in the inheritance of number of seeds siliqua^{-1} in cross IV; length of main branch in cross IC 491446 × GM 2; test weight in cross IC 491446 × GM 2 and PM 67 × Varuna with greater magnitude of dominance × dominance interaction (l). The additive × additive (i) interaction had the greater magnitude in protein content in cross IC 491446 × GM 2. The $\chi 2$ value of joint scaling test was found significant in most of the characters in all the crosses. Duplicate epistasis was evident for most of the characters of yield and its attributes in different crosses.

Singh *et al.* (2014) performed generation mean analysis using two crosses (Maya × BPR_ 543-2) and (BPR_ 543-2 × BPR_ 2) to study the nature and magnitude of gene effects on seed yield and physiological characters in Indian mustard. The F_1, F_2, BC1 and BC2 of these crosses, along with P_1 and P_2, were studied for physiological traits. As to the water use efficiency, the dominance (h) and dominance × dominance (l) non-allelic interactions were found to be the most important in BPR_ 543-2 × BPR_ 2 cross. In Maya × BPR_ 543-2, negative significant values of h and l were observed. Water use efficiency also showed duplicate-type epistasis in both crosses; indicating that l gene interaction effect or other types of digenic complementary gene interaction could be exploited effectively by selection for improvement of this trait. The seed yield plant^{-1} in Maya × BPR-543-2 showed d, h, and additive × additive (i) types of gene interaction, indicating this trait was under the control of fixable and non-fixable gene effects. The i gene interaction and duplicate epistasis suggested possibilities of obtaining transgressive segregants in later generations.

Mumtaz *et al.* (2015) used the Hayman and Jinks model to estimate gene action on oil quality related traits using four lines (UAF-11, Toria, BSA and TP-124–1) and their hybrids in a diallel fashion. All traits other than oil percent and linolenic acid were controlled by dominant gene action. Absence of epistasis was observed for all traits. Number of frequency of dominant genes was more frequent towards better parents, and recessive genes were greater than dominant genes in all traits, except in the case of lenolenic acid. The best

parents were TP-124–1 and UAF-11, which had the maximum dominant and recessive genes, for the best traits can be used as parents in future hybrid breeding programs.

Parihar *et al.* (2016) investigated six generations derived from three different crosses in grass pea. The significance of additive-dominance model, gene action involved in inheritance of quantitative characters and heritability. Non-allelic interactions influencing the traits were detected by the both scaling test and joint scaling test, indicating the inadequacy of the additive-dominance model in explaining the manifestation of complex traits such as yield. Additive (d) and dominance (h) gene effects, different types of inter-allelic interactions (i, j, l) contributed towards the inheritance of traits in the given crosses. Duplicate epistasis was prevalent in most of the cases for traits like plant height, seeds pod^{-1}, 100-seed weight and pod width. In view of the diverse gene actions, i.e. additive, dominant and epistasis, playing important roles in the manifestation of complex traits like yield, therefore, implementation of population improvement techniques in particular reciprocal recurrent selection was suggested to improve productivity gains in grass pea.

Prabhu *et al.* (2017) studied gene action for yield and related characters in two selected crosses of rice, involving three parents, including their F_1s, F_2s, and their back cross populations. The significant scaling test indicated digenic epistasis in all the characters studied except in grain yield $plant^{-1}$ which showed simple additive and dominance effect. Since the segregation generations did not follow Mendalian inheritance, high selection pressure is expected in later generations due to probable successful exploitation of additive and dominance component.

Singh *et al.* (2017) studied six generations in three crosses to estimate gene effects in yield and its related attributes by generation mean analysis and scaling test for ten physiological traits and revealed three cross families showed the significant differences among the progenies (generations) within family for most of the quantitative traits. Six parameters genetic model revealed the presence of additive (d), dominant (h) and epistasis (i, j, l) for most of the evaluated traits. Significant differences for two or more individual scaling tests (A, B, C, and D) in all three crosses indicating the sight of non-allelic interactions. Further, it was confirmed by joint scaling test. All the crosses showed significant chi-square values for all the evaluated characters except for days to maturity in NDYS 427 × YST-151. The significant chi-square values indicated the presence of epistasis or inadequacy of additive-dominance model.

Pallavi *et al.* (2019) carried out generation mean analysis in cowpea to estimate the gene action in the inheritance of yield and its components using six basic generations of two different crosses namely PGCP-63 × Pant Lobia-1 and Pant Lobia-3 × Pant Lobia-1. In most traits, additive, dominant, additive × additive, additive × dominance and dominance × dominance were significant. Additive effect significantly contributed for number of pods plant^{-1} and 100-seed weight. Dominance effect was significant for the pod length in both families. Additive × dominance type of interaction contributed significantly for days to flowering and pod maturity and seed yield hectare^{-1}. Duplicate type of epistasis was observed for days to flowering, and pod length in both family. The study suggested recurrent selection for cowpea improvement.

Philanim *et al.* (2019) studied the nature and magnitude of gene effects for the yield and important yield contributing characters in mustard. Six generations of two crosses viz; MRNJ 88-1 × JMWR 9081-1 (Family A), MRNJ 131 × JMWR 9081-2 (Family B) were investigated and showed the predominance of both Main effect (additive-dominance) and interaction effect for most of the studied traits except in number of primary and secondary branches plant^{-1}. Presence of interaction effects and duplicate epistasis suggested the possibilities of obtaining transgressive segregants in later generations. The role of fixable and non-fixable gene action in controlling different traits was also apparent. This will help in deciding effective selection and breeding strategies for desirable improvement in yield and related traits.

Fouad *et al.* (2020) estimated gene effects through generation mean analysis in two faba bean crosses. Heritability in broad sense were higher than in narrow sense for all traits in both crosses. Heterosis over the better and the mid parents and inbreeding depression were positive and degree of dominance was higher than one for all traits in both crosses. The significant positive additive gene effect for days to 50% flowering and plant height in cross I and yield and 100 seed weight in cross II, indicated effective selection for these traits. Dominance effects were greater the additive effects for all traits. Complementary epistasis type for traits like PH and NS P^{-1} in cross I and DF, PH and 100 seed weight in cross II indicates selected parents for crossing are different. Predominant duplicate epistasis than complementary epistasis indicating recurrent selection could improve these traits in advanced generations.

Abdelsatar *et al.* (2021) evaluated gene action and epistasis for yield and related traits. Scaling and joint scaling tests revealed inadequacy of simple additive-dominance model in the inheritance of all studied traits in corresponding crosses at both locations. Significant negative heterosis and heterobeltiosis were found for days to first flower, plant height and first siliqua height, whereas it was significant positive for seed weight plant^{-1} and its components in the corresponding crosses at both locations. High to moderate heritability (Ns) were detected for days to the 1st flower in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, 1st siliqua height in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish and seeds weight plant^{-1} in the 1st cross at both locations. The dominance gene effects as the ratio ((H/D) $^{0.5}$>1) with the duplicate epistasis was detected in most of the traits in the corresponding crosses at both locations. Therefore, delay selection to advanced generation is advisable for improving most traits in most cases.

Rajanna *et al.* (2021) undertaken a study to know the nature of gene action governing the characters. Generation mean analysis was performed to decide the breeding program that suit for the improvement of traits being analyzed. In majority of the yield traits F_2 mean was lower than their corresponding F_1 for characters like, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and yield plant^{-1}. six generations mean analysis in the cross PCL-55 × LLA-5 revealed that dominance genetic variance was documented for the important yield traits like, number of capsules plant^{-1}, 1000 test weight and yield plant^{-1}.

2.5 Genotypic and phenotypic variability

Improvement in any crops depends mainly on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. So, the genetic variability of the germplasm should be evaluated. The review of literature concerning the studies are presented here:

Alam (2010) conducted an experiment by using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* L. to study the variation among them and found the higher phenotypic variation than the genotypic variation.

Singh *et al.* (2010a) studied on 62 F_1 and 24 parental lines of *Brassica juncea* and observed the higher genotypic variation in seeds plant^{-1}, primary and secondary branches plant^{-1}, 1000 seed weight and seeds siliqua^{-1}.

Roy *et al.* (2011) conducted an experiment on *Brassica* spp. to study variability. The result revealed significant varietal difference except the number of siliqua on main recyme. The PCV and the GCV was high in secondary branches plant^{-1} and number of siliqua plant^{-1}.

Yadava *et al.* (2011) evaluated 30 released varieties of *Brassica juncea* (L.) Czern and Coss. 14 quantitative traits was studied and pooled analysis over the environments. The mean, range, phenotypic, genotypic and environmental variance, genotypic and phenotypic coefficient of variation were calculated and found diverse nature in used material.

Kahrizi and Alaahvarand (2012) carried out a study to estimate genetic variability parameters in 17 spring rapeseed genotypes. The characters studied were grain yield, some phenological, morphological and physiological traits. Statistical analysis showed significantly differences among the genotypes based on the most studied traits. This indicated that there was sufficient variability available to have an effective selection. Genotypic and phenotypic coefficients of variations were high for grain yield, crown to first node distance (CND), Harvest Index (HI). High genetic gain was observed for HI (42.91%) and CND (39.25%).

Abideen *et al.* (2013) studied eight genotypes of *Brassica napus* and observed that there were highly significant variations among the genotypes for most of the traits studied. Non-significant differences were in primary branches plant^{-1} and pods plant^{-1} among the genotypes.

Ahmad *et al.* (2013) studied 35 advanced mutant lines along with a cheek variety of *Brassica napus* called Abasin-95 for variability analysis and reported that seed yield and days to flowering showed the high genetic variability. The mutant lines 0A5, G1 and 06 showed their superiority in the high seed yield, 1000 seed weight and earliness in flowering.

Ali *et al.* (2013) conducted an experiment with 30 lines of *Brassica carinata* and reported thatPCV and GCV ranged from 4.92-48.24% and 3.2-38.1%, respectively.

Khan *et al.* (2013) evaluated 30 F_7 segregating lines and two parents of *Brassica rapa* to study variability. The result revealed that except 1000 seed weight, significant variation was presented among all the genotypes for all the characters. The highest

genotypic, phenotypic and environmental variances were observed in plant height while the lowest one was in length of siliqua followed by 1000 grain weight.

Uddin *et al.* (2013) conducted an experiment to study the variability among seven parental genotypes and their 21 F_2 progenies of *Brassica rapa* at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The phenotypic variances were higher than the genotypic variances. Least genotypic and phenotypic variance was observed among all the parental genotypes and their F_2 progenies for all the characters studied except for siliqua plant^{-1}. The highest genotypic coefficient of variation value was observed for secondary branches plant^{-1}.

Ejaz-Ul-Hasan *et al.* (2014) carried a research on nine genotypes of *Brassica napus* to evaluate components of variability for yield and various yield components. Significant variation was found at phenotypic and genotypic level of seed yield plant^{-1}, plant height, siliqua plant^{-1}, siliqua length, seeds siliqua^{-1}, days to maturity and 1000 seed weight, days to flowering.

Halder *et al.* (2014) assessed variability among 11 advanced lines of *Brassica rapa* with three popular check varieties. Significant variations were found in yield hectare^{-1} and all the yield components. The highest yield hectare^{-1} (2111.33 kg) was found in TORI-7 × BARI Sarisha-9. The advanced line BARI Sarisha-6×TORI-7 matured early (83.67 days) and produced moderate yield (1662.00 kg). The highest GCV (20.06%) and PCV (31.71%) were observed in number of siliqua plant^{-1}. Genotypic variance was lower than phenotypic variance for all characters except yield hectare^{-1}.

Hussain *et al.* (2014) carried out an experiment with 24 genotypes including four check varieties of *Brassica rapa* L. for estimating the variations in characters. The phenotypic variances were higher than the genotypic variances. Days to 50% flowering and 80% maturity showed moderate difference between the phenotypic and genotypic variance whereas minimum differences were found in number of primary and secondary branches plant^{-1}, number of seeds siliqua^{-1}, siliqua length and 1000 seed weight and yield plant^{-1}.

Iqbal *et al.* (2014) carried out a study to check ten locally collected *Brassica rapa* accessions for genetic variability estimation. The highly significant differences were observed in all traits except siliqua width. Hence, these great proportion of genetic variability could be manipulated in future breeding programs to fully utilize their genetic potential.

Jahan *et al.* (2014) conducted a field experiment to study variability in ten F_4 line of *Brassica rapa*. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters the high GCV was observed for number of secondary branches plant^{-1}, siliqua plant^{-1}, yield plant^{-1}, whereas days to maturity showed very low GCV.

Mekonnen *et al*. (2014) evaluated 36 genotypes of *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. The high GCV estimates were observed for number of pods plant^{-1}, primary and secondary branches plant^{-1}, seed yield plot^{-1}, and seed yield hectare^{-1}. The highest PCV was in primary branches plant^{-1}. The higher GCV and PCV for seed yield, number of pods plant^{-1}.

Muhammad *et al.* (2014) studied four parental genotype along with twelve F_2 generation of *Brassica napus* and reported days to 50% flowering were significantly different. Plant height and pod length showed the high heritability and days to 50% flowering showed the moderate heritability.

Walle *et al.* (2014) carried out a study to estimate the genotypic variability of Ethiopian mustard. Highly significant values for days to maturity, grain filling period, secondary branches plant^{-1}, harvest index, seed yield plot^{-1}, seed yield hectare^{-1} and oil content were found. Significant differences were noted for days to flowering, plant height, primary branch plant^{-1}, oil yield plot^{-1}. GCV % was lower than PCV % for all the traits studied.

Iqbal *et al.* (2015) carried out an investigation in 49 genotypes of *Brassica rapa* to study the genetic variability for various traits. PCV was higher than corresponding GCV for all the studied traits. The high GCV was in seed yield plant^{-1}, whereas the moderate GCV was revealed in number of primary and secondary branches plant^{-1}.

Naznin *et al.* (2015) conducted an experiment with 33 genotypes of *Brassica rapa* L. to find out their inter-genotypic variability for yield and its component characters. BARI sarisha-6 × Tori-7 showed the best result in terms of early maturity (75 days) and the higher seed yield plant^{-1} (5.28g) than check varieties. Plant height was highly influenced by the environment whereas, all other characters influenced the least. Number of secondary branches plant^{-1} showed the highest PCV and GCV. Therefore, number of primary and secondary branches plant^{-1} and siliqua plant^{-1} can be used as selection criteria to increase seed yield plant^{-1}.

Bibi *et al.* (2016) conducted an experiment to observe genetic variability of ten *Brassica juncea* genotypes. Highly significant differences were observed in days to 50% flowering, days to 70% maturity, plant height, number of primary branches, silique length, number of seeds siliqua^{-1}, 1000 seed weight and seed yield plant^{-1}.

Joya *et al.* (2016) evaluated 38 rapeseed genotypes to estimate the genetic variability of eight quantitative characters. A considerable amount of genetic variability were found in 1000 seed weight (11.09g) to harvest index (44.00%) and phenotypic variability for plant height (13.36m) to harvest index (44.14%).

Yared and Misteru (2016) studied 64 *Brassica* breeding lines to investigate the extent and nature of genetic variability. Considerable genetic variation was found among the lines for further selection and hybridization efforts.

Afrin *et al.* (2017) evaluated 30 BC_1F_6 populations of *Brassica napus* to study the genetic variability for yield and yield component traits and revealed significant variations were observed among the genotypes for all the traits. Considering genetic parameters, the high GCV were observed for number of secondary branches plant^{-1} and seed yield plant^{-1}.

Salam *et al.* (2017) carried out a research on 30 F_1 to estimate the genetic variability. Sufficient variability except for days to maturity and oil content (%) was revealed. PCV was higher than the GCV. The high GCV and PCV were observed for number of branches plant^{-1} and harvest index. The traits plant height, siliqua length, number of siliqua plant^{-1}and seed yield plant^{-1} had the moderate GCV and PCV.

Sikarwar *et al.* (2017) carried out an experiment to assess the genetic variability in 21 genotypes of *Brassica rapa* L. for ten yield and its contributing traits. The high PCV and GCV were observed for number of secondary branches plant^{-1} followed by seed yield plant^{-1}, number of primary branches plant^{-1} and number of siliqua on main raceme. Days to flowering, plant height and length of siliqua showed low PCV and GCV.

Singh *et al.* (2017) carried out a study in six parental genotypes, twelve F_1 and F_2 populations to assess the variation in quantitative traits and revealed significant differences for all yield and quality traits indicated the presence of sufficient genetic variability for effective selection.

Karmokar (2018) conducted an experiment to evaluate genetic variability for ten yield and its contributing characters of 13 advanced line of *Brassica rapa* L. The phenotypic variance

was considerably higher than the genotypic variance for all the characters studied. Number of primary and secondary branches plant^{-1}, length of siliqua and 1000 seed weight and yield plant^{-1} showed least difference between genotypic and phenotypic variance while Days to 80% maturity, plant height, number of sliliqua plant^{-1} showed much difference. The high GCV and PCV was found for number of secondary branches, siliqua and yield plant^{-1}.

Rauf and Rahim (2018) evaluated 35 genotypes of *Brassica napus*. The significant variation were found for most of the traits. Phenotypic variances were comparatively higher than the genotypic variances for most of the traits. The high GCV was observed for seed yield plant^{-1}.

Singh *et al.* (2018) evaluate sixty germplasms of Indian mustard to estimate genetic variability for yield and its contributing traits. The highly significant variations were observed for all the traits. The high PCV was recorded for seed yield, secondary and primary branches plant^{-1}, 1000-seed weight and the highest GCV was for seed yield plant^{-1} followed by secondary branches plant^{-1}, 1000-seed weight, length of main raceme and plant height.

Ullah (2018) evaluate genetic variability for ten yield and its contributing characters of eight advanced populations of *Brassica rapa* L. For all the traits the genotypic variance was lower than the phenotypic variance. Number of primary and secondary branches, seed yield plant^{-1}, siliqua length and 1000 seed weight showed the least difference between genotypic and phenotypic variance. The low GCV and PCV was observed for days to 50% flowering and 80% maturity, plant height, number of primary branches and siliqua plant^{-1}, siliqua length and number of seeds siliqua^{-1} except number of secondary branches and seed yield plant^{-1}and 1000-seed weight. The differences between PCV and GCV for the characters were narrow.

Gupta *et al.* (2019) carried out an experiment to estimate genetic variability among 35 genotypes of oilseed *Brassica*. Considerable variability was observed among the genotypes for all the fourteen characters. The estimates of GCV and PCV were comparatively higher for plant height, primary and secondary branches plant^{-1}, number of siliqua plant^{-1}, siliqua length, seeds siliqua^{-1}, 1000 seed weight, seed yield plant^{-1} and oil yield plant^{-1}.

Rout *et al.* (2019) examine the genetic variability in 38 genotypes of Indian mustard. Significant variability were found among the genotypes for all the traits. PCV and GCV were observed moderate for number of primary and secondary branches, siliqua, biological weight, and seed yield plant^{-1}, number of seed siliqua^{-1}, harvest index and 1000 seed weight. The difference between the values of GCV and PCV were observed low for all the traits.

Aktar *et al*. (2019) conducted an experiment with eighteen *Brassica* genotypes to estimate genetic variability. Significant variation was found among the genotypes for all the studied traits. The PCV was higher than the GCV for all the characters measured.

2.6 Heritability and genetic advance

Knowledge about heritability and genetic advance is helpful for quick improvement by selecting suitable genotypes through appropriate breeding methodologies. Related works for heritability and genetic advance are reviewed below.

Alam (2010) studied the heritability and genetic advance in 26 F_4 populations of *Brassica rapa* L. High heritability with high genetic advance was found in plant height, number of primary and secondary branches plant^{-1} and number of siliqua plant^{-1}.

Singh *et al.* (2010a) studied 62 F_1 and 24 parental lines of *Brassica juncea* and observed that high heritability and high genetic advance in primary and secondary branches plant^{-1}, seeds plant^{-1}, 1000-seed weight and seed siliqua^{-1}.

Afrin *et al.* (2011) studied heritability in *Brassica napus*. The plant height showed the highest heritability (BS) while the number of siliqua, primary and secondary branches plant^{-1}, siliqua length, number of seed siliqua^{-1}, 1000-seed weight and seed yield plant^{-1} showed the moderate broad sense heritability. Days to 80% maturity showed the lowest heritability.

Roy *et al.* (2011) conducted an experiment on *Brassica* spp. and studied heritability. The high heritability along with high genetic advance as percent of mean was reported in plant height, seed yield, secondary branches plant^{-1}, siliqua plant^{-1} and seeds siliqua^{-1}.

Tahira *et al.* (2011) studied ten genetically wide ranged variety of *Brassica juncea* to study heritability in broad sense. Siliqua length, plant height and seed yield had the high values.

Yadava *et al.* (2011) evaluated thirty released varieties of *Brassica juncea*. 14 quantitative traits was evaluated. Heritability in broad sense and genetic advance were calculated. The high heritability coupled with high genetic advance for 1000-seed weight was found.

Kahrizi and Alaahvarand (2012) carried out a study to estimate heritability in seventeen spring rapeseed genotypes. The high heritability was found in all phonological traits and chlorophyll content but the low heritability was found for the grain yield and HI.

Ahmad *et al.* (2013) estimated heritability in 30 advanced lines and a cheek variety of *Brassica napus*. The high heritability with high genetic advance was found in seed yield plant^{-1}.

Ali *et al.* (2013) conducted an experiment with 30 *Brassica carinata* genotypes and found the highest heritability for pod length followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield plant^{-1} and pods on main raceme.

Khan *et al.* (2013) evaluated 30 F_7 lines and two parents of *Brassica rapa* to study heritability and genetic advance. 1000 seed weight, number of secondary branches plant^{-1}, seeds siliqua^{-1} and siliqua length showed the high heritability with low genetic advance in percent of mean.

Uddin *et al.* (2013) studied the heritability and genetic advance in seven parental genotypes and 21 F_2 progenies of *Brassica rapa*. The number of secondary branches plant^{-1} showed the high heritability with the high genetic advance in percent of mean.

Ejaz-Ul-Hasan *et al.* (2014) studied heritability in nine genotypes of *Brassica napus*. Heritability in broad sense ($h^2_{B.S}$) was evaluated for yield and various yield components. Seed plant^{-1} was showed the maximum heritability in broad sense ($h^2_{B.S.}$).

Halder *et al.* (2014) assessed heritability and genetic advance in eleven advanced lines of *Brassica rapa* and three popular check varieties. The high heritability (BS) was observed for days to 50% flowering and 80% maturity. The highest genetic advance was found for number of siliqua plant^{-1}. The low heritability and high genetic advance was found for yield hectare^{-1}.

Hussain *et al.* (2014) studied 24 genotypes and four check varieties of *Brassica rapa* L. to estimate heritability and genetic advance. Number of secondary branches plant^{-1} showed the high heritability with the high genetic advance in percent of mean. 50% flowering, number of siliqua and yield plant^{-1} showed the high heritability with the moderate genetic advance in percent of mean. Days to 80% maturity, number of primary branches plant^{-1}, number of seed siliqua^{-1} showed the high heritability coupled with the low genetic advance in percent of mean.

Iqbal *et al.* (2014) carried out a study to check heritability and genetic advance in ten locally collected *Brassica rapa L.* accessions. The highest heritability coupled with the higher genetic advance was noticed in plant height while rest of the traits exhibited variable trends.

Jahan *et al.* (2014) studied ten F_4 lines and eight released varieties of *Brassica rapa* to estimate heritability and genetic advance in percent of mean. The high heritability with the low genetic advance in percent of mean was found for days to maturity. The high heritability with the moderate genetic advance in percent of mean was found in plant height and days to flowering.

Mekonnen *et al.* (2014) evaluated 36 genotypes of *Brassica carinata* to study heritability. The higher heritability along with the higher genetic advance was observed in days to maturity, days to flowering, grain-fill period, number of pods plant^{-1}, secondary branches plant^{-1}, plant height, seed yield plot^{-1} and hectare while the lowest one was in primary branches plant^{-1}.

Muhammad *et al.* (2014) studied four parental genotype with 12 F_2 generation of *Brassica napus* and reported that plant height and pod length showed the high heritability and days to 50% flowering showed the moderate heritability.

Walle *et al.* (2014) estimated the heritability and genetic advance of Ethiopian mustard. The high genetic advance along with the high heritability was found in plant height, plant biomass, number of secondary branch plant^{-1}, days to 80% maturity and grain filling period.

Iqbal *et al.* (2015) studied the heritability in 49 genotypes of *Brassica rapa*. The high values of heritability was recorded for 50 % flowering, 80 % maturity, number of primary and secondary branches plant^{-1} and seed yield ha^{-1}.

Naznin *et al.* (2015) evaluated heritability and genetic advance in percent of mean for yield and its component characters in 33 *Brassica rapa* L. genotypes. The number of siliqua, number of primary and secondary branches plant^{-1} showed the high heritability couple with the high genetic advance in percent of mean.

Bibi *et al.* (2016) checked heritability and genetic advance in *Brassica juncea L*. The high heritability along with the high genetic advance was noted in plant height, siliqua length and seed yield while days to flowering and maturity, number of branches plant^{-1}, number of seeds siliqua^{-1} and 1000 seed weight exhibited variable trends.

Joya *et al.* (2016) evaluated 38 rapeseed genotypes to estimate heritability. The high heritability was found for all traits except 1000 seed weight. The minimum genetic advance was observed for 1000 seed weight which was maximum for plant height. The lowest

genetic advance in percent of mean was found in 1000 seed weight and the highest in harvest index.

Yared and Misteru (2016) studied 64 *Brassica* lines to identify the extent and nature of genetic heritability for some morphological traits. Number of secondary branches plant^{-1} and yield plot^{-1} were the major positive contributor while 1000 seed weight recorded the high heritability values in broad sense along with the high genetic advance as percent of mean.

Afrin *et al.* (2017) evaluated 30 BC_1F_6 populations of *Brassica napus* to study the heritability and genetic advance for yield and yield contributing traits. The high heritability coupled with the high genetic advances in percent mean were obtained for number of secondary branches, number of siliqua and seed yield plant^{-1}.

Salam *et al.* (2017) estimated the heritability in 30 F_1 of *Brassica campestris*. The high heritability was observed for erucic acid content followed by plant height, branches, seed yield plant^{-1}, siliqua length, days to 50% flowering and harvest index (%). Genetic advance as percent of mean was high for number of siliqua plant^{-1}, followed by seed yield plant^{-1}, days to maturity and plant height.

Sikarwar *et al.* (2017) assessed the heritability and the genetic advance in 21 genotypes of *Brassica rapa* for yield and its contributing traits. The heritability (BS) were observed for all the characters. The high heritability coupled with the high genetic advance was observed for number of primary and secondary branches, seed yield plant^{-1}, length of main raceme, number of siliqua on main raceme, number of seeds siliqua^{-1}. The high heritability with the moderate genetic advance in case of siliqua length and 1000 seed weight and the high heritability and the low genetic advance for days to flowering and plant height was estimated.

Singh *et al.* (2017) assessed the heritability and the genetic advance in six intra-specific crosses in yellow sarson. The high heritability coupled with the high genetic advance were noticed for length of fruiting zone (Ragni x YST-151) and for seed yield plant^{-1} in Jagrati × YST151, NDYS-427 × YST-151, Pusa Gold × Jagrati and Ragni × NDYS-425 crosses.

Karmokar (2018) conducted an experiment to estimate heritability and genetic advance for ten yield and related characters of thirteen advanced line of *Brassica rapa* L. The high heritability coupled with the high genetic advance in percent of mean were observed for days to 50% flowering, seeds siliqua^{-1}, secondary branches, siliqua, and yield plant^{-1}.

Rauf and Rahim (2018) evaluated 35 genotypes of *Brassica napus*. Seed yield plant^{-1} exhibitedthe highest value of heritability followed by number of siliqua plant^{-1} while plant height exhibited the lowest value of heritability.

Singh *et al.* (2018) evaluated heritability and genetic advance of 60 Indian mustard germplasms. The high heritability estimates were found for days to 50% flowering and 80% maturity, plant height, oil content, 1000-seed weight and yield plant^{-1}. The genetic advance as percent of mean was high for seed yield plant^{-1}, 1000-seed weight, secondary branches plant^{-1}, plant height and main raceme length. The high heritability coupled with high genetic advance was found for 1000 seed weight, plant height and seed yield plant^{-1}.

Ullah (2018) estimated heritability and genetic advance of eight advanced lines of *Brassica rapa* L. The high heritability were observed for days to 50% flowering and 80% maturity, plant height, number of primary and secondary branches plant^{-1}, number of siliqua plant^{-1}, length of siliqua, number of seeds siliqua^{-1}, 1000 seed weight. Seed yield plant^{-1} recorded the moderate genetic gain. The high heritability coupled with the moderate genetic advance was found in plant height and number of siliqua plant^{-1}.

Gupta *et al.* (2019) estimated heritability and genetic advance in 35 genotypes of *Brassica*. The high heritability were recorded for all the characters. Genetic advance were also high for number of siliqua plant^{-1} and plant height. Number of siliqua plant^{-1} showed the high heritability with the high genetic advance and genetic advance in percent of mean.

Rout *et al.* (2019) evaluated 38 genotypes of Indian mustard to examine the heritability and genetic advance in percent of mean. The high heritability with the high genetic advance as percent of mean were observed for number of primary and secondary branches, number of siliqua and seed yield plant^{-1}, number of seeds siliqua^{-1}, harvest index, and 1000-seed weight.

Aktar *et al*. (2019) estimated the heritability and genetic advances in percent of mean in 18 *Brassica* genotypes. All traits showed the high heritability. The high heritability with high genetic advance in percent of mean was observed for number of branches, number of pods and seed yield plant^{-1}, number of seeds pod^{-1}.

2.7 Fatty acid content

Mustard and rapeseed oil has a special fatty acid composition and the quality of oil depends on its fatty acid composition. Oleic acid, linoleic acid, linolenic acid, palmitic acid and

stearic acid are the most important and essential fatty acids in rapeseed oil. The review of literature concerning the studies are presented here:

Niraj *et al.* (2001) evaluated 21 genotypes of the Indian mustard and reported a considerable variation in fatty acid profile and the low erucic acid (40.12 to 49.7 %) in many genotypes.

Bhowmik (2003) reported Indian rapeseed and mustard oils are inferior in quality as contain the high amount of erucic acid (28.0-53.0%). They reported Linolenic acids (8.5-22.7%), linoleic (12.0-21.0%) and oleic acid (10.0-24.0%) in oil which are nutritionally good.

Sengupta *et al.* (2003) conducted an experiment on fatty acid composition in seven edible oils and reported that saturated, mono and poly-unsaturated fatty acid 6.73 and 21% respectively. They also noted that the amount of linoleic acid (18:2) ranges from 11-22%.

Siddiqui *et al.* (2004) carried out nutritional analysis on different rapeseed varieties viz. *Brassica carinata* (IGC-01 and Pusa Gaurav), *Brassica juncea* cultivars (Jagannath, Kranti, Rohini and TERI (OE) M 21-Swarna) and *Brassica napus* CV. (Hyola PAC-401) and reported that Jagannath, Kranti and Rohini had the highest amount of linolenic acid (22.76%), erucic acid (43.30%) and palmitic acid (5.63%).

Nasr *et al*. (2006) studied five important fatty acids, i.e. oleic, linoleic, linolenic, stearic and palmitic acid in ten rapeseed released and line cultivars where oleic and stearic acid had the highest and the lowest %, respectively. Oleic acid levels in different rapeseed released and line cultivars were 51% to 62%, while 18-32% linoleic acid, 2-16% linolenic acid, 0.15-2.2% stearic acid and 4-8% palmitic acid and oil percentages among rapeseed released and line cultivars and mentioned the mean variation of seed oil percentages to be 37-42 in them.

Pospišil *et al*. (2007) reported that the fatty acid profile in rapeseed hybrids and its double low cultivars were affected by released and line cultivars to a great extent. In the new varieties and advanced lines, instead of erucic acid, other fatty acids such as oleic acid (more than 60%) and linoleic acid (10-20%) increased, while linolenic acid had decreased (less than10%).

Moser *et al*. (2009) observed mustard oil contains about 20–28% oleic acid, 10–12% linoleic, 9.0–9.5% linolenic acid, and 30–40% erucic acid.

Fadl *et al.* (2011) reported the high erucic acid (37.89 and 23.90 %) in the yellow and brown mustard oils respectively. Both yellow and brown mustard seeds oils contained a little amounts of saturated fatty acids (8.45 to 8.94%) as compared to the other edible oils. Oleic

acid was the prevalent unsaturated fatty acids (19.08 to 20.24 %) followed by linoleic acid (12.37 to 21.36 %) of total fatty acid profiles in both yellow and brown mustard oils.

Chauhan and Kumar (2011) evaluated that the concentration of oleic acid (18:1), a beneficial monounsaturated fatty acid, ranges from 3.6-32.2% in rapeseed-mustard oil.

Amir *et al.* (2012) studied fatty acids in rapeseed released and line cultivars and reported oleic acid (63.62-67.38%), linoleic acid (15.87-19.06%), linolenic acid (7.55-9.76%), palmitic acid (3.55-4.51%) and stearic acid (1.54-2.3%). Moreover, the arachidic acid, the erucic acid and the palmitoleic acid were also found in the lowest percentages (Less than 1%).

Mubashir *et al.* (2012) reported mustard oil possess 60% monounsaturated fatty acids of which 42% erucic acid and 12% oleic acid while 21% polyunsaturated fatty acids of which 6% is the ω-3 alpha-Linolenic acid and 15% ω-6 linoleic acid with 12% saturated fats.

Kumar (2013) studied 24 parents and 80 F_1 crosses of Indian mustard to assess the fatty acid profile and oil content. The PCV varied from 4.6% for oil content to 50.9% for oleic acid. The GCV were high for oleic, palmitic + stearic, erucic and linolenic acid, erucic acid and palmitic + stearic acid had the least genotypic variation (GCV: 16.3 to 16.9%). The heritability in broad-sense was relatively high for oleic (61.5%) and erucic (56.3%). Erucic acid had significant and negative correlation with all of the fatty acids except linolenic acid. Although, oil content had very low direct effect (-0.011) on erucic acid but its positive association was the result of its strong positive indirect effect through oleic acid (0.435), which was partially neutralized by negative indirect effects (-0.112) through linolenic acid.

Sharafi *et al*. (2015) studied 20 accessions of *Brassica* species to estimate oil and fatty acid composition. Oil content varied from 21 (*Brassica nigra*) to 46% (*Brassica napus*). Among wild species, *Brassica rapa* and *Brassica oleracea* had the highest oil content (31 and 28%, respectively). Oleic, linoleic, linolenic, erucic, palmitic, and stearic acids accounted for 89–94% of the total fatty acids in all species. Cultivated species of *Brassica napus* had the highest oleic acid 31(61%) and the lowest erucic acid (1%). *Brassica rapa* and *Brassica oleracea* had the highest erucic acid (41and 46%, respectively). The highest content of linolenic (20%) and linoleic (19%) acid was observed for *Brassica juncea*.

Nath *et al.* (2016) reviewed that popularity of rapeseed oil being declined due to presence of erucic acid and glucosinolates. Breeders got success in developing '00'-quality rapeseed,

known as ‘Canola’. Mutagenesis of fae-1 and fae-2 of *Brassica napus* ensured such success. Thereafter, ‘canola’ regains its market as a healthy vegetable oil. The high oleic acid (86%) rapeseed lines, have been developed by using chemical mutagenesis of FAD_2 alleles responsible for desaturation of oleic acid to linoleic acid.

Ko *et al.* (2017) studied 447 accessions of *Brassica* spp. for fatty acid compositions. Among the *Brassica* sp., *Brassica rapa* sub sp. *trilocularis* had the highest oil, stearic and erucic acid. *Brassica carinata* had the highest palmitic, oleic and linoleic acid. *Brassica rapa* sub sp. *dichotoma* and *Brassica rapa* sub sp. *oleifera* had the highest linoleic and behenic acid. *Brassica rapa* sub sp. *trilocularis* had the highest erucic acid. Significant positive relationship was found between oleic and linoleic acid.

Ullah *et al.* (2017) investigated genetic variability, heritability and correlation among different biochemical traits in *Brassica rapa* L. Significant variations were observed for glucosinolate, oil and protein content, oleic, linolenic and erucic acid composition. Genotypic variances were greater than the environmental variances with the high heritability for majority of the traits.

Niemann *et al.* (2020) made a study in winter oilseed rape (*Brassica napus* L.) to estimate heterosis for oil quality of the newly developed *Brassica* interspecific hybrids, using selected parental lines. Five parental genotypes and 22 inter-specific cross derived *Brassica* lines were evaluated. Variation among genotypes was evident for most of the fatty acids studied, but the differences between genotypes were not always significant when based on individual fatty acids (FAs). However, the highest number of significant heterosis effects was observed for behenic and lignoceric acids for *Brassica* hybrid line H_1.

CHAPTER III

MATERIALS AND METHODS

The investigation was carried out in the research field of Sher-e-Bangla Agricultural University (SAU), Dhaka, in three consecutive rabi seasons of 2017 to 2020 (Nov-March) and the lab experiments were conducted at Biochemistry and Agricultural Chemistry and Environmental Science laboratory of SAU during 2020 to 2021 with seven selected *Brassica rapa* genotypes. The experiments conducted during the study periods are cited below:

Experiment 1: Characterization of selected *Brassica rapa* genotypes and their F_1s for morphological traits

Experiment 2: Heterosis and combining ability analysis in *Brassica rapa*

Experiment 3: Study on the gene actions involved for yield and related attributes in *Brassica rapa*

Experiment 4: Study on the oil content and quality characteristics of selected *Brassica rapa* genotypes

Experiment 1: Characterization of selected *Brassica rapa* genotypes and their F_1s for morphological traits

Different *Brassica rapa* genotypes were collected from BARI (Bangladesh Agriculture Research Institute), BINA (Bangladesh Institute of Nuclear Agriculture) and SAU (Sher-e-Bangla Agricultural University). Then seven materials were selected on the basis of their yield, duration, oil content and quality characteristics and grown each with three replications to study their morphological characteristics (Table 1).

1.1 Experimental site

The experiment was conducted at the research Farm, Sher-e-Bangla Agricultural University, Dhaka-1207 from November 2017 to February 2018. The experimental area was situated at 23°46'16" N latitude and 90°22'46" E longitude at an altitude of 8.8 meter above the sea level. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28. The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

Table 1. List of selected *Brassica rapa* genotypes used in the experiment to study the morphological traits

Selected *Brassica rapa* materials	Sources	Yield (t ha^{-1})	Duration (Days)	Criteria for selection
P_1 (BARI Sarisha-14)	BARI, Gazipur, Dhaka	1.4-1.6	75-80	Yield and duration
P_2 (Brown Special)	GEPB, SAU, Dhaka	1.8 -2.5	75-80	Yield and duration
P_3 (Yellow Special)	GEPB, SAU, Dhaka	1.6 -1.9	85-90	Yield
P_4 (Tori-7)	BARI, Gazipur, Dhaka	0.9-1.0	70-80	Duration
P_5 (BARI Sarisha-17)	BARI, Gazipur, Dhaka	1.7-1.8	80-85	Yield and duration
P_6 (BARI Sarisha-15)	BARI, Gazipur, Dhaka	1.4-1.7	80-85	Yield and duration
P_7 (BARI Sarisha-6)	BARI, Gazipur, Dhaka	1.9-2.2	90-100	Yield

Source: BARI Krishi Projukti Hatboi 2019 (9th Edition) Final Book and Dept. of GEPB, SAU.
Note: BARI-Bangladesh Agriculture Research Institute; GEPB, SAU- Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University.

Table 2. Fertilizers and manures with doses and application procedures

Sl. No.	Fertilizers/ manures	Doses		Application procedure
		Applied in the plot	Quantity ha^{-1}	
1.	Urea	7 kg	225 kg	50% basal and 50% at the time of flower initiation
2.	TSP	4.75 kg	235 kg	as basal
3.	MOP	2.25 kg	78 kg	as basal
4.	Gypsum	4 kg	135 kg	as basal
5.	Boric acid	320 g	11 kg	as basal
6.	ZnO	80g	3 kg	as basal
7.	Cow dung	100 kg	5 ton	as basal

1.2 Soil and climate

The soil of the experimental fields was clay loam. The land was medium high and the fertility level was medium. The site was in the subtropical climate zone. Climatic feature of this region was wet summer and dry winter. During the Rabi season, generally the rainfall is very few, the temperature is moderate and the day length is short.

1.3 Planting materials

Seven *Brassica rapa* materials were selected on the basis of their yield, duration, oil content and quality characteristics. The list of selected materials are shown in Table 1.

1.4 Experimental layout

The field experiment was designed in Randomized Complete Block Design (RCBD) with three replications. The plot size was 225 m^2 of which the evaluation plot was120 m^2 and the crossing plot was 105m^2. Row length was maintained as 3.5 m having 1.0 m irrigation channels among the rows. For evaluation plot line to line distance was 30 cm and plant to plant distance was 10 cm and for crossing plot line to line distance was 50 cm and plant to plant distance was 10 cm.

1.5 Field practices

1.5.1 Soil and field preparation

The field was prepared through several ploughing and cross ploughing followed by laddering and harrowing using power tiller to have fine tilth and optimum level of moisture condition. Weeds and stubbles were removed from the field. During final land preparation, cow dung was applied and leveled the field properly.

1.5.2 Fertilizer and manure application

Urea, triple super phosphate (TSP), Muriate of potash (MOP), gypsum, zinc oxide (ZnO) and boric acid were applied at the proper rate and proper time. Urea was applied in two installments. 1st half of urea and total TSP, MOP, gypsum, boric acid, ZnO and cowdung were applied during final land preparation as a basal dose. The remaining half of urea was applied as a top dressing at the time of flower initiation. The rate of fertilizer and manure is shown below in Table 2.

1.5.3 Seed selection and sowing time

Healthy and pure seeds were taken and sown in lines in the experimental field on 1st November, 2017. Unfilled seeds were avoided. Seeds were placed at about 1.5 cm deep furrows with watering in the soil. Clods were removed before seed sowing.

1.5.4 Intercultural operations

Different intercultural operations like weeding, thinning, irrigation, top dressing; pest management and etc. were carried out in appropriate time to ensure proper growth and development of the plants. A good drainage system was maintained to release the rain water immediately from the experimental field.

1.5.4.1 Tagging and tying

Tagging of each population of all replication was done during sowing (Plate 1). The field was bound with rope to protect the plants from leaning by using bamboo.

1.5.4.2 Weeding and thinning

Two times weeding and thinning was done according to the requirement of maintaining uninterrupted growth of the crop. The first weeding was done after 14 days of sowing. Thinning was done at the same time for maintaining 30 cm from line to line and 10 cm from plant to plant. Second weeding was done after 21 days of sowing.

1.5.4.3 Irrigation and after care

The experimental plot was lightly irrigated after sowing by watering canes to bring proper moisture condition of the soil ensuring uniform germination of seeds. Second irrigation was given (20 DAS) before the flower initiation (Plate 2). Third irrigation was given (40 DAS) when the pod appeared. Fourth irrigation was given (60 DAS) when seeds appeared in the pod (Plate 3). Good drainage system was maintained to drain out the excess water. During irrigation, special care was taken to prevent breaking the shoots of the plants.

1.5.4.4 Pesticide application

Aphid infection was found during the vegetative and siliqua development stage. Ripcord-10 EC @ 1mL/liter of water was sprayed to flea beetle and Malathion-57 EC @ 2mL/liter to control aphids. Insecticide was applied in the afternoon to protect the beneficial insect.

1.6 Crossing among selected *Brassica rapa* genotypes

The selected *Brassica rapa* genotypes (Table 1) were subjected for crossing in all possible combinations in a 7×7 full diallel fashion. For this purpose they were grown on the plot in different block each in three times at 10 days interval, i.e. 1 November 2017, 12 November 2017 and 22 November 2017 to obtain the maximum buds for emasculation and pollination.

1.6.1 Experimental layout for crossing plot

The field experiment was designed in Randomized Complete Block Design (RCBD). The total plot size was 225 m^2 of which the evaluation plot was120 m^2 and the crossing plot was

Plate 1. Experimental field view showing tag of each treatment

Plate 2. The experimental field view at flowering stage

Plate 3. The experimental field view at fruiting stage

105 m^2. Row length was maintained as 3.5 m having 1.0 m irrigation channels among the rows. For crossing plot line to line distance was 50 cm and for plant to plant distance was 10 cm. Each material sown in two to three rows. Location, duration, fertilizers and intercultural operation was same as described before.

1.6.2 Crossing modes

The parents were crossed with each other in all possible combination in a 7×7 full diallel fashion (Table 3).

1.6.3 Crossing techniques

Crossing was made by hand pollination among desirable genotypes to get the desired combinations. Bagging method was used for making hand pollination (Plate 4 and 5). Ethyl alcohol was used for hand washing during crossing. Emasculation was done in every day morning. Floral buds of each of the female parents which were ready to open were emasculated and the remaining buds were removed. Emasculated buds were covered with thin yellow paper bag. Then emasculated buds were dusted with freshly collected male pollen of desired parents (Plate 4). After pollination, pollinated buds were covered with a paper bag and were tagged properly (Plate 5). The bags were removed after seven to eight days allowing the siliqua to grow normally.

1.6.4 Collection of seeds from the crossed materials

After ripening, pods from each of the cross materials were collected carefully. Then seeds from the pods were collected, counted, maintained separately, packed and stored for evaluation in the next season.

1.6.5 Crossability study

Total number of buds crossed, number of pods attained to maturity and total number of seeds pod^{-1} $cross^{-1}$ were recorded. The crossability among the selected *Brassica rapa* genotypes were determined on the basis of the number of hybrid seeds produced by the cross among the respective parents.

1.7 Harvesting

Harvesting was started at 3rd February and continued to 18th February, 2018 depending upon maturity of the plants. Plants were harvested at 80% maturity stage. Ten plants were selected for morphological analysis from each of the populations. The sample plants were harvested by uprooting and tagging was done for analyzing morphological and quality traits.

Table 3. Crossing mode among the selected parents in all possible combination

Male / Female	P_1	P_2	P_3	P_4	P_5	P_6	P_7
P_1	-	√	√	√	√	√	√
P_2	√	-	√	√	√	√	√
P_3	√	√	-	√	√	√	√
P_4	√	√	√	-	√	√	√
P_5	√	√	√	√	-	√	√
P_6	√	√	√	√	√	-	√
P_7	√	√	√	√	√	√	-

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. (BARI-Bangladesh Agriculture Research Institute).

Plate 4. Hand pollination at flowering stage for making desirable cross

Plate 5. Bagging method used in the experiment after hand pollination

1.8 Collection of data

To study the mean performance and different genetic parameters the following ten characters were evaluated: 1. Plant height, 2. Days to 50% flowering, 3. Days to 80% maturity, 4. Number of primary branches plant^{-1}, 5. Number of secondary branches plant^{-1}, 6. Number of

siliqua plant^{-1}, 7. Length of siliqua, 8. Number of seeds siliqua^{-1}, 9. Thousand seed weight and 10. Seed yield plant^{-1}.

1.9 Data collection methods

1.9.1 Days to 50% flowering

Days to 50% flowering was counted from the date of sowing to the date of 50% flowering of each population.

1.9.2 Days to 80% maturity

Days to 80% maturity was counted from the date of sowing to the date of 80% maturity.

1.9.3 Plant height (cm)

Ten plants were selected randomly and plant height was measured from the base of the plant to the tip of the longest inflorescence with the help of meter scale in cm after final harvest. Mean height was recorded.

1.9.4 Number of primary branches plant^{-1}

The total number of branches emerged from the main stem was counted as the number of primary branches plant^{-1}.

1.9.5 Number of secondary branches plant^{-1}

The total numbers of branches originated from the primary branches of the plant were counted as the number of secondary branches plant^{-1}.

1.9.6 Number of siliqua plant^{-1}

Total number of siliqua of each plant was counted from the selected ten plants and considered as the number of siliqua plant^{-1}.

1.9.7 Length of siliqua (cm)

Five representative siliqua were selected randomly and measurement was taken in centimeter from the base to the tip of a siliqua without beak.

1.9.8 Number of seeds siliqua^{-1}

Five siliqua from the sample plants were collected randomly. Seeds obtained from each siliqua were counted and average numbers of the seeds siliqua^{-1} was recorded.

1.9.9 Thousand-seed weight (g)

Ten plants of each line were selected and thousand seed weight was recorded in grams (g).

1.9.10 Yield plant^{-1}. (g)

All the seeds produced by a representative plant were weighted in g by considering it as the seed yield plant^{-1}.

1.10 Characterization of selected *Brassica rapa* genotypes and their F_1s

Forty two F_1s obtained from the full diallel crosses among the selected *Brassica rapa* genotypes were grown with their parents each with three replications to study their morphological characteristics in comparison to their parents. Characterization was carried out on the basis of qualitative and quantitative characters of the genotypes. The characters were evaluated for screening the genotypes into different groups.

1.10.1 Planting materials

The parents and the F_1s which were used in this experiment for morphological characterization are listed below (Table 5).

1.10.2 Experimental layout

The field experiment was designed in RCBD with three replications. The plot size was 267 m^2. Row length was maintained as 3.5 m having 1.0 m irrigation channels among the rows. Row number for each parents was two and each F_1 is one for each replication. The distance between line to line was 30 cm and plant to plant was 10 cm.

1.10.3 Field practice

Soil and field preparation, fertilizer, manure and pesticide application, other intercultural operations, and harvesting were done as in the same way as above description.

1.10.4 Collection of data

Morphological characterization was carried out on the basis of qualitative and quantitative characters of the genotypes. Total twenty eight characters were evaluated of which five quantitative leaf characters, three quantitative flower and pod characters, ten quantitative yield and yield related characters and ten qualitative leaf, flower and pod characters.

The following qualitative and quantitative characters were taken into consideration for morphological characterization:

Table 4. List of the parents and F_1s used for morphological characterization

Parents	F_1s
P_1 (BARI Sarisha-14)	$P_1 \times P_2$ = BARI Sar-14 × Brown Special
P_2 (Brown Special)	$P_1 \times P_3$ = BARI Sar-14 × Yellow Special
P_3 (Yellow Special)	$P_1 \times P_4$ = BARI Sar-14 × Tori-7
P_4 (Tori-7)	$P_1 \times P_5$ = BARI Sar-14 × BARI Sar-17
P_5 (BARI Sarisha-17)	$P_1 \times P_6$ = BARI Sar-14 × BARI Sar-15
P_6 (BARI Sarisha-15)	$P_1 \times P_7$ = BARI Sar-14 × BARI Sar-6
P_7 (BARI Sarisha-6)	$P_2 \times P_1$ = Brown Special × BARI Sar-14
	$P_2 \times P_3$ = Brown Special × Yellow Special
	$P_2 \times P_4$ = Brown Special × Tori-7
	$P_2 \times P_5$ = Brown Special × BARI Sar-17
	$P_2 \times P_6$ = Brown Special × BARI Sar-15
	$P_2 \times P_7$ = Brown Special × BARI Sar-6
	$P_3 \times P_1$ = Yellow Special × BARI Sar-14
	$P_3 \times P_2$ = Yellow Special × Brown Special
	$P_3 \times P_4$ = Yellow Special × Tori-7
	$P_3 \times P_5$ = Yellow Special × BARI Sar-17
	$P_3 \times P_6$ = Yellow Special × BARI Sar-15
	$P_3 \times P_7$ = Yellow Special × BARI Sar-6
	$P_4 \times P_1$ = Tori-7 × BARI Sar-14
	$P_4 \times P_2$ = Tori-7 × Brown Special
	$P_4 \times P_3$ = Tori-7 × Yellow Special
	$P_4 \times P_5$ = Tori-7 × BARI Sar-17
	$P_4 \times P_6$ = Tori-7 × BARI Sar-15
	$P_4 \times P_7$ = Tori-7 × BARI Sar-6
	$P_5 \times P_1$ = BARI Sar-17 × BARI Sar-14
	$P_5 \times P_2$ = BARI Sar-17 × Brown Special
	$P_5 \times P_3$ = BARI Sar-17 × Yellow Special
	$P_5 \times P_4$ = BARI Sar-17 × Tori-7
	$P_5 \times P_6$ = BARI Sar-17 × BARI Sar-15
	$P_5 \times P_7$ = BARI Sar-17 × BARI Sar-6
	$P_6 \times P_1$ = BARI Sar-15 × BARI Sar-14
	$P_6 \times P_2$ = BARI Sar-15 × Brown Special
	$P_6 \times P_3$ = BARI Sar-15 × Yellow Special
	$P_6 \times P_4$ = BARI Sar-15 × Tori-7
	$P_6 \times P_5$ = BARI Sar-15 × BARI Sar-17
	$P_6 \times P_7$ = BARI Sar-15 × BARI Sar-6
	$P_7 \times P_1$ = BARI Sar-6 × BARI Sar-14
	$P_7 \times P_2$ = BARI Sar-6 × Brown Special
	$P_7 \times P_3$ = BARI Sar-6 × Yellow Special
	$P_7 \times P_4$ = BARI Sar-6 × Tori-7
	$P_7 \times P_5$ = BARI Sar-6 × BARI Sar-17
	$P_7 \times P_6$ = BARI Sar-6 × BARI Sar-15

Note: BARI-Bangladesh Agriculture Research Institute

A. Quantitative characters

i) Leaf characteristics	ii) Flower and pod characteristics	iii) Yield and yield related Characteristics
1. Leaf length	1. Petal length and width	1. Days to 50% flowering
2. Leaf width	2. Silique length and width	2. Days to 80% maturity
3. Number of leaf lobes	3. Beak length	3. Plant height
4. Petiole length		4. Number of primary branches plant^{-1}
5. Petiole width		5. Number of secondary branches plant^{-1}
		6. Number of siliqua plant^{-1}
		7. Siliqua length
		8. Number of seeds siliqua^{-1}
		9. Thousand seed weight
		10. Seed yield plant^{-1}

B. Qualitative characters

i) Leaf Characteristics		ii) Flower and Pod Characteristics
1. Leaf type	5. Leaf apex shape	1. Flower colour
2. Leaf arrangement	6. Leaf blade edges	2. Silique shape
3. Leaf angle	7. Leaf hairiness	3. Silique angle
4. Leaf blade shape		

For quantitative yield and yield related characteristics data collection methods was as same as mentioned above.

1.11 Statistical analysis

Data were recorded for analyzing mean performance for yield related characters mentioned above. The mean values of ten randomly selected plants used for recording observations were computed for each of the traits for each population in each replication and were subjected to statistical analysis. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C and OPSTAT software.

Experiment 2: Heterosis and combining ability analysis in *Brassica rapa*

This field experiment was conducted at the research field of Sher-e-Bangla Agricultural University, Dhaka-1207 from November/2018 to March/2019. Seeds of forty two F_1s obtained from the full diallel crossing were grown with their parents in the plot in different blocks each with three replications to study the general combining ability (GCA) of parents, specific combining (SCA) ability of crosses and combined heterotic effect of the F_1s for yield and contributing traits (Plate 6, 7 and 8). In addition to this backcrosses were carried out among twenty one selected F_1s with their parents to obtain BC_1 and BC_2. F_1s were selected on the basis of their cross ability. All the necessary data has been recorded for the analysis.

Experimental site, soil and climate, planting materials, experimental layout and field practice were as same as experiment-1.

2.1 Harvesting

Harvesting continued from 29 January to 13 February, 2019 depending on the maturity of the plants. Plants were harvested when 80% showed symptoms of maturity such as, straw color of siliqua, leaves, stem and desirable seed color in the mature siliqua (Plate 8). At maturity, 10 plants were selected for morphological analysis from each of the populations. The sample plants were harvested by uprooting and tagging was done specifically for analyzing morphological and quality traits.

2.2 Collection of data

To study the heterosis and the combining ability the following ten characters were taken into consideration: 1. Plant height, 2. Days to 50% flowering, 3. Days to 80% maturity, 4. Number of primary branches plant^{-1}, 5. Number of secondary branches plant^{-1}, 6. Number of siliqua plant^{-1}, 7. Length of siliqua, 8. Number of seeds siliqua^{-1}, 9. Thousand seed weight and 10. Seed yield plant^{-1}.

Data collection methods was same as experiment-1.

2.3 Statistical analysis

Data were recorded for estimating heterosis, analyzing combining ability in relation to diallel cross for ten yield related characters mentioned above.

Plate 6. Experimental field view at flower initiation stage

Plate 7. Experimental field view at fruiting stage

Plate 8. Experimental field view at maturity stage

2.3.1 Estimation of heterosis

The amount of heterosis in the F_1 was calculated using the following formula:

Heterosis over better parent % $= \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$

Here, $\overline{F_1}$= Mean of F_1 individuals

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

Heterosis over mid parent% $= \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$

Here, $\overline{F_1}$= Mean of F_1 individuals

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

CD (Critical Difference) values were used for testing significance of heterotic effects.

Critical Differences (CD) = $t \times \frac{\sqrt{2EMS}}{\sqrt{r}}$

Here,

EMS = Error Mean Sum of square,

r = Number of replication,

t = Tabulated t value at error df

CD values were compared with the values come from F_1-Better Parent (BP) and F_1-Mid Parent (MP) to test significance of respective heterotic effects.

2.3.2 Combining ability in relation to diallel cross

Giriffing (1956) proposed four methods of analysis depending on the materials involved. Grffling has also considered Eisenhart's model I (fixed effect) and model II (random effect) situation in the analysis. In the present research work combining ability analysis were done following method 1 (including reciprocals) and Model-I.

The mathematical model for the analysis was:

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

Where,

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

K = 1, 2, ..., b

L = 1, 2, ..., c

P = Number of parents

B = Number of blocks or replications

c = Number of observation in each plot

Y_i = The mean of i x jth genotype over K and I.

m = The population mean.

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

g_j = The GCA of jth parent

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

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

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 (diallel family) as follows:

Table 5. The analysis of variance for combining ability was carried out using replication mean of each entry.

ANOVA

Item	d.f.	Sum of Square	MSS	Expected MSS
GCA	p-1	S_g	M_g	$\sigma_e^2 + (P+2)\frac{1}{(P-1)}\sum g_i^2$
SCA	p(p-1)/2	S_s	M_s	$\sigma_e^2 + \frac{2}{P(P-1)}\sum_i \sum_j S_{ij}^2$
Error	(b-1)(e-1)	S_e	M_e	σ_e^2

Where,

GCA = general combining ability

SCA = specific combining ability

p = Number of parents

b = Number of blocks or replications

e = Number of entry (family)

Yi = Array total of the ith parent

Yjj = Mean value of the ith parent

Yg = Grand total of the P (P-l)/2 crosses and parental lines

Yij= Progeny mean values in the diallel table

S_e = Sum of square due to error

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

$$Ss = \sum_i \sum_j Y_{ij}^2 \frac{1}{(P+2)} \sum (Y_i + Y_{ii})^2 + \frac{2}{(P+1)(P+2)} Y_{..}^2$$

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

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

$$S_{ij} = Y_{ij} - \frac{1}{(P+2)} \sum_i \left(y_i + y_{ii} + y_j + y_{ji}\right) + \frac{2}{(p+1)(p+2)} y.$$

The variance of GCA and SCA were,

$$Var(g_i) = \frac{(P-1)}{P(P+2)} \sigma_e^2$$

$$Var(S_{ij}) = \frac{2(P-1)}{(P+1)(P+2)} \sigma_e^2 (i \neq j)$$

Standard error (SE) of an estimate was calculated the square root of the variance of concerned estimate eg. j Var (g;) and j Var (s.)

$$\sqrt{Var(g_i)} \text{ and } \sqrt{Var(S_{ij})}$$

2.4 Backcrossing

Backcrossing was performed among twenty one selected F_1s (Table 6) with their parents to obtain BC_1 and BC_2. F_1s were selected on the basis of their crossability (on the basis of number of hybrid seeds production). The selected F_1s with their parents were grown in the plot in different blocks each in three times at ten days interval, i.e. 29 October, 10 November and 21 November 2018 to obtain maximum number of buds for emasculation and pollination.

2.4.1 Crossing techniques

Crossing was made by hand pollination in desirable parents to obtain the desired combinations. Bagging method was used for making hand pollination (Plate 4 and plate 5). Emasculation was done in every day morning. Floral buds of each of the parents of the selected F_1s which were ready to open were emasculated and the remaining buds were removed. Emasculated buds were covered with thin yellow paper bags. Then emasculated buds were dusted with freshly collected male pollen of desired F_1 plants. After pollination pollinated buds were covered with a cellophane paper bag and were tagged properly. The bags were removed after seven to eight days allowing the siliqua to grow normally. The desired twenty

Table 6. Selected *Brassica rapa* genotypes and their F_1s used for backcrossing program

Sl. No.	Parents	F_1s
1.	**P_1** (BARI Sarisha-14)	**P_1 × P_2** = BARI Sar-14 × Brown Special
2.	**P_2** (Brown Special)	**P_1 × P_3** = BARI Sar-14 × Yellow Special
3.	**P_3** (Yellow Special)	**P_1 × P_5** = BARI Sar-14 × BARI Sar-17
4.	**P_4** (Tori-7)	**P_1 × P_6** = BARI Sar-14 × BARI Sar-15
5.	**P_5** (BARI Sarisha-17)	**P_1 × P_7** = BARI Sar-14 × BARI Sar-6
6.	**P_6** (BARI Sarisha-15)	**P_2 × P_3** = Brown Special × Yellow Special
7.	**P_7**(BARI Sarisha-6)	**P_2 × P_4** = Brown Special × Tori-7
8.		**P_2 × P_5** = Brown Special × BARI Sar-17
9.		**P_2 × P_7** = Brown Special × BARI Sar-6
10.		**P_3 × P_5** = Yellow Special × BARI Sar-17
11.		**P_3 × P_6** = Yellow Special × BARI Sar-15
12.		**P_3 × P_7** = Yellow Special × BARI Sar-6
13.		**P_4 × P_1** = Tori-7 × BARI Sar-14
14.		**P_4 × P_3** = Tori-7 × Yellow Special
15.		**P_4 × P_5** = Tori-7 × BARI Sar-17
16.		**P_4 × P_6** = Tori-7 × BARI Sar-15
17.		**P_4 × P_7** = Tori-7 × BARI Sar-6
18.		**P_5 × P_6** = BARI Sar-17 × BARI Sar-15
19.		**P_5 × P_7** = BARI Sar-17 × BARI Sar-6
20.		**P_6 × P_2** = BARI Sar-15 × Brown Special
21.		**P_6 × P_7** = BARI Sar-15 × BARI Sar-6

Note: BARI-Bangladesh Agriculture Research Institute

Table 7. Backcross combinations among selected *Brassica rapa* genotypes

BC_1				BC_2		
$P_1 \times P_2 \rightarrow F_1$	×			$P_4 \times P_1 \rightarrow F_1$	×	P_1
$P_1 \times P_3 \rightarrow F_1$	×			$P_1 \times P_2 \rightarrow F_1$	×	P_2
$P_1 \times P_5 \rightarrow F_1$	×	P_1		$P_6 \times P_2 \rightarrow F_1$	×	
$P_1 \times P_6 \rightarrow F_1$	×			$P_1 \times P_3 \rightarrow F_1$	×	
$P_1 \times P_7 \rightarrow F_1$	×			$P_2 \times P_3 \rightarrow F_1$	×	P_3
$P_2 \times P_3 \rightarrow F_1$	×			$P_4 \times P_3 \rightarrow F_1$	×	
$P_2 \times P_4 \rightarrow F_1$	×	P_2		$P_2 \times P_4 \rightarrow F_1$	×	P_4
$P_2 \times P_5 \rightarrow F_1$	×			$P_1 \times P_5 \rightarrow F_1$	×	
$P_2 \times P_7 \rightarrow F_1$	×			$P_2 \times P_5 \rightarrow F_1$	×	
$P_3 \times P_5 \rightarrow F_1$	×			$P_3 \times P_5 \rightarrow F_1$	×	P_5
$P_3 \times P_6 \rightarrow F_1$	×	P_3		$P_4 \times P_5 \rightarrow F_1$	×	
$P_3 \times P_7 \rightarrow F_1$	×			$P_1 \times P_6 \rightarrow F_1$	×	
$P_4 \times P_1 \rightarrow F_1$	×			$P_3 \times P_6 \rightarrow F_1$	×	
$P_4 \times P_3 \rightarrow F_1$	×	P_4		$P_4 \times P_6 \rightarrow F_1$	×	P_6
$P_4 \times P_5 \rightarrow F_1$	×			$P_5 \times P_6 \rightarrow F_1$	×	
$P_4 \times P_6 \rightarrow F_1$	×			$P_1 \times P_7 \rightarrow F_1$	×	
$P_4 \times P_7 \rightarrow F_1$	×			$P_2 \times P_7 \rightarrow F_1$	×	
$P_5 \times P_6 \rightarrow F_1$	×	P_5		$P_3 \times P_7 \rightarrow F_1$	×	
$P_5 \times P_7 \rightarrow F_1$	×			$P_4 \times P_7 \rightarrow F_1$	×	P_7
				$P_5 \times P_7 \rightarrow F_1$	×	
$P_6 \times P_2 \rightarrow F_1$	×	P_6		$P_6 \times P_7 \rightarrow F_1$	×	
$P_6 \times P_7 \rightarrow F_1$	×					

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. (BARI-Bangladesh Agriculture Research Institute)

one BC_1 and 21 BC_2 combinations were made. Total number of buds crossed, total number of pods attained to maturity and total number of seed pod^{-1} $cross^{-1}$ were recorded. Backcrosses were made following the combinations mentioned above (Table 7).

2.4.2 Seed collections

After ripening, pods within each cross were collected carefully. Then seeds from the pods were collected, counted, maintained separately, packed and stored for evaluation in the next season.

Experiment 3: Study on the gene actions involved for yield and related attributes in *Brassica rapa*

This experiment was conducted at SAU Research Farm, Sher-e-Bangla Agricultural University, Dhaka-1207 from November/2019 to March /2020. Twenty one F_1s, F_2s, BC_1s and BC_2s obtained from the previous experiment through diallel crosses and backcrosses were grown with their parents each with three replications to study their generation means, gene actions for yield and related attributes. All the data has been recorded for analysis. Experimental site, soil and climate, soil and field preparation and intercultural operations were as same as described in experiment -1.

3.1 Materials

Seeds of seven parents, twenty one F_1s and their F_2s, BC_1s and BC_2s were selected to study the gene actions for yield and related attributes. F_1s were selected on the basis of their crossability. Crossability was determined on the basis of the number of hybrid seeds produced by each cross among the respective parents. The materials used in the experiment are listed below (Table 8).

3.2 Experimental layout

The field experiment was designed in Randomized Complete Block Design (RCBD) with three replications. The plot size was 506 (23×22) m^2. Row length was maintained as two meters having 0.50 m irrigation channels among the rows. The distance between line to line was 30 cm and plant to plant was 10 cm. The number of rows for each parent was three, each F_1, BC_1 and BC_2 were two and for each F_2 was four for each replication.

3.3 Seed selection and sowing time

Healthy and pure seeds were taken and unfilled seeds were avoided. The seeds were sown in the lines in about 1.5 cm deep furrows with watering the soil in the experimental field on 15 November, 2019.

3.4 Collection of data

To study the generation means, gene interactions and genetics for yield and related attributes, following parameters were taken into considerations: 1. Plant height, 2. Days to 50% flowering, 3. Days to 80% maturity, 4. Number of primary branches $plant^{-1}$, 5. Number of secondary branches $plant^{-1}$, 6. Number of siliqua $plant^{-1}$, 7. length of siliqua, 8. Number of seeds $siliqua^{-1}$, 9. Thousand seed weight and 10. Seed yield $plant^{-1}$.

Table 8. List of parents, F_1s, F_2s, BC_1s and BC_2s used for gene interaction study

Parents	F_1s	F_2s	BC_1s	BC_2s
P_1 (BARI Sarisha-14)	$P_1 \times P_2$	$P_1 \times P_2$	$P_1 \times P_2$	$P_1 \times P_2$
P_2 (Brown Special)	$P_1 \times P_3$	$P_1 \times P_3$	$P_1 \times P_3$	$P_1 \times P_3$
P_3 (Yellow Special)	$P_1 \times P_5$	$P_1 \times P_5$	$P_1 \times P_5$	$P_1 \times P_5$
P_4 (Tori-7)	$P_1 \times P_6$	$P_1 \times P_6$	$P_1 \times P_6$	$P_1 \times P_6$
P_5 (BARI Sarisha-17)	$P_1 \times P_7$	$P_1 \times P_7$	$P_1 \times P_7$	$P_1 \times P_7$
P_6 (BARI Sarisha-15)	$P_2 \times P_3$	$P_2 \times P_3$	$P_2 \times P_3$	$P_2 \times P_3$
P_7 (BARI Sarisha-6)	$P_2 \times P_4$	$P_2 \times P_4$	$P_2 \times P_4$	$P_2 \times P_4$
	$P_2 \times P_5$	$P_2 \times P_5$	$P_2 \times P_5$	$P_2 \times P_5$
	$P_2 \times P_7$	$P_2 \times P_7$	$P_2 \times P_7$	$P_2 \times P_7$
	$P_3 \times P_5$	$P_3 \times P_5$	$P_3 \times P_5$	$P_3 \times P_5$
	$P_3 \times P_6$	$P_3 \times P_6$	$P_3 \times P_6$	$P_3 \times P_6$
	$P_3 \times P_7$	$P_3 \times P_7$	$P_3 \times P_7$	$P_3 \times P_7$
	$P_4 \times P_1$	$P_4 \times P_1$	$P_4 \times P_1$	$P_4 \times P_1$
	$P_4 \times P_3$	$P_4 \times P_3$	$P_4 \times P_3$	$P_4 \times P_3$
	$P_4 \times P_5$	$P_4 \times P_5$	$P_4 \times P_5$	$P_4 \times P_5$
	$P_4 \times P_6$	$P_4 \times P_6$	$P_4 \times P_6$	$P_4 \times P_6$
	$P_4 \times P_7$	$P_4 \times P_7$	$P_4 \times P_7$	$P_4 \times P_7$
	$P_5 \times P_6$	$P_5 \times P_6$	$P_5 \times P_6$	$P_5 \times P_6$
	$P_5 \times P_7$	$P_5 \times P_7$	$P_5 \times P_7$	$P_5 \times P_7$
	$P_6 \times P_2$	$P_6 \times P_2$	$P_6 \times P_2$	$P_6 \times P_2$
	$P_6 \times P_7$	$P_6 \times P_7$	$P_6 \times P_7$	$P_6 \times P_7$

Note: BARI-Bangladesh Agriculture Research Institute

3.5 Statistical analysis

3.5.1 Generation Mean Analysis

Data were subjected to statistical analysis and mean values has been computed for six generations for each crosses. The generation mean analysis was carried out following the methodology of Hayman (1958) using six generations and estimated the gene effects viz., M (mean), D (additive effect), H (dominant effect), I (additive × additive interaction effect), J (additive × dominance interaction effect) and L (dominance × dominance interaction effect).

3.5.2 Scaling test

Scaling tests A, B, C and D as described by Mather (1949) and Hayman and Mather (1955) has been performed to check the adequacy of simple additive-dominance model. The means of different generations were used to calculate the scales. The variances of A, B, C and D scales has been computed by utilizing the variance of different generations. The standard error of A, B, C and D was made by taking the square root of respective variances. To test the significance of the scales, 't' test was performed.

3.5.3 Joint scaling test

In some cases, Mather's scaling test becomes inadequate to explain the additive-dominance model completely. Hence, joint scaling test (Cavalii 1952) was performed which explains multiple scaling tests to test the efficiency of simple additive-dominance model or to detect epistasis for all the measured traits using $\chi 2$ test. The simple genetic model (m, d and h) was applied when epistasis was absent. Whereas, six parameters genetic model according to Hayman (1958) was proceeded in presence of non-allelic interaction.

3.5.4 Estimation of gene effects

Where $\chi 2$ and/or scaling tests, i.e. the simple additive-dominance model is inadequate, six parameter model or digenic interaction model by Hayman (1958) approach was used to provide information on the inheritance of various characters to estimate main gene effects. These parametes represent mean effect (M), genetic effects including additive (D) and dominance (H), and gene interaction effects comprising additive × additive (I), additive × dominance (J) and dominance × dominance (L). The square roots of respective variances were used for the computation of standard error which were used to calculate the 't' values for testing significance of the corresponding gene effects.

3.5.5 Estimation of variance components

The components of variation in six generations were determined according to Mather and Jinks 1982 as follows:

Environmental variance, $Ew = (vP_1 + vP_2 + 2vF_1)/4$

Additive genetic variance, $D = 4vF_2 – 2(vBC_1 + vBC_2)$

Dominance variance, $H = 4(vBC_1 + vBC_2 – vF_2 – vEw)$

Genotypic variance, V_G = Additive variance + Dominance variance + Epistatic variance

Phenotypic variance, V_P = Genotypic variance, V_G / Heritability in broad sense

Degree of dominance h/d was calculated according to (Mather,1949).

3.5.6 Heritability and Genetic advance

Heritability in broad sense (Hb) and in narrow sense (Hn) were calculated as follows:

Heritability in broad sense, $Hb = [vF_2 - (vP_1 + vP_2 + vF_1) / 3] / vF_2$

Heritability in narrow sense, $Hn = [2vF_2 - (vBC_1 + vBC_2)] / vF_2$

Genetic advance, $Ga = i \times Hb \times \sqrt{vF_2}$ (Johnson *et al*. 1955)

where, Ga estimated with 5% selection intensity of I = 2.063 for all traits and v = variance

3.5.7 Heterosis and Inbreeding depressions

The amount of heterosis in the F_1 was calculated using the following formula:

Heterosis over better parent % $= \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$

Here, $\overline{F_1}$= Mean of F_1 individuals

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

Heterosis over mid parent% $= \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$

Here, $\overline{F_1}$= Mean of F_1 individuals

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

CD (Critical Difference) values were used for testing significance of heterotic effects.

Critical Differences (CD) $= t \times \frac{\sqrt{2EMS}}{\sqrt{r}}$

Here, EMS = Error Mean Sum of square, r = Number of replication, t = Tabulated t value at error df

CD values were compared with the values come from F_1-Better Parent (BP) and F_1-Mid Parent (MP) to test the significance of respective heterotic effects.

Inbreeding depression (ID) % = (Mean of F_1 individuals - Mean of F_2 individuals) / (Mean of F_1 individual) × 100

Experiment 4: Study on the oil content and quality characteristics of selected *Brassica rapa* genotypes

This experiment was conducted at the Biochemistry and Agricultural Chemistry and Environmental Science Laboratory of Sher-e-Bangla Agricultural University, Dhaka-1207. Rapeseed-mustard oil quality is determined by the constituent of fatty acids composition which is highly influenced by the variety type (Nasr *et al.* 2006 and Javidfar *et al.* 2007). Therefore, seven parents, six F_1s, five F_2s, five BC_1s and five BC_2s **depending on their yield performance and duration studied in the previous experiment** were selected to study their oil content and quality. All the necessary data has been recorded for statistical analysis. The materials and methods related to this experiment are presented here.

4.1 Materials

Seeds seven parents, six F_1s, five F_2s, five BC_1s and five BC_2s which were selected for studying the oil content and quality are listed below (Table 9). These samples were cleaned, sun-dried and stored into plastic container in a cool place until chemical analysis was done.

4.2 Methods

4.2.1. Extraction and Estimation of oils

4.2.1.1. Reagents & Equipments

1. Petrolium ether (60 to 90˚C)
2. Soxhlet, flask and condenser
3. Hot water bath

4.2.1.2. Procedure

Dried mustard grinded sample was weighed out into an extraction thimble. Weight of thimble and sample were recorded in laboratory book. The thimble was placed into the soxhlet and 150-200 ml petrolium ether was added to the soxhtet flask, then it was connected to holder and condenser. Soxhlet flask was placed on a round bottle flask on hot water bath and distilled at 80˚C temperature for eight hours (Plate 9). After extraction it was turned off and allowed to cool. When distillation was ceased, the extraction thimble was removed and allowed to air dry for 30-40 minutes the thimble was weighed out. Then the oil content was determined by the procedure described by Hughes (1965).

% Crude fats/Oil (on a dry weight basis) = Weight of thimble & sample before extraction - Weight of thimble & sample after extraction / Weight of sample before extraction × 100

Table 9. List of *Brassica rapa* materials used for studying the oil content and quality characteristics

Parents	F_1s	F_2s	BC_1s	BC_2s
P_1 (BARI Sarisha-14)	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_2$	$P_2 \times P_4$
P_2 (Brown Special)	$P_2 \times P_3$	$P_2 \times P_4$	$P_1 \times P_3$	$P_2 \times P_5$
P_3 (Yellow Special)	$P_2 \times P_5$	$P_3 \times P_6$	$P_3 \times P_6$	$P_3 \times P_2$
P_4 (Tori-7)	$P_2 \times P_7$	$P_4 \times P_3$	$P_4 \times P_1$	$P_3 \times P_7$
P_5 (BARI Sarisha-17)	$P_4 \times P_3$	$P_6 \times P_2$	$P_4 \times P_3$	$P_4 \times P_1$
P_6 (BARI Sarisha-15)	$P_6 \times P_2$			
P_7 (BARI Sarisha-6)				

Note: BARI-Bangladesh Agriculture Research Institute

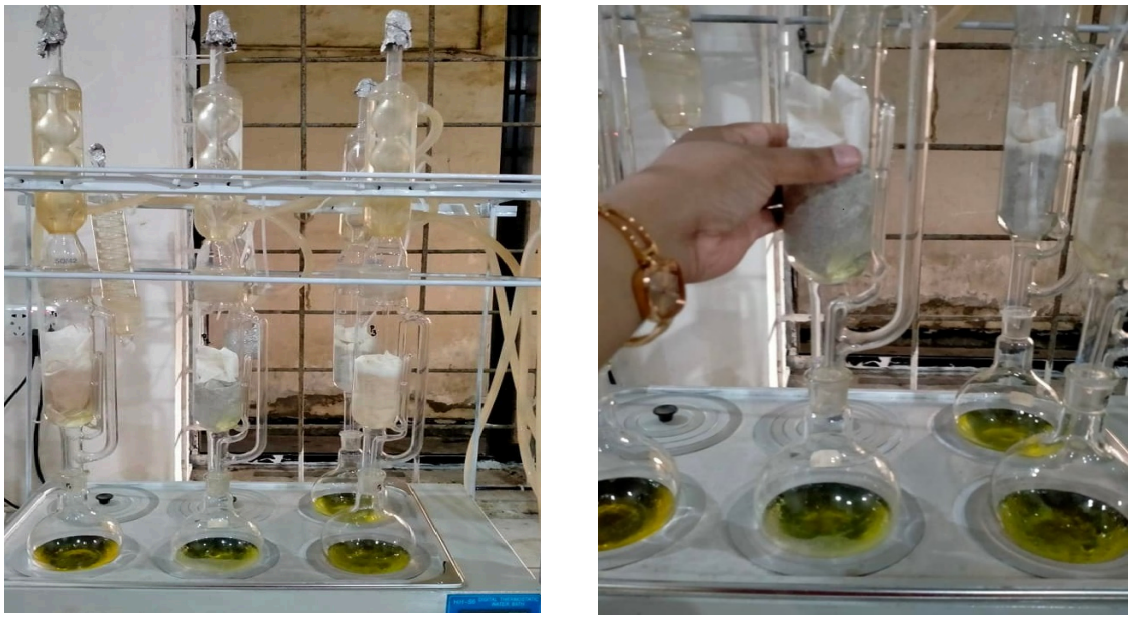


Plate 9. Oil extraction using the Soxhlet method

4.2.2. Estimation of fatty acid composition by gas chromatography

4.2.2.1. Preparation of oil samples

After the extraction procedure, the solvents were evaporated under vacuum, and the samples were subsequently stored at 4 °C.

4.2.2.2. Methylation of oil sample for FAME (Fatty Acid Methyl Ester) synthesis

Two-step methylation procedure was followed. Oils obtained after the extraction of samples were converted to the corresponding FAMEs according to O'Fallon *et al.* (2007). In this procedure, 40 µL of extracted oil was placed into 10 mL centrifuge tubes to which 0.7 mL of potassium hydroxide (10 M) solution and 5.3 mL of methanol were added. The reaction was performed at 55 °C for 1.5 h with mixing for 5 s every 20 min. After cooling to room temperature, 0.58 mL of sulfuric acid (10 M) solution was added and the reaction was continued at 55 °C for 1.5 h with mixing for 5 s every 20 min. After cooling to room temperature, 3 mL of n-hexane was added and mixed for 5 min. Subsequently, the tubes were centrifuged for 5 min and the extracts were removed for GC analysis.

4.2.2.3. Analysis of FAME products by GC (Gas Chromatography)

The fatty acid composition of the FAMEs from oil was determined using an Agilent 6820 gas chromatograph equipped with a Supelco capillary column (hp-innowax, Agilent, 100 m×0.25 mm, i.d. 0.20 µm), a flame ionization detector and split injection port. The initial oven temperature was 200 °C, which was held for one min, subsequently increased to 230 °C at 1.5 °C min^{-1} and then held for one min. The injector was set at 250 °C, and the detector at 280 °C. Nitrogen was used as the carrier gas at a flow rate of 1 ml/min. The split ratio was 50:1, and the sample size was 1 µl.

4.3 Statistical analysis

Data were recorded for palmitic acid (C16:0), stearic acid (C18:0), arachidic acid (C20:0), lignoceric acid (C24:0), palmitoleic acid (C16:1), oleic acid (C18:1,c9), octadecenoic acid (C18:1,t9), linoleic acid (C18:2), linolenic acid (C18:3),eicosenoic acid (C20:1), arachidonic acid (C20:4) and erucic acid (C22:1) content in %. The mean values were estimated using MSTAT-C software.

CHAPTER IV

RESULTS AND DISCUSSION

Four separate experiments were conducted to achieve the objectives of the study. The objectives of the study was to select short duration, high yielding and low erucic acid containing genotypes of *Brassica rapa*. The results of the research works are presented experiment wise with relevant sub heads as follows:

Experiment 1: Characterization of selected *Brassica rapa* genotypes and their F_1s for morphological traits

1.1 Morphological characterization of selected *Brassica rapa* genotypes

Morphologically seven *Brassica rapa* genotypes were characterized on the basis of their qualitative and quantitative characters.

1.1.1 Qualitative leaf characteristics

1.1.1.1 Leaf types and arrangements

For all the genotypes the leaf type was simple (i.e., not separated into leaflets) and the leaf arrangement was of alternate type (i.e., one leaf node^{-1} along the stem).

1.1.1.2 Leaf angles

Brown Special, Yellow Special, Tori -7 and BARI Sar-6 had an open type leaf angle (~ 65 º) while BARI Sar-14 and BARI Sar-15 had semi prostrate (~ 45 º) type leaf angle only BARI Sar-17 had prostrate (< 30 º) type leaf angle (Table 10). The above results were supported by Hilty (2019) and Native Plant Trust (2021) where they found that different varieties of *Brassica rapa* had the simple and alternate type leaves having prostrate (< 30 º) to open (~ 70 º) type leaf angle.

1.1.1.3 Leaf blade shapes and edges

Two types of leaf blade shape were observed viz. lyrated and runcinated. Tori -7 and BARI Sar-15 had lyrated type leaf blade shape and the remaining genotypes had runcinated type of leaf blade shape. The middle and upper leaves were lanceolate-oblong in shape. Leaf blade edge was lobed for all the genotypes but it was crenated for BARI Sar-14, Yellow Special, Tori-7 and BARI Sar-6, semi crenated for Brown Special and serrated for BARI Sar-17 and BARI Sar-15. The middle and upper leaves had margins that were smooth or bluntly dentate (Plate 10).

Table 10: Characterization of *Brassica rapa* genotypes based on qualitative leaf characteristics

Selected genotypes	Leaf types	Leaf arrangement	Leaf angle	Leaf blade shape	Leaf apex shape	Leaf blade edges	Leaf hairiness
P_1	Simple	Alternate	Semi prostrate (~ 45 º)	Runcinate	Acute	Lobed and crenated	Very sparse
P_2	Simple	Alternate	Open (~ 65 º)	Runcinate	Semi acute	Lobed and slightly crenated	Sparse
P_3	Simple	Alternate	Open (~ 65 º)	Runcinate	Semi acute	Lobed and crenated	Very sparse
P_4	Simple	Alternate	Open (~ 65 º)	Lyrate	Round	Lobed and crenated	Sparse
P_5	Simple	Alternate	Prostrate (< 30 º)	Runcinate	Acute	Lobed and serrated	Sparse
P_6	Simple	Alternate	Semi prostrate (~ 45 º)	Lyrate	Round	Lobed and serrated	Sparse
P_7	Simple	Alternate	Open (~ 65 º)	Runcinate	Acute	Lobed and crenated	Very sparse

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6.

BARI Sarisha-14

Brown Special

Yellow Special

Tori-7

BARI Sarisha-17

BARI Sarisha-15

BARI Sarisha-6

Plate 10: Middle leaves of *Brassica rapa* genotypes at 50% flowering stage

1.1.1.4 Leaf apex shapes

BARI Sar-14, BARI Sar-17 and BARI Sar-6 had acute type leaf apex shape while it was found to be semi acute for Brown Special and Yellow Special butTori-7 and BARI Sar-15 had rounded type leaf apex shape (Plate 10).

1.1.1.5 Leaf hairiness

In Brown Special, Tori -7, BARI Sar-17 and BARI Sar-15 leaf hairs were sparsely distributed while in BARI Sar-14, Yellow Special and BARI Sar-6 leaf hairiness was very sparse (Table 10).

The findings of this study were more or less similar with the findings of DiTomaso and Healy (2007), eFloras (2008), Gulden *et al.* 2008 and Warwick (2010) who found that the basal leaves were lyrate, setose, with toothed to pinnatifid margins. Stem leaves were lanceolate, glaucous, simply toothed, sessile and clasping with stem.

1.1.2 Quantitative leaf characteristics

Significant variation was found in all quantitative leaf characteristics among different selected genotypes.

1.1.2.1 Leaf length and width

The basal leaves were long. The leaf length ranged from 9.07 cm to 21.08 cm and the leaf width ranged from 4.57 cm to 9.65 cm in contrast, the middle to upper leaves were smaller in size. The highest leaf length and width were measured in BARI Sar-6 (21.08 cm and 9.65 cm respectively) followed by Brown Special (18.41 cm and 7.87 cm respectively) and Tori-7 (17.78 cm and 7.08 cm respectively) while the lowest leaf length and width were measured in BARI Sar-14 (9.07 cm and 4.57 cm respectively) preceded by BARI Sar-17 (11.30 cm and 5.10 cm respectively) (Table 11). The results matched with the findings of DiTomaso and Healy (2007), eFloras (2008), Gulden *et al.* 2008 and Warwick (2010) who found that the basal leaves were 10 to 40 cm long and 3 to 10 cm in width. According to Minnesota Wild Flowers (2021) the length and width of basal leaves were up to 40 cm and 12 cm respectively. In case of leaf width the result was slightly different from the findings of iNaturalist org. (2021) where they found that the basal leaf length and width of different *Brassica rapa* varieties were up to 25.40 cm and 5.08 cm respectively. Young-Mathews (2012) observed that basal leaf length of *Brassica rapa* varieties was up to 30.48 cm.

Table 11: Characterization of *Brassica rapa* genotypes based on quantitative leaf characteristics

Selected genotypes	Basal leaf length (cm)	Basal leaf width (cm)	Number of leaf lobes	Petiole length (Basal leaf) (cm)	Petiole width (Basal leaf) (cm)
BARI Sarisha-14	9.07 g	4.57 f	9.13 a	3.70 e	0.59 f
Brown Special	18.41 b	7.87 b	8.66 ab	6.40 b	0.95 b
Yellow Special	14.73 e	6.35 d	6.53 b	4.50 d	0.71 d
Tori-7	17.78 c	7.08 c	6.06 b	5.25 c	0.80 c
BARI Sarisha-17	11.30 f	5.10 e	7.88 b	3.80 e	0.53 g
BARI Sarisha-15	15.89 d	6.60 cd	6.66 b	4.55 d	0.65 e
BARI Sarisha-6	21.08 a	9.65 a	8.33 ab	7.60 a	1.10 a
Minimum	9.07	4.57	6.06	3.70	0.53
Maximum	21.08	9.65	9.00	7.60	1.10
Mean	15.46	6.74	7.28	5.11	0.76
CV%	2.14	4.37	17.17	3.59	3.86
LSD	0.59	0.52	1.63	0.32	0.05

1.1.2.2 Petiole length and width

Both the basal and lower leaves had stout petioles. The petiole length and width of basal leaves ranged from 3.70 cm to 7.60 cm and 0.53 cm to 1.10 cm respectively and was significantly differed from each other. The highest basal leaf petiole length and width was measured in BARI Sar-6 (7.60 cm and 1.10 cm respectively) followed by Brown Special (6.40 cm and 0.95 cm respectively) and Tori-7 (5.25 cm and 0.80 cm respectively) while the lowest basal leaf petiole length was measured in BARI Sar-14 (3.70 cm) and the lowest petiole width was measured in BARI Sar-17 (0.53 cm) (Table 11). The middle and upper leaves had bases that usually clasped their stems, although some of them were sessile. The result was supported by Warwick, (2010) and Young-Mathews (2012) who stated that lower leaves were long with long petiole and upper leaves were smaller, non-lobed, and had a pointed tip and widened, clasping base. According to Minnesota Wild Flowers (2021) and iNaturalist org. (2021) basal leaves had stout petioles while the middle to upper leaves had bases that usually clasped their stems and were usually sessile. Native Plant Trust (2021) reported that lower leaves had long petiole which was 1.00 to 17.00 cm long and 0.50 to 2.00 cm in width and the present result was within that findings.

1.1.2.3 Number of leaf lobes

The edge of the leaf blade had lobes or teeth or it had both teeth and lobes. The number of leaf lobes ranged from six to nine. The highest number of leaf lobes was found in BARI Sar-14 (nine) followed by Brown Special, BARI Sar-17 and BARI Sar-6 each of the genotypes had eight leaf lobes and the lowest number of leaf lobes (six) was found in Yellow special, Tori-7 and BARI Sar-15 (Table 11). The result was more or less similar with the findings of PROTA (2018) where it was reported that *Brassica rapa* varieties had one to five pairs of small lateral lobes and large terminal lobes. Warwick (2010) and Young-Mathews (2012) found that *Brassica rapa* varieties had one to four pairs of lateral lobes towards the base and the terminal lobes were larger than the lateral lobes. The result was also supported by DiTomaso and Healy (2007) and eFloras (2008).

1.1.3 Qualitative flower characteristics

1.1.3.1 Flowers colour

The flowers were yellow in colour for all genotypes except BARI Sar-15 having whitish yellow flowers and the flowers were radially symmetrical for all varieties (Plate 11).

BARI Sarisha-14

Brown Special

Yellow Special

Tori-7

BARI Sarisha-17

BARI Sarisha-15

BARI Sarisha-6

Plate 11: Flowers of *Brassica rapa* genotypes used as parents

1.1.4 Quantitative flower characteristics

1.1.4.1 Flower length

There were four petals, sepals, or tepals in the flowers, both the petals and sepals were separate and not fused (Plate 11). Stamen number was six. Significant variations were found in flower length, petal length and width. The flower length ranged from 0.70 cm to 1.10 cm. The highest flower length was measured in Tori-7 (1.10 cm) followed by BARI Sar-6 and Brown Special (0.98 cm and 0.92 cm respectively) while the lowest flower length was measured in BARI Sar-14 (0.70 cm) (Table 12). The result was more or less similar with the findings of Hilty (2019) who reported that the length of the flowers of *Brassica rapa* ranged from 0.85 cm to 1.27 cm. Young-Mathews (2012) and Minnesota Wild Flowers (2021) found that the flowers of *Brassica rapa* was usually 0.64 to 1.27 cm.

1.1.4.2 Petal length and width

Petal length and width ranged from 0.58 cm to 0.94 cm and 0.28 cm to 0.45 cm respectively. The highest petal length was measured in Tori-7 (0.94 cm) followed by BARI Sar-6 and Brown Special (0.86 cm and 0.80 cm respectively) while the lowest petal length was measured in BARI Sar-14 (0.58 cm). The highest petal width was measured in BARI Sar-6 (0.45 cm) followed by Tori-7 (0.42 cm) while the lowest was in BARI Sar-14 (0.28 cm) (Table 12). According to DiTomaso and Healy (2007), eFloras (2008), Gulden *et al*. (2008), Warwick (2010) and Native Plant Trust (2021) the length and width of the flowers petal of *Brassica rapa* ranged from 0.60 cm to 1.0 cm and 0.30 cm to 0.60 cm respectively. Vélez-Gavilán (2018) and Vibrans (2018) reported petal length of *Brassica rapa* ranged from 0.70 cm to 1.10 cm which supported the present findings.

1.1.5 Qualitative pod characteristics

1.1.5.1 Pod shape

The pods were elongated cylindrical, round slender and flattened in shape. All capsule splits open at the base to release the seeds at maturity. Each part of the pod had a single prominent lengthwise vein that distinguishes it from other *Brassica* species (Plate 12)

1.1.5.2 Pod angle

On the basis of siliqua or pod angle, *Brassica rapa* genotypes were grouped into three categories, viz. long, erect and semi-erect type. Brown Special and Tori-7 had long angle while BARI Sar-6 and BARI Sar-15 had semi erect pod angle. The rest of the genotypes

Table 12: Characterization of *Brassica rapa* genotypes based on qualitative and quantitative flower and pod characteristics

Selected genotypes	Qualitative characteristics			Quantitative characteristics					
	Flower colour	Siliqua shape	Siliqua angle	Flower length (cm)	Petal length (cm)	Petal width (cm)	Siliqua length (cm)	Siliqua width (cm)	Beak length (cm)
P_1	Yellow	Cylindrical	Erect	0.70 g	0.58 g	0.28 f	2.80 e	0.96 b	1.20 c
P_2	Yellow	Rounded	Long	0.92 c	0.80 c	0.40 c	5.08 a	0.56 d	1.31 bc
P_3	Yellow	Flattened	Erect	0.86 e	0.75 e	0.37 d	3.66 cd	0.78 c	1.45 b
P_4	Yellow	Round and slender	Long	1.10 a	0.94 a	0.42 b	3.98 c	0.40 e	1.16 c
P_5	Yellow	Cylindrical	Erect	0.78 f	0.65 f	0.33 e	3.00 e	1.10 a	1.35 bc
P_6	Whitish yellow	Flattened	Semi-erect	0.90 d	0.78 d	0.40 c	3.41 d	0.63 d	0.93 d
P_7	Yellow	Flattened	Semi-erect	0.98 b	0.86 b	0.45 a	4.46 b	0.75 c	1.68 a
Minimum	-	-	-	0.70	0.58	0.28	2.80	0.40	0.93
Maximum	-	-	-	1.40	0.94	0.45	5.08	1.10	1.68
Mean	-	-	-	0.93	0.76	0.38	3.84	0.74	1.33
CV%	-	-	-	0.78	0.64	1.00	5.31	6.50	8.48
LSD	-	-	-	0.05	0.06	0.07	0.36	0.08	0.20

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6.

BARI Sarisha-14

Brown Special

Yellow Special

Tori-7

BARI Sarisha-17

BARI Sarisha-15

BARI Sarisha-6

Plate 12: Siliqua or pods of *Brassica rapa* genotypes

had erect type pod angle (Plate 12). Turner and Gustafson (2006), DiTomaso and Healy (2007), eFloras (2008), Warwick (2010), Jepson Flora Project (2012), Young-Mathews (2012) and Hilty (2019) reported erect and semi-erect type siliqua/pod in different *Brassica rapa* varieties.

1.1.6 Quantitative siliqua or pod characteristics

1.1.6.1 Siliqua or pod length and width

The siliqua length and width varied significantly from each other among the studied genotypes. The siliqua length and width ranged from 2.80 cm to 5.08 cm and 0.40 cm to 1.10 cm respectively. The highest siliqua length was measured in Brown Special (5.08 cm) followed by BARI Sar-6 (4.46 cm) and the lowest siliqua length was measured in BARI Sar-14 (2.80 cm) preceded by BARI Sar-17 (3.00 cm) while the highest siliqua width was measured in BARI Sar-17 (1.10 cm) followed by BARI Sar-14 (0.96 cm) and it was lowest in Tori-7 (0.40 cm) (Table 12).

1.1.6.1 Beak length

The beak length of the siliqua or pods also varied significantly from each other among the selected genotypes. The highest beak length was measured in BARI Sar-6 (1.90 cm) and the lowest was in BARI Sar-15 (0.93 cm) (Table 12).

The result of the present study was supported by Hilty (2019) who stated that each flower was replaced by an ascending cylindrical pod (siliqua) that was 3.18 cm to 5.72 cm long at maturity. Each seedpod terminated in a seedless beak that was about 0.80 cm to 1.43 cm in length. The result was also remained within the findings of Native Plant Trust (2021) where they reported that the fruit was roughly cylindrical and was 2.00 cm to 11.00 cm long and 0.20 cm to 1.10 cm wide at maturity having beak that was about 0.80 cm to 1.5 cm in length. Turner and Gustafson (2006), Warwick (2010), Jepson Flora Project (2012) and Young-Mathews (2012) reported that the fruit was elongated, two-parted capsule that splits open at the base to release the seeds at maturity and the silique was 1.90 cm to 10.16 cm long and 0.15 cm to 1.15 cm wide with a narrow beak at the tip. The present result was also matched with the findings of DiTomaso and Healy (2007) and, eFloras (2008) where they estimated that the pods were 3.00 cm to 8.00 cm long and gradually narrow to form beaks that were 1.0 to 1.5 cm long. According to Minnesota Wild Flowers (2021) pods of *Brassica rapa* varieties are slender, round, 2.54 cm to 5.08 cm long and the tip end had a beak 0.85 cm to 1.27 cm long that looked like part of the pod which was more or less similar with the present

findings. The result also matched with the findings of PROTA (2018) where they reported that siliqua of *Brassica rapa* varieties were linear, 4.00 cm to 10.00 cm long and 0.20 cm to 0.40 cm in width with a tapering beak 0.50 cm to 2.00 cm long.

1.2 Morphological characterization of F_1s

Morphologically forty two F_1s obtained from 7×7 full diallel crosses among seven *Brassica rapa* materials were characterized on the basis of their qualitative and quantitative characters. The results of characterization and frequency distribution of each descriptor of the genotypes (F_1s) were presented in table 13.

1.2.1 Qualitative characters

1.2.1.1 Leaf characteristics

1.2.1.1.1 Leaf types and arrangements

For all the F_1s the leaf type was simple (i.e., not separated into leaflets) and the leaf arrangement was of alternate type (i.e., one leaf node^{-1} along the stem).

1.2.1.1.2 Leaf angle

In case of leaf angle, among the F_1s about 76.19 % genotypes had the open (~ 65 º) type leaf angle, 14.29% genotypes had the semi-prostrate (~ 45 º) leaf angle and 9.52% genotypes had the prostrate (< 30 º) leaf angle (Table 13). The results of the present study was supported by Hilty (2019) and Native Plant Trust (2021) where they found that different varieties of *Brassica rapa* had the simple and alternate leaves having prostrate (< 30 º) to open (~ 70 º) type leaf angle.

1.2.1.1.3 Leaf blade shape

According to leaf blade shape F_1s had been grouped into two categories, viz. lyrated and runcinated. Out of the forty two F_1s about 23.81 % genotypes had the lyrated type leaves and 76.19% genotypes had the runcinated type leaves (Table 13). These findings were more or less similar with the findings of DiTomaso and Healy (2007), eFloras (2008), Gulden *et al.* (2008) and Warwick (2010) who found basal leaves were lyrated, runcinated, elliptic or obovate while stem leaves were lanceolate in different *Brassica rapa* varieties.

1.2.1.1.4 Leaf apex shape

On the basis of leaf apex shape F_1s had been grouped into three categories, viz. acute, semi-acute and rounded. Among the hybrids about 52.38 % genotypes had the acute type leaf apex, 23.81 % genotypes had the semi-acute type leaf apex and remaining 23.81% genotypes had the rounded type leaf apex (Table 13). Warwick (2010) and Young-Mathews

Table 13. Characterization and frequency distribution of forty two F_1s for different qualitative and quantitative characters.

SL. No.	Plant descriptors	State of expression	Number of F_1s belonging to each class	Frequency (%)
1.	Leaf length	Long	7	16.66
		Intermediate	31	73.81
		Short	4	9.52
2.	Leaf width	Large	5	11.90
		Intermediate	34	80.95
		Narrow	3	7.14
3.	Leaf angle	Open	32	76.19
		Semi-prostrate	6	14.29
		Prostrate	4	9.52
4.	Leaf blade shape	Lyrate	10	23.81
		Runcinate	32	76.19
5.	Leaf apex shape	Acute	22	52.38
		Semi acute	10	23.81
		Rounded	10	23.81
6.	Leaf blade edges	Lobed and crenated	30	71.43
		Lobed and Serrated	12	28.57
7.	Leaf hairiness	Very sparse	14	33.33
		Sparse	26	61.90
		Absent	2	4.76
8.	Number of leaf lobes	High	6	14.29
		Medium	30	71.43
		Low	6	14.29
9.	Petiole length	Long	6	14.29
		Intermediate	34	80.95
		Short	2	4.76
10.	Petiole width	Broad	12	28.57
		Intermediate	30	71.43

Table 13 (Cont'd).

11.	Flower colour	Yellow	42	100.00
12.	Petal length	Long	6	14.29
		Medium	34	80.95
		Short	2	4.76
13.	Petal width	Broad	6	14.29
		Medium	34	80.95
		Narrow	2	4.76
14.	Siliqua shape	Cylindrical	2	4.76
		Rounded	11	21.43
		Thin and Rounded	7	16.66
		Flattened	16	42.86
		Thin and Flattened	6	14.29
15.	Siliqua length	Long	25	59.52
		Intermediate	15	35.71
		Short	2	4.76
16.	Siliqua width	Broader	2	4.76
		Medium	27	64.29
		Narrow	13	30.95
17.	Siliqua angle	Long	16	38.10
		Erect	10	23.81
		Semi-erect	16	38.10
18.	Beak length	Long	6	14.29
		Intermediate	32	76.19
		Short	4	9.52

(2012) reported that leaves of *Brassica rapa* varieties had acute, semi-acute, intermediate and rounded apex. Yadav (2013) also reported acute, intermediate and rounded leaf apex in Indian mustard.

1.2.1.1.5 Leaf blade edges

Leaf blade edges were lobed for all varieties but it was crenated or serrated. Out of the forty two F_1s about 71.43 % genotypes had the lobed and crenated type leaf blade edges and 28.57 % genotypes had the lobed and serrated type leaf blade edges (Table 13). These findings were more or less similar with the findings of DiTomaso and Healy (2007), eFloras (2008), Gulden *et al.* (2008) and Warwick (2010) who found that basal leaves had toothed to pinnatifid edges and stem leaves were simply toothed and clasping with stem.

1.2.1.1.6 Leaf hairiness

In case of leaf hairiness F_1s had been grouped into three categories, viz. very sparse, sparse and absent. Among the F_1s leaf hair was very sparse in 33.33 % genotypes, sparse in 61.90 % genotypes and in remaining 4.76 % genotypes leaf hair was absent (Table 13). This findings were more or less similar with the findings of Gulden *et al.* (2008) and Warwick (2010) who found that leaves were simply hairy in most of the *Brassica rapa* varieties.

1.2.1.2 Flower and pods or siliqua characteristics

1.2.1.2.1 Flowers colour

Usually two flower colours are found in most of the *Brassica rapa* varieties. However, in this study all the F_1s produced bright yellow coloured flower although one of the selected parent (BARI Sar-15) had whitish yellow colored flowers. Young-Mathews (2012), Hilty (2019) and Minnesota Wild Flowers (2021) found that flowers of *Brassica rapa* was usually bright yellow while few varieties have whitish flowers. DiTomaso and Healy (2007), eFloras (2008), Gulden *et al*. (2008), Warwick (2010), Vélez-Gavilán (2018), Vibrans (2018) and Native Plant Trust (2021) also reported that flowers of *Brassica rapa* were usually bright yellow in colours.

1.2.1.2.2 Pods or siliqua shape

F_1s had been grouped into five categories according to their siliqua shape viz. round, cylindrical, thin and rounded, flattened, thin and flattened. Among the F_1s about 4.76 % were cylindrical, 26.19% were rounded, 16.66% were thin and rounded, 38.10 % were flattened while 14.29 % genotypes were thin and flattened (Table 13). Hilty (2019) and

Native Plant Trust (2021) stated that *Brassica rapa* had cylindrical seed pod. Jepson Flora Project (2012) and Young-Mathews (2012) reported that the fruit of *Brassica rapa* were elongated, two-parted capsule. The result also matched with DiTomaso and Healy (2007) and eFloras (2008) where they found that the pods of *Brassica rapa* were usually cylindrical or flattened. According to Minnesota Wild Flowers (2021) that pods of *Brassica rapa* varieties were slender or round. PROTA (2018) also reported that siliqua of *Brassica rapa* varieties were linear.

1.2.1.2.3 Siliqua angle

On the basis of siliqua angle, F_1s had been grouped into three categories, viz. long, erect and semi-erect. Out of forty two hybrids about 38.10 % genotypes had long siliqua angle, 23.81 % genotypes had erect siliqua and 38.10 % genotypes had semi-erect siliqua (Table 13). DiTomaso and Healy (2007), Warwick (2010), Young-Mathews (2012) and Hilty (2019) reported erect and semi-erect type siliqua in different *Brassica rapa* varieties.

1.2.2 Quantitative characters

1.2.2.1 Leaf characteristics

1.2.2.1.1 Leaf length

On the basis of leaf length, F_1s had been grouped into three categories, viz. long (> 20 cm), intermediate (< 20 cm) and short (< 10 cm). Among the F_1s about 16.66 % genotypes had the long leaves, 73.81% genotypes had the intermediate leaf length and 9.52% genotypes had the short leaves (Table 13). The results matched with DiTomaso and Healy (2007), eFloras (2008), Gulden *et al.* (2008), Warwick (2010) and Minnesota Wild Flowers (2021) who reported that basal leaves were 10 to 40 cm long in different *Brassica rapa* genotypes.

1.2.2.1.2 Leaf width

The middle to upper leaves were smaller in size. Among the F_1s about 11.90 % genotypes had the larger leaf width (> 7 cm), 80.95% genotypes had the intermediate leaf width (< 7 cm) and 7.14% genotypes had the narrower leaf width (< 4 cm) (Table 13). The results matched with the findings of DiTomaso and Healy (2007), eFloras (2008), Gulden *et al.* (2008), Warwick (2010) and Minnesota Wild Flowers (2021) who reported that the basal leaves were 3.00 to 10.00 cm in width in different *Brassica rapa* genotypes.

1.2.2.1.3 Number of leaf lobes

According to the number of leaf lobes F_1s had been grouped into three categories i.e. High (>10 lobes), medium (<10 lobes) and low (<5 lobes). About 14.29 % genotypes had the high

i.e. more than 10 lobes in the leaves, 71.43% genotypes had the medium i.e. more than five but less than 10 lobes in the leaves and 14.29% genotypes had the low i.e. less than five lobes in the leaves (Table 13). The result was more or less similar with the findings of PROTA (2018) where it was reported that *Brassica rapa* varieties had one to five pairs of small lateral lobes and large terminal lobes. Warwick (2010) and Young-Mathews (2012) found that the leaves of *Brassica rapa* varieties had one to four pairs of lateral lobes towards the base. The result was also supported by DiTomaso and Healy (2007) and eFloras (2008).

1.2.2.1.4 Petiole length

Both the basal and lower leaves had stout petioles. On the basis of petiole length, F_1s had been grouped into three categories, viz. long (> 8 cm), intermediate (< 8 cm) and short (< 4 cm). Among the hybrids about 14.29 % genotypes had the long petioles, 80.95% genotypes had the intermediate type petiole length and 4.76 % genotypes had the short petioles (Table 13). The result was supported by Warwick, (2010), Young-Mathews (2012), Minnesota Wild Flowers (2021) and iNaturalist org. (2021) who stated that the lower leaves were long with long petiole and upper leaves were smaller with clasping base in *Brassica rapa* varieties. Native Plant Trust (2021) reported that the lower leaves of different *Brassica rapa* varieties had long petiole (1.00 cm to 17.00 cm) and the present results was remained within this findings.

1.2.2.1.5 Petiole width

Among the F_1s about 28.57 % genotypes had the broad petiole width (> 1 cm), 71.43% genotypes had the intermediate petiole width (< 1 cm). Native Plant Trust (2021) reported lower leaves had long petiole which is 0.50 cm to 2.00 cm in width and the result of the present study was found within this findings. Warwick, (2010), Young-Mathews (2012) found broad and intermediate type leaf petiole in different *Brassica rapa* varieties. Yadav (2013) reported broad, intermediate and narrow type leaf petiole in Indian mustard.

1.2.2.2 Flower and pod or siliqua characteristics

1.2.2.2.1 Petal length and width

On the basis of petal length, F_1s had been grouped into three categories, viz. long (> 1 cm), medium (< 1 cm) and short (< 0.5 cm). On the other hand hybrids had been grouped into three categories according to their petal width viz. broad (> 0.5 cm), medium (< 0.5 cm) and narrow (< 0.2 cm). Out of forty two F_1s about 14.29 % genotypes had the long petal with the broad petal width, 80.95 % genotypes had the medium petal length and width and 4.76 %

genotypes had the short and the narrow petal (Table 13). The result was more or less similar with the findings of Hilty (2019) who reported that the length of the flowers of *Brassica rapa* ranged from 0.85 cm to 1.27 cm. Young-Mathews (2012) and Minnesota Wild Flowers (2021) found that the flowers of *Brassica rapa* was usually 0.64 cm to 1.27 cm. According to DiTomaso and Healy (2007), eFloras (2008), Gulden *et al*. (2008), Warwick (2010) and Native Plant Trust (2021) the length and width of the flowers petal of *Brassica rapa* ranged from 0.60 cm to 1.0 cm and 0.30 cm to 0.60 cm respectively. Vélez-Gavilán (2018) and Vibrans (2018) reported that the length of the flowers petal of *Brassica rapa* ranged from 0.70 cm to 1.10 cm which matched with the present findings.

1.2.2.2.2 Siliqua length and width

On the basis of siliqua length, F_1s had been grouped into three categories, viz. long (> 3.5 cm), intermediate (< 3.5 cm) and short (< 2.0 cm) while according to siliqua width F_1s had been also grouped into three categories viz. large (> 1 cm), medium (< 1 cm) and narrow (< 0.5 cm). Out of forty two F_1s about 59.52 % genotypes had the long siliqua, 35.71 % genotypes had the intermediate siliqua length and 4.76 % genotypes had the short siliqua while 4.76 % genotypes had the larger siliqua width, 64.29 % genotypes had the medium siliqua width and 30.95 % genotypes had the narrower siliqua length (Table 13). The result matched with Hilty (2019) and Native Plant Trust (2021) who stated that pods (siliqua) were 3.18 cm to 5.72 cm and 2.00 cm to 11.00 cm long respectively while 0.20 cm to 1.10 cm and 1.2 cm to 1.5 cm wide respectively at maturity. Warwick (2010), Jepson Flora Project (2012) and Young-Mathews (2012) reported that the siliqua were 1.90 cm to 10.16 cm long and 0.15 cm to 1.15 cm wide. The present result was also matched with the following findings of DiTomaso and Healy (2007) and, eFloras (2008) where they estimated that the pods were 3.00 cm to 8.00 cm long. According to Minnesota Wild Flowers (2021) pods of *Brassica rapa* varieties were 2.54 cm to 5.08 cm long which was more or less similar with the present findings. PROTA (2018) also reported that siliqua of *Brassica rapa* varieties were 4.00 cm to 10.00 cm long and 0.20 cm to 0.40 cm in width.

1.2.2.2.3 Beak length

On the basis of beak length, F_1s had been grouped into three categories, viz. long (> 1.5 cm), intermediate (< 1.5 cm) and short (< 0.8 cm). Out of forty two F_1s about 14.29 % genotypes had the long beak, 76.19 % had the intermediate beak length and 9.52 % genotypes had the

short beak (Table 13). The result was supported by Hilty (2019) and Native Plant Trust (2021) who stated that beak length was about 0.80 cm to 1.43 cm and 0.80 cm to 1.5 cm respectively. DiTomaso and Healy (2007) and, eFloras (2008) found that the beaks were 1.0 to 1.5 cm long. PROTA (2018) and Minnesota Wild Flowers (2021) reported *Brassica rapa* pods had a beak of about 0.50 cm to 2.00 cm and 0.85 cm to 1.27 cm long respectively.

1.2.2.3 Yield and yield related quantitative characters

Mean performance of ten quantitative yield and yield related traits of parents and their F_1s were estimated and showed in Table 14.

1.2.2.3.1 Days to 50% flowering

In case of days to 50% flowering, it ranged from 34.00 to 62.00 days for parent. The parent Tori-7 flowered within the lowest time (34.00 days) while the parent BARI Sar-6 took the highest duration (62.00 days). The result was more or less similar with the findings of Ali *et al.* (2002), Karmokar (2018) and Ullah (2018) who reported days to 50% flowering for different lines and varieties of *Brassica rapa* ranged from 39.00 to 46.00 days, 33.00 to 57.33 days and 27.33 to 35.66 days respectively. On the other hand, the F_1-Tori-7 × Brown Special produced 50 % flower within the lowest growth duration (35 days) and the reciprocal F_1-BARI Sar-6 × BARI Sar-17 produced 50 % flower within the highest duration (57 days) (Table 14). Ferdous (2019) observed days to 50% flowering, ranged from 29.00 to 39.00 days for parent and from 31.00 to 37.00 days in F_1s of *Brassica rapa*.

1.2.2.3.2 Days to 80% maturity

The parent Brown Special showed the lowest duration (80.66 days) for maturation and BARI Sar-6 had taken the highest duration (110.00 days). The shortest time (81 days) was required for 80% maturity in Tori-7 was reported by Ali *et al.* (2002). The result exceeded the findings of Karmokar (2018) and Ullah (2018) who reported that it ranged from 78.00 to 89.67 days and 78.33 to 87.33 days respectively for different lines and varieties of *Brassica rapa* while in the reciprocal F_1- Tori-7 × Brown Special matured within the lowest duration (80.00 days) followed by F_1- Brown Special × BARI Sar-14 (82.00 days), F_1-Yellow Special × Brown Special (83 days) and the F_1-BARI Sar-14 × Tori-7 (83 days) while the F_1-BARI Sar-6 × BARI Sar-17 required the maximum duration (103.00 days). Ferdous (2019) observed that it ranged from 86.00 to 99.00 days for parent and from 82.00 to 95.00 days in F_1s of *Brassica rapa*.

Table 14. Mean performance of ten yield and yield contributing traits of *Brassica rapa* genotypes and their F_1s

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% Maturity	Plant height (cm)	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length (cm)	Number of seeds siliqua^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
A.	**Parents**										
1.	P_1	40.00	85.00	95.66	6.66	1.09	97.66	3.30	25.03	3.35	5.20
2.	P_2	34.66	80.66	109.38	6.15	4.73	210.63	4.52	18.30	3.62	5.88
3.	P_3	44.00	88.00	112.26	5.46	0.26	137.73	3.94	21.28	4.62	5.36
4.	P_4	34.00	81.66	73.46	6.23	9.60	250.53	3.00	12.18	2.82	4.25
5.	P_5	51.33	96.00	100.90	5.13	2.12	102.66	3.66	30.04	4.00	6.97
6.	P_6	43.00	90.33	114.30	8.76	1.23	165.40	3.59	22.78	4.76	6.43
7.	P_7	62.00	110.00	148.56	8.73	0.80	175.20	4.10	22.47	4.78	8.41
B.	**Crosses**										
1.	$P_1 \times P_2$	44.00	90.00	132.30	9.10	9.80	386.68	3.84	10.40	4.25	18.67
2.	$P_1 \times P_3$	43.00	89.00	124.80	7.70	0.33	190.24	3.62	21.92	3.92	12.09
3.	$P_1 \times P_4$	38.00	83.00	128.96	8.40	7.30	428.53	3.16	9.20	4.11	13.27
4.	$P_1 \times P_5$	42.00	88.00	111.63	4.10	1.93	101.00	4.47	26.46	3.47	10.20
5.	$P_1 \times P_6$	44.00	90.00	122.96	7.80	1.03	183.36	3.63	15.56	4.30	12.04
6.	$P_1 \times P_7$	46.00	92.00	125.53	8.46	1.53	232.73	3.79	16.40	4.39	14.11
7.	$P_2 \times P_3$	41.00	87.00	118.62	10.13	2.40	270.86	4.12	17.24	4.24	18.34
8.	$P_2 \times P_4$	40.00	86.00	112.86	10.40	10.60	305.13	3.00	9.08	2.98	15.75
9.	$P_2 \times P_5$	48.00	94.00	125.80	8.13	14.50	420.33	2.04	9.30	3.74	23.55

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6.

Table 14 (Cont'd).

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% Maturity	Plant height (cm)	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length (cm)	Number of seeds siliqua^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
10.	$P_2 \times P_6$	40.00	85.00	148.00	14.75	21.00	1029.00	2.89	3.86	4.02	26.02
11.	$P_2 \times P_7$	39.00	84.33	122.13	8.93	5.13	276.26	4.06	16.72	5.04	12.44
12.	$P_3 \times P_4$	39.00	84.00	120.96	8.73	8.76	506.73	3.14	10.92	3.44	15.02
13.	$P_3 \times P_5$	42.00	88.00	116.46	7.60	2.73	160.13	4.08	21.80	4.72	15.80
14.	$P_3 \times P_6$	48.00	94.24	120.33	9.00	2.34	211.86	3.64	17.72	4.08	12.25
15.	$P_3 \times P_7$	50.25	96.66	128.60	7.60	2.40	230.73	4.65	24.56	3.20	13.70
16.	$P_4 \times P_5$	49.00	95.50	114.98	8.60	16.93	617.05	3.76	16.85	4.40	16.37
17.	$P_4 \times P_6$	50.33	96.00	133.73	12.26	17.26	620.26	3.13	5.72	2.81	15.54
18.	$P_4 \times P_7$	42.00	86.66	125.13	12.73	7.13	385.86	4.14	16.00	4.14	13.53
19.	$P_5 \times P_6$	46.33	91.33	126.60	8.53	0.60	180.13	3.38	14.00	3.19	10.55
20.	$P_5 \times P_7$	43.00	89.38	130.50	6.40	1.06	166.99	3.52	12.49	3.71	9.53
21.	$P_6 \times P_7$	47.00	93.00	134.00	8.78	4.80	341.23	3.76	10.33	5.41	12.66
C.	**Reciprocals**										
22.	$P_2 \times P_1$	37.00	82.00	128.51	8.00	6.06	312.93	3.21	11.40	3.08	11.59
23.	$P_3 \times P_1$	40.33	86.00	117.33	5.60	2.60	123.83	3.91	23.42	5.20	9.69
24.	$P_3 \times P_2$	38.00	83.00	129.26	9.46	5.73	350.00	3.67	13.04	4.15	15.79
25.	$P_4 \times P_1$	47.50	94.25	134.53	10.46	9.60	426.46	3.88	11.20	4.02	16.19
26.	$P_4 \times P_2$	35.00	80.00	116.46	11.00	10.06	401.73	4.26	12.28	4.37	13.24
27.	$P_4 \times P_3$	50.33	96.00	130.00	9.33	16.40	555.93	3.62	11.44	5.42	27.67
28.	$P_5 \times P_1$	46.00	91.00	110.60	6.13	6.94	120.53	3.76	35.68	4.37	11.82

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6.

Table 14 (Cont'd).

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% Maturity	Plant height (cm)	Number of primary branches plant^{-1}	Number of secondary branches/ plant^{-1}	Number of siliqua plant^{-1}	Siliqua length (cm)	Number of seeds siliqua^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
29.	$P_5 \times P_2$	44.00	89.00	119.00	8.66	2.46	314.46	3.44	11.92	3.60	11.15
30.	$P_5 \times P_3$	48.00	93.00	121.90	7.90	0.80	168.70	3.97	22.24	3.00	9.66
31.	$P_5 \times P_4$	44.00	90.00	124.00	9.40	10.26	453.00	3.79	11.16	5.37	16.23
32.	$P_6 \times P_1$	42.00	88.00	118.66	7.33	9.99	171.30	3.50	15.08	3.53	8.37
33.	$P_6 \times P_2$	46.44	92.88	121.26	11.00	22.00	591.20	3.22	15.30	5.58	22.34
34.	$P_6 \times P_3$	44.00	89.00	129.40	7.66	0.26	164.93	3.27	15.72	3.10	9.52
35.	$P_6 \times P_4$	41.00	85.00	139.96	14.06	18.40	823.86	3.01	9.92	3.01	19.61
36.	$P_6 \times P_5$	49.00	95.00	120.96	5.83	7.09	169.36	3.42	14.18	2.81	7.80
37.	$P_7 \times P_1$	47.00	93.00	141.53	11.90	2.53	234.50	3.16	12.60	2.44	12.21
38.	$P_7 \times P_2$	42.00	87.00	130.16	9.26	3.11	258.62	4.80	16.36	4.42	14.04
39.	$P_7 \times P_3$	49.00	95.00	128.53	7.00	2.10	131.40	4.17	21.08	2.10	10.36
40.	$P_7 \times P_4$	44.00	90.00	137.86	9.60	8.93	463.40	4.14	13.32	3.10	16.60
41.	$P_7 \times P_5$	57.00	103.00	139.20	10.24	1.66	225.08	3.63	13.73	5.69	13.33
42.	$P_7 \times P_6$	54.00	99.00	136.66	7.80	1.13	240.06	3.14	10.48	3.27	9.32
	Minimum	34.00	80.00	73.46	4.10	0.26	97.66	2.04	3.86	2.10	4.21
	Maximum	62.00	110.00	148.56	14.75	22.00	1029.00	4.80	35.68	5.69	27.67
	Mean	44.42	90.12	123.57	8.63	6.28	307.88	3.65	15.92	3.94	13.07
	CV (%)	8.78	1.48	2.09	12.19	17.31	2.47	6.03	8.20	4.78	1.18
	LSD	1.88	1.06	4.20	1.70	1.55	12.32	0.35	2.11	0.30	1.73

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6

1.2.2.3.3 Plant height

For parents, plant height ranged from 73.46 cm to 148.56 cm. The lowest plant height was recorded in Tori-7 (73.46 cm) and the highest was in BARI Sar-6 (148.56 cm). For F_1s, plant height ranged from 110.60 cm to 148.00 cm. F_1-BARI Sar-17 × BARI Sar-14 (110.60 cm) showed the lowest plant height preceded by F_1-BARI Sar-14 × BARI Sar-17 (111.63 cm). Therefore, they could be used as the materials for getting dwarf plants. Whereas, among the F_1s the highest plant height was found in F_1- Brown Special × BARI Sar-15 (148.00 cm) followed by F_1-BARI Sar-6 × BARI Sar-14 (141.53 cm). The plant height was higher in F_1s than the parents. The result was slightly different from Karmokar (2018) and Ullah (2018) who reported that the plant height for different lines and varieties of *Brassica rapa* ranged from 80.77 cm to 111.47 cm and 94.56 cm to 107.73 cm respectively.

1.2.2.3.4 Number of primary branches plant^{-1}

In parents, it ranged from 5.13 to 8.76. BARI Sar-17 showed the lowest number (5.13) and BARI Sar-15 showed the highest value (8.76). Among the F_1s, F_1- Brown Special × BARI Sar-15 showed the highest number (14.75) and F_1-BARI Sar-14 × BARI Sar-17 showed the lowest number (4.10). The result was supported by Ferdous (2019) who observed that it ranged from 3.57 to 6.33 for parents while for their F_1s it was 4.53 to 14.00. Karmokar (2018) also reported that it ranged from 5.13 to 10.33 in *Brassica rapa* but was higher than the findings of Ullah (2018) who estimated that it was between 5.67 and 4.12.

1.2.2.3.5 Number of secondary branches plant^{-1}

It ranged from 0.26 to 9.60 in parents while 0.26 to 22.00 in F_1s. In parents, the highest value was recorded in Tori-7 (9.60) and among F_1s, the highest value was recorded in F_1-BARI Sar-15 × Brown Special (22.00). The lowest number was found in reciprocal F_1-BARI Sar-15 × Yellow Special and the parent Yellow Special (0.26). The F_1s were almost two times higher than the parental average. For parents the result was supported by Karmokar (2018) who reported that it ranged from 0.50 to 10.93 for different lines and varieties of *Brassica rapa* but higher than the findings of Ullah (2018) who estimated that it was between 1.45 and 2.27. Ferdous (2019) also observed more or less similar result in parents 4.45 and in their F_1s up to 21.07.

1.2.2.3.6 Number of siliqua plant^{-1}

It ranged from 97.66 to 250.53 in parents where Tori-7 produced the highest and BARI Sar-14 produced the lowest number. This Results exceeded the ranges reported by Naznin *et al.*

(2015), Karmokar (2018) and Ullah (2018) who found that it ranged from 59.48 to 124.29, 96.54 to 124.44 and 78.00 to 180.33 respectively for different lines and varieties of *Brassica rapa*. In F_1s, siliqua plant^{-1} ranged from 101.00-1029.00. The F_1- Brown Special × BARI Sar-15 produced the highest number which was much higher than their parents while F_1- BARI Sar-14 × BARI Sar-17 produced the lowest number. Ferdous (2019) observed number of siliqua plant^{-1} in parents ranged from 54.87 to 143.33 and for their F_1s it was up to 856.33 which was more or less similar to the present results.

1.2.2.3.7 Siliqua length

Siliqua length of parent ranged from 3.00 cm to 4.52 cm. The parent Brown Special produced the longest siliqua (4.52 cm) while Tori-7 produced the shortest siliqua (3.00cm). The result was more or less similar with the findings of Karmokar (2018) and Ullah (2018) who reported that it ranged from 4.67 cm to 5.96 cm and 5.07 cm to 6.38 cm respectively for different lines and varieties of *Brassica rapa*. The length varied from 2.04 cm to 4.80 cm in F_1s. The F_1-BARI Sar-6 × Brown Special exhibited the highest length (4.80 cm) and that was little bit higher than it's either parent while F_1- Brown Special × BARI Sar-17 showed the lowest length. Ferdous (2019) observed that it ranged from 3.83 cm to 5.07 cm in parents and for their F_1s it was 3.13 cm to 4.86 cm.

1.2.2.3.8 Number of seeds siliqua^{-1}

It ranged from 12.18 to 30.04 in parents. The parent BARI Sar-17 produced the highest number of seeds (30.04) while Tori-7 produced the lowest number of seeds siliqua^{-1} (12.18). Karmokar (2018) and Ullah (2018) found that it ranged from 11.98 to 16.22 and 12.83 to 20.87 respectively for different varieties of *Brassica rapa*. The result exceeded this findings. In the F_1s, it ranged from 3.86 to 35.68. The F_1-BARI Sar-17 × BARI Sar-14 produced the highest seeds siliqua^{-1} (35.68) and F_1- Brown Special × BARI Sar-15 produced the lowest seeds siliqua^{-1} (3.86). Ali *et al.* (2002) observed that the F_1s of *Brassica rapa* produced 25.06 seeds siliqua^{-1} which was much higher than their parents. Ferdous (2019) also observed that it ranged from 13.06 to 26.20 in parents and 5.01 to 25.41in their F_1s.

1.2.2.3.9 Thousand seed weight

Thousand seed weight in parents ranged from 2.82 g to 4.78 g. However, the heaviest seeds were produced by BARI Sar-6 while the lowest seed weight was recorded for Tori-7. The result was more or less similar with the findings of Karmokar (2018) and Ullah (2018) who reported that it ranged from 3.33 g to 4.53 g and 2.50 g to 3.63 g respectively in *Brassica*

rapa. The F_1-BARI Sar-6 × BARI Sar-17 (5.69 g) followed by F_1-BARI Sar-15 × Brown Special (5.58 g) produced the highest weighted seeds which were higher than it's both parents (Table 14) and the F_1-BARI Sar-6 × Yellow Special (2.10 g) produced the lowest weighted seeds. Ali *et al.* (2002) found variation in thousand seed weight in *Brassica rapa* which ranged from 5.33 g to 5.83 g in parent and from 3.60 g to 6.33 g in F_1s. Ferdous (2019) observed that thousand seed weight in parents varied from 3.50 g to 5.53 g and from 1.82 g to 5.69 g in F_1s of *Brassica rapa*.

1.2.2.3.10 Seed yield plant^{-1}

Seed yield plant^{-1} ranged from 4.25 g to 8.41 g in parents and from 4.21 g to 27.67 g in F_1s. The highest seed yield was found in parent, BARI Sar-6 (8.41 g plant^{-1}). Similarly, among the F_1s, the highest seed yield was recorded in the reciprocal F_1-Tori-7 × Yellow special (27.67 g plant^{-1}) while the lowest seed yield was found in the parent, Tori-7 (4.25 g plant^{-1}) and among the F_1s, it was lowest in the reciprocal F_1-BARI Sar-15 × BARI Sar-17 (7.80 g plant^{-1}). Most of the F_1s showed seed yield above 10.00 g plant^{-1}. Karmokar (2018) and Ullah (2018) found that the yield plant^{-1} for different lines and varieties of *Brassica rapa* ranged from 3.53 g to 7.31 g and 5.65 g to 7.48 g respectively. The result remained within the range of this findings for parents. Ferdous (2019) observed that seed yield plant^{-1} in parents ranged from 4.16 g to 7.07 g and from 4.88 g to 20.09 g in F_1s of *Brassica rapa*.

1.3 Identification of F_1s

The F_1s were identified at the flowering and pod formation stage by visual observation of different morphological features which was different from their parents. The F_1s plants are usually intermediate in different characteristics between two parents in respect of leaf, inflorescence and siliqua but sometimes the F_1s had become more resemble to their female parent. However, in some cases the F_1 plants showed different characteristics in respect of leaf, inflorescence and siliqua from the both parents.

The F_1 plants obtained from the cross BARI Sar-14 × Brown Special and their reciprocal cross Brown Special × BARI Sar-14 both represented similar leaf angle, leaf apex shape, leaf hairiness and siliqua angle (open, semi-acute, sparse and long) to Brown Special and leaf blade edges like to BARI Sar-14 (lobed and crenated). However, the leaf blade shape was more or less similar in both F_1s with their parents (all were runcinate type) but had high number of leaf lobes. Both F_1s had different siliqua shape from their parents round for BARI

Sar-14 × Brown Special and thin and round for their reciprocal cross Brown Special × BARI Sar-14). Rest of the characters were intermediate type for both F_1s (Plate 13). From the cross BARI Sar-14 × Yellow Special and their reciprocal cross combination Yellow Special × BARI Sar-14 the F_1 plants obtained both produced similar siliqua shape to Yellow Special (flattened) and leaf angle, leaf apex shape was like to BARI Sar-14 (semi prostrate, acute). However, leaf blade shape, leaf blade edges and leaf hairiness was similar in both F_1s and their parents (all were runcinated, lobed and crenated, very sparse type) but both had more siliqua length from the both parents and semi erect type siliqua angle. The two F_1s differed from each other in leaf length and width, the F_1s obtained from reciprocal cross (Yellow Special × BARI Sar-14) had short and narrow leaf length and width while other F_1s produced intermediate type. Other characters were intermediate type for both F_1s. However, the both F_1 plants obtained from the cross BARI Sar-14 × Tori-7 and their reciprocal cross Tori-7 × BARI Sar-14 exhibited similar leaf angle to Tori-7 (open type) but leaf blade edges was similar in both F_1s and both parents (all were lobed and crenated type). The two F_1s differed from each other in leaf blade shape, leaf apex shape, leaf hairiness, siliqua shape, the F_1s obtained from BARI Sar-14 × Tori-7 had lyrate, rounded, sparse, thin and rounded type while the F_1s obtained from their reciprocal cross (Tori-7 × BARI Sar-14) had runcinaate, semi acute, no hair, thin and flattened type. However, both had narrow siliqua width and long siliqua angle which was different from the both parents. Rest of the characters were intermediate type for both F_1s while the F_1 plants obtained from the cross BARI Sar-14 × BARI Sar-17 and their reciprocal cross BARI Sar-17 × BARI Sar-14 exhibited different leaf angle, leaf blade edges and leaf hairiness, the F_1s obtained from BARI Sar-14 × BARI Sar-17 had semi prostrate, lobed and crenated and very sparse type which was similar to BARI Sar-14 while the F_1s obtained from their reciprocal cross (BARI Sar-17 × BARI Sar-14) had prostrate, lobed and serrated and sparse type which was similar to BARI Sar-17. However, leaf blade shape, leaf apex shape, siliqua shape and angle were similar in both F_1s and their parents (all were runcinated, acute, cylindrical and erect type) but had short and narrow leaf, small sized flower with short and narrow petals, short and broader siliqua which was different from the both parents. Rest of the characters were intermediate type (Plate 13). The F_1 plants originated from the cross BARI Sar-14 × BARI Sar-15 showed similar leaf blade shape and leaf hairiness to BARI Sar-14 (runcinated and very sparse type) but had similar leaf blade edges, siliqua shape and angle (lobed and

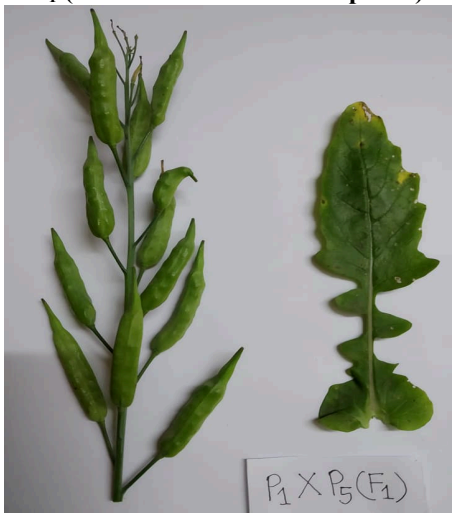
BARI Sar-14

F_1 (BARI Sar-14 × Brown Special)

F_1 (Brown Special × BARI Sar-14)

Brown Special

BARI Sar-14

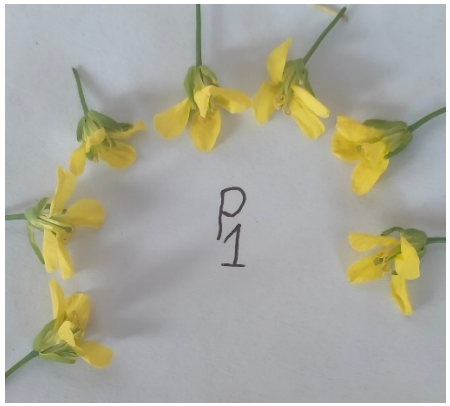


F_1 (BARI Sar-14 × BARI Sar-17)

F_1 (BARI Sar-17 × BARI Sar-14)

BARI Sar-17

Plate 13. Leaves and Siliqua of F_1s developed from the 7 × 7 full diallel crosses among different *Brassica rapa* genotypes



BARI Sar-14

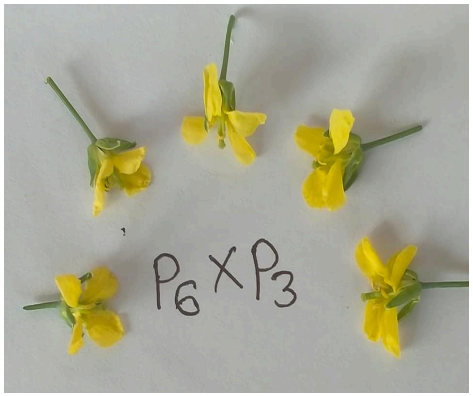
F_1 (BARI Sar-14 × BARI Sar-15)

F_1 (BARI Sar-15 × BARI Sar-14)

BARI Sar-15

Yellow Special

F_1 (Yellow Special × BARI Sar-15)



F_1 (BARI Sar-15 × Yellow Special)

BARI Sar-15

Plate 14. Flowers of F_1s developed from the 7 × 7 full diallel crosses among different *Brassica rapa* genotypes

serrated, flattened, semi erect type) to BARI Sar-15 while the F_1 plants obtained from the reciprocal cross BARI Sar-15 × BARI Sar-14 exhibited similar leaf blade shape, leaf hairiness and siliqua angle to BARI Sar-15 (lyrate, sparse and semi erect type) but had leaf blade edges (lobed and crenated) similar to BARI Sar-14 and different siliqua shape from both parents i.e. thin and flattened. However, leaf angle was similar in both F_1s and their parents (all were semi prostrate) but had semi acute leaf apex, long siliqua with short beak which was different from the both parents. Rest of the characters were intermediate type (Plate 14). The F_1 plants from the cross BARI Sar-14 × BARI Sar-6 and their reciprocal cross BARI Sar-6 × BARI Sar-14 exhibited similar siliqua shape to BARI Sar-6 (flattened) and siliqua angle to BARI Sar-14 (erect) and leaf blade shape, leaf apex shape, leaf blade edges and leaf hairiness was similar in both F_1s and their parents (all were runcinated, acute, lobed and crenated and very sparse type) but had more number of leaf lobes which was different from the both parents. Two F_1s differed from each other in leaf length and angle, the F_1s from BARI Sar-14 × BARI Sar-6 produced medium and semi prostrate type leaves while their reciprocal BARI Sar-6 × BARI Sar-14 produced long and open leaves while other characters were intermediate.

The both F_1 plants obtained from the cross Brown Special × Yellow Special and their reciprocal cross Yellow Special × Brown Special exhibited similar leaf hairiness (sparse) to Brown Special. Both F_1s and their parents had identical leaf angle, leaf blade shape, leaf blade edges (all were open, runcinated, lobed and crenated type). But both F_1s had similar petiole width, siliqua length and angle (broad, long and long) which were different from the both parents. The two F_1s differed from each other in leaf apex shape, siliqua width and shape, the F_1 plants originated from the cross Brown Special × Yellow Special produced semi acute, medium and rounded types while the F_1s from their reciprocal cross Yellow Special × Brown Special produced acute, broad and flattened types while other characters were intermediate type. The F_1s from the cross Brown Special × Tori-7 showed runcinated, semi-acute type leaves, thin and rounded siliqua like Brown Special while the F_1s from their reciprocal cross Tori-7 × Brown Special produced lyrate and rounded type leaves, thin and flattened siliqua like Tori-7. However, both F_1s and their parents showed similar leaf blade edges, leaf hairiness and leaf angle (all were lobed and crenated, sparse, open type) but both F_1s had long and broad petiole length and width, larger flower with long and broad petal, long siliqua angle which was different from the both parents. Rest of the characters were

intermediate type. The both F_1 plants obtained from the cross Brown Special × BARI Sar-17 and their reciprocal cross BARI Sar-17 × Brown Special exhibited different leaf angle and leaf blade edges, siliqua shape and angle, the F_1s from the cross Brown Special × BARI Sar-17 produced open, lobed and crenated type leaves, rounded and long siliqua while the F_1s from their reciprocal cross BARI Sar-17 × Brown Special produced semi prostrate, lobed and serrated type leaves, flattened and semi-erect type siliqua but both F_1s produced similar leaf apex shape like BARI Sar-17 (acute). However, leaf blade shape and leaf hairiness of both F_1s and their parents was similar (all were runcinated and sparse). While other characters were intermediate type. In the cross Brown Special × BARI Sar-15 and their reciprocal cross BARI Sar-15 × Brown Special the F_1 plants originated both showed similar leaf angle (open) like Brown Special and leaf blade shape, leaf apex shape, leaf blade edges, (lyrate, rounded, lobed and serrated) like BARI Sar-15. Both F_1s differed from each other in siliqua shape and angle, the F_1s from the cross Brown Special × BARI Sar-15 produced rounded and long siliqua while the F_1s from their reciprocal cross BARI Sar-15 × Brown Special produced thin and rounded, semi-erect type siliqua. However, leaf hairiness of both F_1s and their parents was similar (all were sparse type). While other characters were intermediate type. The both F_1 plants obtained from the cross Brown Special × BARI Sar-6 and their reciprocal cross BARI Sar-6 × Brown Special exhibited different siliqua shape and angle, the F_1s from the cross Brown Special × BARI Sar-6 produced long, thin and round siliqua with long angle while the F_1s from their reciprocal cross BARI Sar-6 × Brown Special produced long, flattened type siliqua with semi-erect angle but both F_1s produced similar leaf apex shape and leaf hairiness to BARI Sar-6 (acute and very sparse). However, leaf angle, leaf blade shape, leaf blade edges of both F_1s and their parents were similar (all were open, runcinated, lobed and crenated) but both F_1s had long and large leaves, more number of leaf lobes, long and broad petiole, long siliqua with long beak which was different from the both parents while other characters were intermediate.

In the cross Yellow Special × Tori-7 and their reciprocal cross (Tori-7 × Yellow Special) the F_1 plants originated both showed similar leaf blade shape and leaf apex shape to Yellow Special (runcinated and semi acute) and leaf hairiness like to Tori-7 (sparse). Two F_1s differed from each other in siliqua shape and angle, the F_1s from the cross Yellow Special × Tori-7 produced thin and rounded siliqua with semi erect type angle while the F_1s from their reciprocal cross (Tori-7 × Yellow Special) produced thin and flattened siliqua with long type

angle. However, both F_1s and their parents showed similar leaf blade edges and leaf angle (all were lobed and crenated, open type) but both had less number of leaf lobes, broad petiole width and narrow siliqua which was different from the both parents. Rest of the characters were intermediate type. However, the F_1 plants obtained from the cross Yellow Special × BARI Sar-17 and their reciprocal cross (BARI Sar-17 × Yellow Special) exhibited similar leaf blade edges, leaf apex shape, leaf hairiness, siliqua shape and angle (lobed and crenated, semi acute, very sparse, flattened and erect type) to Yellow Special but two F_1s differed from each other in leaf angle, the F_1s from the cross Yellow Special × BARI Sar-17 produced open type leaf angle while the F_1s from their reciprocal cross (BARI Sar-17 × Yellow Special) produced semi prostrate type leaf angle. However, both F_1s and their parents had identical leaf blade shape (all were runcinated type) but both F_1s had long siliqua which was different from the both parents. Other characters were intermediate type. Both F_1s originated from the cross Yellow Special × BARI Sar-15 and their reciprocal cross (BARI Sar-15 × Yellow Special) showed similar leaf blade shape, leaf apex shape, leaf hairiness and siliqua angle (runcinated, semi acute, very sparse and erect type) to Yellow Special and leaf angle, leaf blade edges (semi prostrate, lobed and serrated) to BARI Sar-15. However, both F_1s and their parents showed similar siliqua shape (all were flattened) but both F_1s had short petiole, less number of leaf lobes and long siliqua which was different from the both parents. Rest of the characters were intermediate type. No special difference was observed between two F_1s (Plate 14). The F_1 plants obtained from the cross Yellow Special × BARI Sar-6 and their reciprocal cross (BARI Sar-6 × Yellow Special) both exhibited similar leaf apex shape and siliqua angle (acute and semi erect) to BARI Sar-6. However, leaf angle, leaf blade shape, leaf blade edges, leaf hairiness was similar in both F_1s and their parents (all were open, runcinated, lobed and crenated, very sparse and) but both F_1 had broad petiole, semi erect type angle and long beak which was different from the both parents while other characters were intermediate type. Two F_1s differed from each other in siliqua shape, the F_1s from the cross Yellow Special × BARI Sar-6 produced short, thin and flattened siliqua while the F_1s from reciprocal cross (BARI Sar-6 × Yellow Special) produced long and flattened siliqua.

From the cross Tori-7 × BARI Sar-17 and their reciprocal cross (BARI Sar-17 × Tori-7) the F_1 plants originated both showed similar leaf blade shape and leaf blade edges (lyrate, lobed and crenated type) to Tori-7. Two F_1s differ from each other in leaf apex shape, leaf

hairiness, leaf angle, siliqua length and width, siliqua shape and angle, the F_1s from the cross Tori-7 × BARI Sar-17 produced rounded, absent, open, long and narrow, thin and rounded siliqua with long angle while the F_1s from their reciprocal cross (BARI Sar-17 × Tori-7) produced semi acute, sparse, semi prostrate, short and broad, flattened siliqua with semi erect angle. Rest of the characters were intermediate type. The F_1 plants obtained from the cross Tori-7 × BARI Sar-15 and their reciprocal cross (BARI Sar-15 × Tori-7) both exhibited similar leaf blade shape, leaf blade edges and leaf angle and siliqua shape (runcinated, lobed and crenated, open, thin and rounded type) to Tori-7 but two F_1s differed from each other in leaf apex shape, siliqua length and width, siliqua angle, the F_1s from the cross Tori-7 × BARI Sar-15 produced acute, long and narrow siliqua with long angle while the F_1s from their reciprocal cross (BARI Sar-15 × Tori-7) produced semi acute, short and narrow siliqua with semi erect angle. However, leaf hairiness was similar in both F_1s and their parents (all were sparse type) but had, less number of leaf lobes, larger flower with long and broad petals and short beak which was different from the both parents while other characters were intermediate type. The both F_1 plants obtained from the cross Tori-7 × BARI Sar-6 and their reciprocal cross (BARI Sar-6 × Tori-7) exhibited similar leaf hairiness and siliqua angle (sparse, long) to Tori-7 while leaf blade shape similar to BARI Sar-6 (runcinated type). However, both F_1s and their parents had identical leaf angle and leaf blade edges (open, lobed and crenated) but had long and larger leaves with long broader petioles and semi acute type leaf apex, larger flowers with long and broad petals different from the both parents. Two F_1s differ from each other in siliqua length and width, shape and angle, F_1s from Tori-7 × BARI Sar-6 produced long and narrow, thin and flattened siliqua with long angle while the F_1s from their reciprocal cross produced short and broader, flattened siliqua with semi erect angle. Other characters were intermediate type.

The F_1 plants originated from the cross BARI Sar-17 × BARI Sar-15 and their reciprocal cross (BARI Sar-15 × BARI Sar-17) both showed similar leaf angle and leaf blade shape (prostrate and runcinated) to BARI Sar-17 while siliqua shape and angle (flattened and semi erect) was similar to BARI Sar-15. However, leaf blade edges, leaf hairiness of both F_1s and their parents were similar (lobed and serrated, sparse type) but both F_1s had semi acute type leaf apex which was different from the both parents. There was no remarkable differences were found between two F_1s while F_1s from BARI Sar-17 × BARI Sar-6 and their reciprocal cross (BARI Sar-6 × BARI Sar-17) both exhibited similar leaf blade edges and siliqua shape

to BARI Sar-6 (lobed and crenated, flattened type) but had sparse leaf hairiness and erect siliqua angle like BARI Sar-17. Two F_1s differed from each other in leaf angle, siliqua length, the F_1s from BARI Sar-17 × BARI Sar-6 produced semi prostrate type leaf angle, medium siliqua while the F_1s from their reciprocal cross produced open type leaf angle, long siliqua. However, leaf blade shape and leaf apex shape in both F_1s and their parents were similar (runcinated and acute type) but had broader siliqua with a long beak which was different from the both parents. Other characters were intermediate.

However, the F_1 plants obtained from the cross BARI Sar-15 × BARI Sar-6 and their reciprocal cross (BARI Sar-6 × BARI Sar-15) both had similar leaf angle, leaf blade shape and leaf apex shape to BARI Sar-6 (open, runcinated and acute type) while leaf blade edges and leaf hairiness similar to BARI Sar-15 (lobed and serrated and sparse type). Both F_1s and their parents had identical siliqua angle (semi-erect type) but had long and larger leaves, broader siliqua which was different from the both parents. Two F_1s differed from each other in siliqua length and shape, the F_1s from the cross BARI Sar-15 × BARI Sar-6 produced medium and flattened siliqua while the F_1s from the reciprocal cross (BARI Sar-6 × BARI Sar-15) produced long and rounded siliqua. Other characters were intermediate.

Findings

Without some exception, most of the F_1s showed intermediate type characteristics between their parents in terms of leaf, flower and pod characteristics.

Tori-7 matured early but had the low yield plant^{-1} (81.66 days and 2.25 g plant^{-1}) while Brown Special matures within a short duration and had moderate yield plant^{-1} (80.66 days and 5.88g plant^{-1}). BARI Sar-15 had moderate yield potential but it required more time to mature (90.33 days and 6.43 g plant^{-1}) than Tori-7 and Brown Special. Another variety of *Brassica rapa* is BARI Sar-6 which required long duration to become matured but had very high yield potential (110.00 days and 8.41 g plant^{-1}).

The F_1, Tori-7 × Brown Special was found to be short durable (80.00 days) and yield was 13.24g plant^{-1} in comparison to Tori-7 (81.66 days and 4.25 g plant^{-1}) and Brown Special (80.66 days and 5.88 g plant^{-1}) while Brown Special × BARI Sar-14 matured in 82.00 days and yield was 11.59 g plant^{-1}, Yellow Special × Brown Special matured in 83.00 days and yield was 15.79 g plant^{-1}, BARI Sar-14 × Tori-7 matured in 83.00 days and yield was 13.27 g plant^{-1} and Brown Special × BARI Sar-15 matured in 85.00 days and yield was 26.02 g

plant^{-1}. These crosses had short duration than BARI Sar-15 (90.33 days) but more than Tori-7 (81.66 days).

While BARI Sar-15 × Brown Special matured in 92.88 days and yield was 22.34 g plant^{-1} and Tori-7 × Yellow Special matured in 96.00 days and yield was 27.67 g plant^{-1} but both showed long duration than Tori-7 and BARI Sar-15 but all the cross combinations had very high yield potential than Tori-7 (4.25 g plant^{-1}) and BARI Sar-15 (6.43 g plant^{-1}). So, these populations possessed excellent potential for use in future trial.

Experiment 2: Heterosis and combining ability analysis in *Brassica rapa*

2.1 Heterosis

Ten yield contributing characters of *Brassica rapa* were studied in seven parental genotypes and their forty two F_1s obtained from 7×7 full diallel crosses. Percent heterosis for ten different yield contributing characters of the F_1s over their respective mid and better parental values were shown in Table 15.

2.1.1 Days to 50% flowering

Significant and negative heterosis over the parents was desirable for the selection of F_1s for short duration. The highest significant negative heterosis for this trait (-35.00%) was found in the reciprocal F_1- BARI Sar-6 × Brown Special over the better parent followed by the F_1- Brown Special × BARI Sar-6 (-30.00%) and reciprocal F_1- BARI Sar-6 × Tori-7 (-30.00%) (Table 15) while the highest significant negative heterosis (-22.75%) was provided by the reciprocal F_1- BARI Sar-6 × BARI Sar-17 over the mid parent followed by the reciprocal F_1- BARI Sar-6 × Brown Special (-17.89%) and the F_1- Brown Special × BARI Sar-6 (-11.58%). Thus they could be used for exploiting desirable heterosis for this trait. F_1- BARI Sar-14 × Tori-7 (18.75%) showed the highly positive significant heterosis over the better parent followed by the F_1-Yellow Special × Tori-7 (17.05%) and the reciprocal F_1-BARI Sar-15 × Tori-7 (17.05%) while the F_1-Yellow Special × Tori-7 (29.05%) and reciprocal F_1-BARI Sar-15 × Tori-7 (29.05%) showed the highly positive significant heterotic effect over the mid parent. The non-significant positive heterosis over the mid parental value was found in F_1-BARI Sar-14 × BARI Sar-17 (0.73%) (Table 15). Barupal *et al.* (2017) also reported the negative and significant heterosis and heterobeltiosis for this trait in Indian mustard hybrids. Ferdous (2019) reported the highest significant negative heterosis (-6.73%) for days to 50% flowering over the mid parent and the non-significant negative heterosis over the better parent. Huq (2006) and Turi *et al.* (2006) also reported the negative and significant heterosis for this trait in the hybrids of *Brassica juncea*.

2.1.2 Days to 80% maturity

The highest significant negative heterosis over the better parent was observed in the F_1- BARI Sar-6 × Brown Special (-23.33%) followed by F_1-BARI Sar-6 × Tori-7 (-21.21%) and F_1- BARI Sar-6 × BARI Sar-17 (-18.75%). F_1- BARI Sar-14 ×Tori-7 showed the highest significant positive heterosis(10.88%) over the better parent followed by the F_1-Yellow

Table 15. Percent heterosis over the mid and the better parents for yield and yield contributing traits in F_1s of *Brassica rapa*

Sl. No.	Genotypes	Plant height (cm)		Number of primary branches plant^{-1}		Number of secondary branches plant^{-1}		Number of siliqua plant^{-1}		Siliqua length (cm)	
	F_1 (Cross)	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP
1.	$P_1 \times P_2$	25.35**	17.49**	24.90**	20.12**	224.64**	62.32**	121.71**	69.49**	-17.90**	-28.98**
2.	$P_1 \times P_3$	14.51**	7.38**	-7.59**	-15.91**	-100.00**	-100.00**	12.88*	1.72	5.25**	-5.32**
3.	$P_1 \times P_4$	38.60**	36.62**	62.36**	57.16**	100.00**	0.00	144.95**	70.22**	23.04**	17.57**
4.	$P_1 \times P_5$	11.96**	8.54**	3.98**	-7.96**	344.21**	-38.22**	32.95**	23.42**	8.04**	2.73**
5.	$P_1 \times P_6$	13.81**	5.13*	-4.92**	-16.34**	-100.00**	-100.00**	30.23**	3.56	2.99**	0.09
6.	$P_1 \times P_7$	15.90**	-4.73*	54.61**	36.26**	384.98**	142.49**	73.45**	35.76**	-15.13**	-23.79**
7.	$P_2 \times P_3$	18.24**	18.17**	62.96**	53.82**	186.98**	53.48**	128.48**	89.57**	-15.14**	-18.80**
8.	$P_2 \times P_4$	12.06**	6.47**	77.65**	76.47**	50.90**	4.79**	84.63**	60.35**	13.20**	-5.75**
9.	$P_2 \times P_5$	12.64**	8.79**	53.66**	40.92**	31.78**	-34.11**	134.42**	70.32**	-15.89**	-23.90**
10.	$P_2 \times P_6$	9.12**	7.43**	47.48**	25.47**	1009.24**	489.28**	237.80**	220.21**	-19.67**	-28.76**
11.	$P_2 \times P_7$	0.92	-12.38**	24.52**	6.10**	30.21**	-16.69**	44.74**	40.07**	10.77**	6.19**
12.	$P_3 \times P_4$	25.16**	18.98**	59.58**	49.68**	232.66**	70.83**	198.67**	121.89**	1.45**	-12.35**
13.	$P_3 \times P_5$	15.46**	11.57**	49.20**	44.69**	515.38**	207.69**	64.27**	38.58**	1.92**	-3.87**
14.	$P_3 \times P_6$	16.51**	14.65**	7.68**	-12.62**	5.40**	0.00	14.88**	-0.28	-14.25**	-20.82**
15.	$P_3 \times P_7$	-0.29	-13.48**	-1.36	-19.85**	-100.00**	-100.00**	-10.75*	-23.93**	0.76**	0.56**
16.	$P_4 \times P_5$	23.77**	21.69**	65.44**	50.80**	113.75**	6.87**	171.10**	80.81**	13.7**	3.55**
17.	$P_4 \times P_6$	32.45**	24.00**	87.46**	60.38**	274.24**	91.66**	296.15**	228.84**	-7.43**	-13.92**
18.	$P_4 \times P_7$	11.61**	-7.20**	28.28**	9.92**	67.80**	-6.98**	118.96**	84.96**	15.75**	-0.16
19.	$P_5 \times P_6$	12.65**	7.17**	-16.04**	-33.46**	-100.00**	-100.00**	36.00**	2.39	-4.42**	-6.56**
20.	$P_5 \times P_7$	11.15**	-6.30**	47.77**	17.29**	218.21**	59.10**	75.57**	30.30**	-7.00**	-12.46**
21.	$P_6 \times P_7$	4.54**	-8.01**	-10.86**	-11.02**	77.02**	8.30**	41.99**	38.98**	-17.83**	-24.27**

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6. *and ** indicate significant at 5% and 1% level of probability respectively; HBP and HMP are Heterosis over Better parents and Mid Parents respectively.

Table 15 (Cont'd).

Sl. No.	Genotypes	Plant height (cm)		Number of primary branches plant^{-1}		Number of secondary branches plant^{-1}		Number of siliqua plant^{-1}		Siliqua length (cm)	
	F_1 (Reciprocal)	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP
22.	$P_2 \times P_1$	29.05**	20.95**	42.07**	36.63**	425.00**	162.50**	173.96**	109.43**	-1.79**	-15.04**
23.	$P_3 \times P_1$	21.80**	14.22**	27.06**	15.61**	153.84**	26.92**	73.42**	56.27**	-2.55**	-12.35**
24.	$P_3 \times P_2$	8.51**	8.45**	74.50**	64.71**	20.20**	-35.71**	76.82**	46.70**	-4.74**	-8.85**
25.	$P_4 \times P_1$	32.86**	30.97**	30.29**	26.12**	52.08**	-23.96**	146.14**	71.05**	0.21	-4.24**
26.	$P_4 \times P_2$	8.60**	3.18	67.96**	66.84**	59.00**	10.41**	40.23**	21.79**	-20.29**	-33.63**
27.	$P_4 \times P_3$	16.47**	10.71**	49.31**	40.05**	77.69**	-8.75**	172.24**	102.26**	-12.00**	-23.97**
28.	$P_5 \times P_1$	13.01**	9.55**	-30.45**	-38.44**	-100.00**	-100.00**	11.40*	3.42	28.35**	22.04**
29.	$P_5 \times P_2$	19.08**	15.01**	44.15**	32.19**	676.78**	288.39**	213.34**	127.66**	-50.12**	-54.87**
30	$P_5 \times P_3$	10.30**	6.59**	43.53**	39.19**	2000.00**	950.00**	55.92**	31.54**	4.75**	-1.21**
31.	$P_5 \times P_4$	14.77**	12.83**	51.36**	37.97**	252.71**	76.35**	269.28**	146.29**	12.80**	2.73**
32.	$P_6 \times P_1$	17.93**	8.94**	1.12	-11.02**	782.86**	341.43**	39.40**	10.86	6.82**	3.81**
33.	$P_6 \times P_2$	33.18**	31.13**	97.76**	68.25**	958.82**	462.50**	487.94**	457.33**	-27.90**	-36.06**
34.	$P_6 \times P_3$	8.34**	6.61**	26.52**	2.66**	-100.00**	-100.00**	47.57**	28.09**	-4.54**	-11.86**
35.	$P_6 \times P_4$	26.56**	18.48**	63.46**	39.85**	251.05**	79.79**	198.25**	147.57**	-3.74**	-10.48**
36.	$P_6 \times P_5$	17.89**	12.17**	22.76**	-2.69**	414.28**	157.14**	44.65**	8.91	-5.54**	-7.65**
37.	$P_7 \times P_1$	2.80	-15.50**	9.92**	-3.13**	193.29**	46.64**	72.14**	34.73**	1.79**	-8.60**
38.	$P_7 \times P_2$	-5.30*	-17.79**	20.04**	2.29**	114.79**	37.41**	54.61**	49.63**	-6.31**	-10.18**
39.	$P_7 \times P_3$	-0.24	-13.44**	7.09**	-12.98**	268.28**	130.03**	56.71**	33.57**	12.36**	12.14**
40.	$P_7 \times P_4$	1.30	-15.77**	70.11**	45.76**	33.98**	-25.73**	82.32**	54.01**	15.75**	-0.16
41.	$P_7 \times P_5$	4.20*	-12.16**	-7.67**	-26.72**	103.19**	1.60*	30.26**	-3.32	-9.82**	-15.11**
42.	$P_7 \times P_6$	2.51	-9.80**	0.34	0.15	651.95**	360.06**	101.83**	97.55**	-1.61**	-9.32**
	Minimum	-5.30	-17.79	-30.45	-38.44	-100.00	-100.00	-10.75	-23.93	-50.12	-54.87
	Maximum	38.60	36.62	97.76	76.47	2000.00	950.00	487.94	457.33	28.35	22.04
	SE	1.83	2.12	0.74	0.86	0.68	0.78	5.38	6.21	0.16	0.18

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6. *and ** indicate significant at 5% and 1% level of probability respectively; HBP and HMP are Heterosis over Better parents and Mid Parents respectively.

Table 15 (Cont'd).

Sl. No.	Genotypes	Number of seeds siliqua^{-1}		1000 seed weight (g)		Days to 50% flowering		Days to 80% maturity		Seed yield plant^{-1} (g)	
	F_1 (Cross)	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP
1.	$P_1 \times P_2$	-43.48**	-54.47**	-14.69**	-14.73**	-1.33**	-7.50**	-0.61	-3.53**	77.27**	47.12**
2.	$P_1 \times P_3$	1.12	-6.47**	26.29**	12.63**	-2.81**	-6.20**	-0.58	-2.27**	46.60**	20.82**
3.	$P_1 \times P_4$	-41.40**	-55.27**	24.72**	11.05**	26.67**	18.75**	14.24**	10.88**	243.98**	211.35**
4.	$P_1 \times P_5$	29.56**	18.77**	14.70**	9.25**	0.73	-10.38**	0.55	-5.21**	80.87**	50.19**
5.	$P_1 \times P_6$	-36.93**	-39.78**	-18.65**	-30.26**	1.20**	-2.33**	1.73*	0.00	53.58**	46.84**
6.	$P_1 \times P_7$	-46.96**	-49.68**	-41.93**	-48.99**	-6.00**	-21.67**	-4.62**	-15.45**	47.02**	7.01**
7.	$P_2 \times P_3$	-28.70**	-38.72**	0.93**	-10.03**	-2.56**	-11.63**	-1.19	-5.68**	98.62**	96.88**
8.	$P_2 \times P_4$	-13.78**	-19.74**	35.75**	20.92**	0.00	0.00	0.00	0.00	118.96**	68.02**
9.	$P_2 \times P_5$	-47.42**	-60.32**	-5.47**	-10.00**	1.93**	-14.28**	1.14	-7.29**	41.59**	41.50**
10.	$P_2 \times P_6$	-19.61**	-32.81**	28.52**	10.13**	19.08**	8.00**	10.57**	5.55**	229.01**	183.50**
11.	$P_2 \times P_7$	-13.38**	-27.20**	5.24**	-7.60**	-11.58**	-30.00**	-8.42**	-20.91**	45.57**	23.05**
12.	$P_3 \times P_4$	-33.62**	-46.24**	45.66**	17.39**	29.05**	17.05**	14.29**	9.09**	352.37**	245.01**
13.	$P_3 \times P_5$	-13.33**	-25.97**	-30.24**	-34.92**	1.77**	-6.49**	1.09	-3.13**	21.59**	20.45**
14.	$P_3 \times P_6$	-28.64**	-30.99**	-35.93**	-38.75**	2.33**	2.33**	1.14	1.14	38.78**	18.70**
15.	$P_3 \times P_7$	-3.64**	-6.20**	-55.26**	-56.03**	-4.85**	-18.33**	-4.04**	-13.64**	6.64**	-9.20**
16.	$P_4 \times P_5$	-48.37**	-62.85**	57.52**	34.42**	1.93**	-14.28**	2.27**	-6.25**	168.63**	106.23**
17.	$P_4 \times P_6$	-44.84**	-56.45**	-23.65**	-40.53**	5.13**	-4.65**	1.19	-3.41**	295.63**	244.04**
18.	$P_4 \times P_7$	-25.29**	-40.73**	-18.35**	-35.05**	-7.37**	-26.67**	-5.26**	-18.18**	112.50**	45.49**
19.	$P_5 \times P_6$	-46.31**	-52.80**	-59.93**	-64.14**	3.89**	-4.54**	3.26**	-1.04	14.96**	-0.89
20.	$P_5 \times P_7$	-47.71**	-54.29**	29.64**	19.02**	2.40**	-5.00**	0.00	-6.36**	38.28**	16.83**
21.	$P_6 \times P_7$	-53.68**	-53.99**	-33.47**	-35.33**	4.85**	-10.00**	0.00	-10.00**	8.94**	-18.32**

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6. *and ** indicate significant at 5% and 1% level of probability respectively; HBP and HMP are Heterosis over Better parents and Mid Parents respectively.

Table 15 (Cont'd).

Sl. No.	Genotypes	Number of seeds siliqua^{-1}		1000 seed weight (g)		Days to 50% flowering		Days to 80% maturity		Seed yield plant^{-1} (g)	
	F_1 (Reciprocal)	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP
22.	$P_2 \times P_1$	-48.44**	-58.47**	17.37**	17.31**	17.33**	10.00**	9.09**	5.88**	185.47**	136.93**
23.	$P_3 \times P_1$	-5.35**	-12.46**	-4.77**	-15.08**	3.61**	0.00	2.89**	1.14	82.90**	50.75**
24.	$P_3 \times P_2$	-5.74**	-18.99**	2.87**	-8.30**	5.13**	-4.65**	3.57**	-1.14	130.69**	128.68**
25.	$P_4 \times P_1$	-51.87**	-63.26**	27.71**	13.72**	1.33**	-5.00**	0.61	-2.35**	181.94**	155.19**
26.	$P_4 \times P_2$	-36.25**	-40.65**	-7.50**	-17.60**	14.29**	14.29**	7.50**	7.50**	160.47**	99.87**
27.	$P_4 \times P_3$	-36.63**	-48.68**	-7.43**	-25.40**	0.00	-9.30**	0.00	-4.55**	145.56**	87.28**
28.	$P_5 \times P_1$	-3.93**	-11.93**	-8.92**	-13.25**	-8.03**	-18.18**	-2.76**	-8.33**	56.08**	29.61**
29.	$P_5 \times P_2$	-58.98**	-69.04**	-1.71**	-6.42**	11.20**	-6.49**	6.82**	-2.08*	199.05**	198.86**
30	$P_5 \times P_3$	-15.04**	-27.43**	9.59**	2.24**	-10.95**	-18.18**	-4.35**	-8.33**	98.87**	97.01**
31.	$P_5 \times P_4$	-22.02**	-43.90**	29.00**	10.08**	13.52**	-4.54**	8.52**	-0.52	170.95**	108.01**
32.	$P_6 \times P_1$	-34.92**	-37.86**	-0.92**	-15.07**	6.02**	2.33**	4.05**	2.27**	120.92**	111.23**
33.	$P_6 \times P_2$	-79.71**	-83.04**	-7.41**	-20.66**	2.56**	-6.98**	1.19	-3.41**	283.26**	230.25**
34.	$P_6 \times P_3$	-19.56**	-22.21**	-15.69**	-19.41**	11.63**	11.63**	7.09**	7.09**	78.57**	52.74**
35.	$P_6 \times P_4$	-68.19**	-74.89**	-28.72**	-44.47**	29.05**	17.05**	14.29**	9.09**	213.52**	172.63**
36.	$P_6 \times P_5$	-46.99**	-53.40**	-29.56**	-36.97**	-1.77**	-9.74**	-0.73	-4.86**	55.54**	34.10**
37.	$P_7 \times P_1$	-30.97**	-34.50**	4.48**	-8.22**	-8.00**	-23.33**	-5.64**	-16.36**	69.90**	23.66**
38.	$P_7 \times P_2$	-11.47**	-25.60**	20.08**	5.44**	-17.89**	-35.00**	-11.23**	-23.33**	28.98**	9.03**
39.	$P_7 \times P_3$	12.27**	9.29**	-31.80**	-32.96**	-2.43**	-16.25**	-2.36**	-12.13**	41.02**	20.07**
40.	$P_7 \times P_4$	-10.26**	-28.80**	8.98**	-13.31**	-11.58**	-30.00**	-8.77**	-21.21**	73.20**	18.58**
41.	$P_7 \times P_5$	-52.43**	-58.42**	-15.52**	-22.44**	-22.75**	-28.33**	-13.22**	-18.75**	-1.14	-16.48**
42.	$P_7 \times P_6$	-54.35**	-54.65**	9.85**	6.78**	-8.74**	-21.67**	-6.06**	-15.45**	47.98**	10.96**
	Minimum	-79.71	-83.04	-59.93	-64.14	-22.75	-35.00	-13.22	-23.33	-1.14	-18.32
	Maximum	29.56	18.77	57.52	34.42	29.05	18.75	14.29	10.88	352.37	245.01
	SE	0.92	1.06	0.13	0.15	0.46	0.54	0.75	0.87	0.82	0.95

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sar-17, P_6 = BARI Sar-15 and P_7 = BARI Sar-6. *and ** indicate significant at 5% and 1% level of probability respectively; HBP and HMP are Heterosis over Better parents and Mid Parents respectively.

Special × Tori-7 (9.09%) and the reciprocal F_1- BARI Sar-15 × Tori-7 (9.09%) (Table 15). The highest significant negative heterosis over the mid parent was found in F_1- BARI Sar-6 × BARI Sar-17 (-13.22%) followed by F_1- BARI Sar-6 × Brown Special (-11.23%) and F_1-BARI Sar-6 × Tori-7 (-8.77%). The highest significant positive heterosis over the mid parent was observed in F_1-Yellow Special × Tori-7 (14.29%) and reciprocal F_1- BARI Sar-15 × Tori-7 (14.29%) followed by F_1- BARI Sar-14 × Tori-7 (14.24%) and F_1- Brown Special × BARI Sar-15 (10.57%). The F_1-BARI Sar-6 × BARI Sar-15, F_1- BARI Sar-6 × BARI Sar-14, F_1-BARI Sar-17 × Yellow Special, F_1-Tori-7 × BARI Sar-6, F_1-Yellow Special × BARI Sar-6, F_1- Brown Special × BARI Sar-6, F_1-BARI Sar-14 × BARI Sar-6 showed the significant negative heterosis over both the better and mid parent (Table 15). Thus these could be used for producing genotypes with earliness. Ferdous (2019) reported the highest and the highly significant negative heterosis (-7.14%) and (-9.95%) for this trait over the better and the mid parent respectively. Huq (2006) and Turi *et al.* (2006) estimated the negative and the significant heterosis for this trait in the hybrids of *Brassica juncea*. Kumar *et al*. (2002) and Mahak *et al.* (2003b) also found the significant heterosis values for this trait over the mid parent and the better parent. Gupta *et al.* (2011) and Barupal *et al.* (2017) showed significant heterosis and heterobeltiosis for this trait in hybrids of Indian mustard.

2.1.3 Plant height

The F_1-BARI Sar-14 × Tori-7 showed the highly significant positive heterotic effect over the better parent (36.62%) followed by the reciprocal F_1-BARI Sar-15 × Brown Special (31.13%) and F_1-Tori-7 × BARI Sar-14 (30.97%) while the highly significant positive heterosis over the mid parent was observed in F_1- BARI Sar-14 × Tori-7 (38.60%) followed by the reciprocal F_1- BARI Sar-15 × Brown Special (33.18%) and F_1-Tori-7 × BARI Sar-14 (32.86%), F_1-Tori-7 × BARI Sar-15 (32.45%), reciprocal F_1- Brown Special × BARI Sar-14 (29.05%) and F_1- BARI Sar-15 × Tori-7 (26.56%) which could be used for exploiting heterosis where tallness is desirable. However, the highly significant negative heterotic effect over the better parent was observed in reciprocal F_1- BARI Sar-6 × Brown Special (-17.79%) preceded by the reciprocal F_1- BARI Sar-6 × Tori-7 (-15.77%) and F_1- BARI Sar-6 × BARI Sar-14 (-15.50%) while the significant negative heterotic effect over the mid parent was observed in reciprocal F_1- BARI Sar-6 × Brown Special (-5.30%) (Table 15). Ferdous (2019) and Wolko *et al.* (2019) also found the highly significant

positive heterotic effect over the mid and the better parent for plant height while Huq (2006) and Turi *et al.* (2006) estimated the negative and the significant heterosis for this trait in the hybrids of *Brassica juncea*. Gupta *et al.* (2011) showed the significant heterosis and heterobeltiosis for plant height. Yadav *et al.* (1998) observed the highest heterosis for plant height.

2.1.4 Number of primary branches plant^{-1}

Heterosis values for the number of primary branches plant^{-1} ranged from -30.45 to 97.76 and -38.44 to 76.47% over the mid parent and the better parent respectively. The reciprocal F_1-BARI Sar-15 × Brown Special showed the highest significant positive heterosis (97.76%) over the mid parent followed by the F_1-Tori-7 × BARI Sar-15 (87.46%) and F_1-Brown Special × Tori-7 (77.65%) while the reciprocal F_1- BARI Sar-17 × BARI Sar-14 (-30.45%) showed the highest significant negative heterosis over the mid parent preceded by the F_1-BARI Sar-17 × BARI Sar-15 (-16.04%) and F_1-BARI Sar-15 × BARI Sar-6 (-10.86%). On the other hand the F_1- Brown Special × Tori-7 (76.47%) showed the highest significant positive heterosis over the better parent followed by the reciprocal F_1- BARI Sar-15 × Brown Special (68.25%) and F_1-Tori-7 × Brown Special (66.84%) while the reciprocal F_1- BARI Sar-17 × BARI Sar-14 (-38.44%) showed the highest significant negative heterosis preceded by the F_1- BARI Sar-17 × BARI Sar-15 (-33.46%) and the reciprocal F_1- BARI Sar-6 × BARI Sar-17 (-26.72%) over the better parent (Table 15). Huq (2006) and Turi *et al.* (2006) also estimated the significant positive heterosis for this trait in most hybrids of *Brassica juncea*. Ferdous (2019) reported that the heterosis values ranged from -3.91 to 143.20 and 4.61 to 173.09 over the better parent and the mid parent respectively for this trait in the hybrids of *Brassica rapa*. Wolko *et al.* (2019) also reported the significant positive and negative heterosis for the number of primary branches plant^{-1} in hybrids of *Brassica napus*.

2.1.5 Number of secondary branches plant^{-1}

Most of the F_1s had the higher number of secondary branches than their parents. All of the forty four F_1s showed the highly significant mid parent heterosis in which thirty six F_1s showed the positive values ranged from 5.40% to 2000.00%. The highest significant and the positive mid-parent heterosis was observed in the reciprocal F_1- BARI Sar-17 × Yellow Special (2000.00%) followed by F_1- Brown Special × BARI Sar-15 (1009.24%) and F_1-BARI Sar-15 × Brown Special (958.82%). Therefore, these F_1s could be utilized for the

further development of heterotic *Brassica* hybrid. On the other hand, twenty six F_1s provided the significant and the positive better parent heterosis which ranged from 1.60 to 950.00%. Out of twenty six F_1s, the highest significant and positive better-parent heterosis was observed in the reciprocal F_1- BARI Sar-17 × Yellow Special (950.00%) followed by F_1- Brown Special × BARI Sar-15 (489.28%) and F_1- BARI Sar-15 × Brown Special (462.50%) (Table 15). Huq (2006) and Turi *et al.* (2006) estimated the significant positive heterosis in most of the hybrids of *Brassica juncea*. Ferdous (2019) reported the highly significant positive values over the mid and the better parents in most of the crosses. Wolko *et al.* (2019) also observed the significant positive and negative heterosis for this trait in the hybrids of *Brassica napus*.

2.1.6 Number of siliqua plant^{-1}

The significant positive heterosis values ranged from 11.40 % to 487.94 % over the mid parent and 21.79% to 457.33% over the better parent. The highest significant positive heterosis over the better parent was estimated in the reciprocal F_1- BARI Sar-15 × Brown Special (457.33%) followed by the F_1- Tori-7 × BARI Sar-15 (228.84%) and F_1- Brown Special × BARI Sar-15 (220.21%) while the highest significant positive heterosis over the mid patent was also found in the reciprocal F_1- BARI Sar-15 × Brown Special (487.94%) followed by the F_1-Tori-7 × BARI Sar-15 (296.15%) and the reciprocal F_1- BARI Sar-17 × Tori-7 (269.28%) whereas the significant negative heterosis was estimated only in the F_1- Yellow Special × BARI Sar-6 (-10.75% and -23.93%) over the mid and the better parents respectively (Table 15). Ferdous (2019) also reported the significant positive heterosis values ranged from 73% to 427.67 % over the better parent and 6.64% to 454.77% over the mid parent while Wolko *et al.* (2019) estimated the significant positive and the negative heterosis for this trait in the hybrids of *Brassica napus*. Rameeh (2019) also reported the significant positive high parent heterosis in most of the hybrids of *Brassica napus*.

2.1.7 Siliqua length

Out of forty two F_1s, forty one showed the significant heterosis over the mid parent whereas eighteen of them showed the positive and the significant heterosis. The highest and highly significant positive heterosis was observed in F_1- BARI Sar-17 × BARI Sar-14 (28.35% and 22.04%) over the both mid and better parents respectively and rest of the F_1s were observed either non-significant positive or significant negative heterosis (Table 15). The highly negative heterosis was found in F_1- BARI Sar-17 × Brown Special over the

better parent (-54.87%) and the mid parent (-50.12%) (Table 15). Ferdous (2019) reported that out of forty two F_1s, thirty eight showed the significant heterosis over the mid parent but only eighteen of them showed the significant positive heterosis. Kumar *et al.* (1990) and Wolko *et al.* (2019) also estimated the significant positive heterosis in the hybrids of *Brassica juncea* and *Brassica napus* respectively.

2.1.8 Number of seeds siliqua^{-1}

All the F_1s showed the highly significant negative heterosis except the F_1- BARI Sar-14 × BARI Sar-17 (29.56% and 18.77%) and the reciprocal F_1- BARI Sar-6 × Yellow Special (12.27% and 9.29%) over the mid and the better parents respectively where they showed the highly significant positive heterosis while the F_1- BARI Sar-14 × Yellow Special showed the non-significant positive heterosis (1.12%) over the mid parent only. The highest and the highly significant negative heterosis was recorded in the reciprocal F_1- BARI Sar-15 × Brown Special (-79.71% and -83.04%) preceded by the reciprocal F_1- BARI Sar-15 × Tori-7 (-68.19% and -74.89%) and F_1- BARI Sar-17 × Brown Special (-58.98% and -69.04%) over the mid and the better parents respectively (Table-15). Therefore, the F_1s that showed the highly significant positive heterosis over the mid parent as well as the better parent could be utilized for further evaluation. Ferdous (2019) also reported that most of the hybrids showed the significant negative heterosis over the mid and the better parents while Wolko *et al.* (2019) estimated significant positive heterosis in the hybrids of *Brassica napus*. Yadav *et al*. (1998) observed 54.1% heterosis over BP and 9.2% negative heterosis over SV in Siifolia × SM-I.

2.1.9 Thousand seed weight

Out of forty two F_1s, only nineteen showed the highly significant positive heterosis over the mid parent. Among them F_1-Tori-7 × BARI Sar-17 (57.52%) gave the highest significance positive heterosis followed by F_1-Yellow Special × Tori-7 (45.66%), F_1-Brown Special × Tori-7 (35.75%) and F_1- BARI Sar-17 × BARI Sar-6 (29.64%) while the highest significant negative heterosis over the mid parent was estimated in F_1- BARI Sar-17 × BARI Sar-15 (-59.93%) preceded by F_1-Yellow Special × BARI Sar-6 (-55.26%) and F_1- BARI Sar-14 × BARI Sar-6 (-41.93%). Similarly, only fourteen showed the highly significant positive heterosis over the better parent. Among them the F_1-Tori-7 × BARI Sar-17 (34.42%) showed the highest significant positive heterosis followed by the F_1-Brown Special × Tori-7 (20.92%), F_1- BARI Sar-17 × BARI Sar-6 (19.02%) while the

highest significant negative heterosis over the better parent was recorded in F_1- BARI Sar-17 × BARI Sar-15 (-64.14%) preceded by F_1-Yellow Special × BARI Sar-6 (-56.03%) and F_1- BARI Sar-14 × BARI Sar-6 (-48.99%) (Table 15). Ferdous (2019) reported the highest significant positive heterosis over the mid parent (41.80 %) and (32.21 %) over the better parent while Wolko *et al.* (2019) estimated the significant positive and negative heterosis for this trait in the hybrids of *Brassica napus*. Gupta *et al.* (2011) showed the significant heterosis and heterobeltiosis for this trait in different crosses. Dar *et al.* (2012) estimated desirable mid and better parent heterosis for this trait in most of the *Brassica rapa* hybrids.

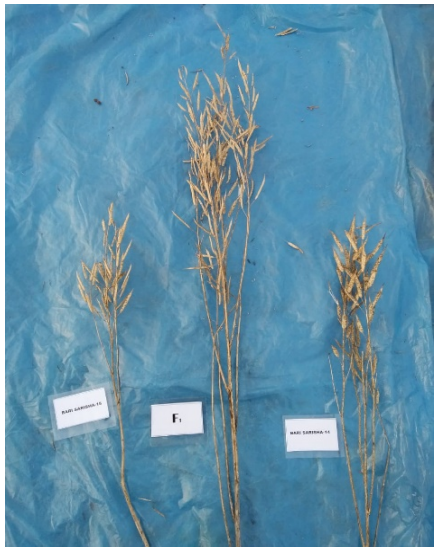
2.1.10 Seed yield plant^{-1}

For this trait out of forty two F_1s, thirty eight showed the highly significant positive heterosis over the better parent and forty one F_1s showed the highly significant positive heterosis over the mid parent. The F_1-Yellow Special × Tori-7 represented the highest and the highly significant positive heterosis for the both mid parent (352.37%) and the better parent (245.01%) followed by F_1-Tori-7 × BARI Sar-15 (295.63% and 244.04% respectively) and F_1- BARI Sar-15 × Brown Special (283.26% and 230.25% respectively) (Table-15). Therefore, these combinations could be selected for the improvement of yield performance. Hybrid vigours in F_1 plants developed from different crosses and reciprocal crosses among selected parents at maturity stage were presented in Plate 15. Ferdous (2019) also represented the highest and the highly significant and positive heterosis for seed yield plant^{-1} over the both mid parent (263.70%) and better parent (191.49 %) in *Brassica rapa*. Rameeh (2019) reported the significant positive high parent heterosis for this trait in most of the hybrids of *Brassica napus*. Singh *et al.* (2017) observed the significant positive standard and better parent heterosis for the trait seed yield plant^{-1} in yellow sarson. Bharti *et al.* (2018) reported the significant positive heterosis for this trait in most of the hybrids of *Brassica juncea*.

F_1 (BARI Sar-14 × Yellow Special)

F_1 (Yellow Special × BARI Sar-14)

F_1 (BARI Sar-14 × BARI Sar-15)



F_1 (BARI Sar-15 × BARI Sar-14)

F_1 (BARI Sar-17 × BARI Sar-15)

F_1 (BARI Sar-15 × BARI Sar-17)

F_1 (Yellow Special × BARI Sar-15)

F_1 (BARI Sar-15 × Yellow Special)

Plate 15. Hybrid vigours in some F_1s developed from 7×7 full diallel crosses among different *Brassica rapa* genotypes at maturity stage

2.2. Combining ability analysis

2.2.1 GCA and SCA Variances

Results from the analysis of variance over GCA and SCA effects for yield and yield contributing components in 7 × 7 full diallel crosses among seven *Brassica rapa* genotypes are presented in Table 16. The significant mean squares for general and specific combining abilities for studied characters indicated significant differences that suggested presence of notable genetic variability among the GCA as well as SCA effects.

2.2.2 General combining ability (GCA) effects

The GCA effects represents the additive nature and magnitude of gene action. A parent with the high GCA variances is a better parent for creating the high specific combination.

The magnitude and direction of the significant GCA effects for seven parents provided the meaningful comparisons and would give clue to the future breeding program. The higher significant GCA effects of a parent represented it as a good general combiner, whereas the parents that possessed the significant but negative or undesirable GCA effects were designated as poor combiners (Ahmed *et al.*, 2014). But in case of days to 50% flowering and 80% maturity and plant height, negative GCA effects are desirable. The estimated GCA effects for seven selected parents were presented in Table 17.

2.2.2.1 Days to 50% flowering

For days to 50% flowering, a significant negative GCA effect was desirable. The highest significant negative GCA effect was observed in the parent Brown Special (-4.06**) preceded by Tori-7 (-2.23**) and BARI Sar-14 (-1.75**) for this trait. Thus there was an opportunity to shorten the duration by using these parents while the highest significant positive GCA effect was observed in the parent BARI Sar-6 (4.20**) followed by BARI Sar-17 (2.83**) and BARI Sar-15 (1.19**) for this trait. Thus they were not suitable for selection for earliness. The parent Yellow Special showed the non-significant negative GCA effect (-0.17) (Table 17). Chowdhury *et al.* (2004), Singh *et al.* (2000) and Verma (2011) found earliness in *Brassica rapa,* in *Brassica campestris* and *Brassica Juncea* respectively. Aghao *et al.* (2010), Singh *et al*. (2010), Gupta *et al.* (2011) and Nasrin *et al.* (2011) also showed the significant GCA effects among the parents.

2.2.2.2 Days to 80% maturity

For the trait days to 80% maturity, also a significant negative GCA effect is desirable. The

Table 16. Analysis of variance (MS value) including GCA and SCA effects for yield and yield contributing components in 7×7 full diallel crosses among *Brassica rapa* genotypes

Source of variation	df	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length	Number of seeds siliqua^{-1}	Thousand seed weight	Days to 50% flowering	Days to 80% maturity	Seed yield plant^{-1}
Progeny	48	393.69	14.47	116.97	112986	0.80	118.02	2.47	86.29	104.14	73.60
Replication	2	43.14	2.58	0.69	406	0.62	2.29	0.00	62.84	60.22	5.21
GCA	6	361.99**	14.42**	161.26**	123871**	0.58**	139.25**	0.14**	120.71**	140.33**	30.62**
SCA	21	150.84**	4.99**	35.49**	42792**	0.27**	41.84**	1.02**	11.79**	16.48**	34.41**
Reciprocal	21	45.69**	1.92**	7.57**	7901**	0.17**	8.29**	0.82**	19.47**	22.77**	12.91**
Error	96	2.24	0.37	0.31	19	0.02	0.57	0.01	0.14	0.38	0.45
GCA : SCA		2.40:1	2.89:1	4.54:1	2.89:1	2.15:1	3.33:1	0.14:1	10.24:1	8.52:1	0.89:1

*** and ** significant at 5% and 1% level of probability, respectively**

Table 17. General combining ability (GCA) effects of seven *Brassica rapa* genotypes for yield and related traits in 7×7 full diallel crosses.

Parents	Days to 50% flowering	Days to 80% maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length	Number of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
BARI Sarisha-14	-1.75**	-1.72**	-3.39**	-0.89**	-2.67**	-84.63**	-0.04	2.64**	-0.05	-1.75**
Brown Special	-4.06**	-4.29**	-0.93*	0.73**	3.05**	71.02**	0.03	-3.20**	0.11*	2.39**
Yellow Special	-0.17	-0.24	-2.25**	-0.87**	-2.66**	-70.24**	0.21**	2.95**	0.05	0.05
Tori-7	-2.23**	-2.42**	-1.42**	1.18**	5.95**	156.91**	-0.15**	-4.20**	-0.16**	1.58**
BARI Sarisha-17	2.83**	2.77**	-5.05**	-1.36**	-1.76**	-73.44**	-0.04	3.39**	0.00	-0.96**
BARI Sarisha-15	1.19**	1.00**	3.00**	0.82**	0.67**	54.65**	-0.30**	-2.06**	-0.05	-0.55*
BARI Sarisha-6	4.20**	4.90**	10.05**	0.38*	-2.57**	-54.27**	0.29**	0.47*	0.10*	-0.75**
SE (gi)	0.09	0.15	0.37	0.15	0.14	1.09	0.03	0.19	0.03	0.17

*** and ** significant at 5% and 1% level of probability, respectively**

Tori-7
(For more number of primary, secondary branches and siliqua plant^{-1})

A

Brown Special
(For earliness, thousand seed weight and seed yield plant^{-1})

B

BARI Sarisha-17
(For dwarfness and more seeds siliqua^{-1})

C

Plate 16. The siliqua of top three good general combiner parents for earliness, yield and other yield contributing traits.

highest significant negative GCA effect was observed in the parent Brown Special (-4.29**) (Plate 16 B) preceded by Tori-7 (-2.42**) and BARI Sar-14 (-1.72**) for this trait. Thus there was an opportunity to shorten the duration by using this parents. The highest significant positive GCA effect was observed in the parent BARI Sar-6 (4.90**) followed by BARI Sar-17 (2.77**) and BARI Sar-15 (1.00**) for this trait. Therefore, there was no opportunity to shorten the duration by using these parents. The parent Yellow Special showed the non-significant negative GCA effect (-0.24) (Table 17). Singh *et al.* (2000), Chowdhury *et al.* (2004) and Verma (2011) reported earliness in YSC-68 in *Brassica campestris*, in Din-2 in *Brassica rapa* and in RC 832 in *Brassica Juncea* respectively. Aghao *et al.* (2010), Singh *et al*. (2010) and Nasrin *et al.* (2011) also observed the significant GCA effects for days to maturity.

2.2.2.3 Plant height

Out of seven parents four parents showed the highly significant negative GCA effect and one parent showed the significant negative GCA effects while other two parents showed the highly significant positive GCA effects. The highest negative and the highly significant GCA effects (-5.05**) was found in BARI Sar-17 (Plate 16 C) preceded by BARI Sar-14 (-3.39**), Yellow Special (-2.25**) and Tori-7 (-1.42**). The other parent which represented negative and significant GCA was Brown Special (-0.93*) while the highest positive and the highly significant GCA effects (10.05**) was found in BARI Sar-6 preceded by BARI Sar-15 (3.00**). Parents with the negative and the highly significant GCA effects were considered as good general combiner for this trait aimed to promote desirable plant height in their crosses (Table 17). Chowdhury *et al.* (2004) and Singh *et al.* (2010) also observed dwarfness in *Brassica campestris* and in *Brassica juncea* respectively. Aghao *et al.* (2010) and Sincik *et al.* (2011) revealed GCA effects was highly significant for plant height.

2.2.2.4 Number of primary branches plant^{-1}

For number of primary branches plant^{-1} the highly significant and the highest positive GCA effects were observed in Tori-7 (1.18**) (Plate 16 A) followed by BARI Sar-15 (0.82**) and Brown Special (0.73**) while BARI Sar-6 showed the significant and positive GCA effects (0.38*) thus they could be considered as the suitable general combiner for this trait. Others parents demonstrated the highly significant and negative GCA effects. The highest negative GCA effects were observed in BARI Sar-17 (-1.36**) followed by BARI Sar-14 (-

0.89**) and Yellow Special (-0.87**) (Table 17). So, they should be avoided in breeding purpose for this trait. Singh *et al.* (2000) and Chowdhury *et al*. (2004) also obtained the highest number of primary branches plant^{-1} in *Brassica juncea* and in *Brassica rapa* respectively. Gupta *et al.* (2011) and Nasrin *et al.* (2011) showed the significant GCA effects among the parents for this trait.

2.2.2.5 Number of secondary branches plant^{-1}

For this trait the highly significant and the highest positive GCA effects were observed in Tori-7 (5.95**) (Plate 16 A) followed by Brown Special (3.05**) and BARI Sar-15 (0.67**) thus they could be considered as the suitable general combiner for this trait. The highly significant negative GCA effects were observed in BARI Sar-14 (-2.67**) followed by Yellow Special (-2.66**), BARI Sar-6 (-2.57**) and BARI Sar-17 (-1.76**) (Table 17). So, they should be avoided in breeding purpose for this trait. Singh *et al.* (2000) and Chowdhury *et al.* (2004) also obtained the highest number of secondary branches plant^{-1} in *Brassica juncea* and in *Brassica rapa* respectively. Gupta *et al.* (2011) showed the significant GCA effects among the parents for this trait.

2.2.2.6 Number of siliqua plant^{-1}

All the parents had highly significant GCA effects of which four were negative and the others had positive values. The parents Tori-7 exhibited the highest positive (156.91**) and the highly significant GCA effects (Plate 16 A) followed by Brown Special (71.02**) and BARI Sar-15 (54.65**) for this trait. Therefore, these three parents could be selected as the best general combiner to improve this trait (Table 17). While, the highest negative and highly significant GCA values were recorded in BARI Sar-14 (-84.63**) preceded by BARI Sar-17 (-73.44**), Yellow Special (-70.24**) and BARI Sar-6 (-54.27**). Chowdhury *et al.* (2004) and Singh *et al.* (2000) also recorded the highest number of siliqua plant^{-1} in *Brassica rapa* and in *Brassica campestris* respectively. Aghao *et al.* (2010), Gupta *et al.* (2011), Rameeh (2011d) and Sincik *et al.* (2011) revealed that the GCA effects was highly significant for siliqua plant^{-1} while Turi *et al.* (2011) reported the non-significant GCA effects for this trait. Atikunnaher, *et al.* (2017) reported that based on GCA effects the best general combiners was Nap-9908 for this trait.

2.2.2.7 Siliqua length

The parents BARI Sar-6 exhibited the highest positive (0.29**) and the highly significant GCA effects followed by Yellow Special (0.21**). So, these two parents could be selected

to improve this trait in *Brassica rapa* (Table 17). Whereas, the highest negative and the highly significant GCA values were recorded in BARI Sar-15 (-0.30**) preceded by Tori-7 (-0.15**). In rest of the parents no significant positive GCA effects was observed for this trait. Thus there was no opportunity to improve the trait by using these parents. Sheikh and Singh (1998) and Acharya and Swain (2004) obtained the maximum siliqua length in *Brassica juncea*. Turi *et al.* (2011) reported the non-significant GCA effects for this trait.

2.2.2.8 Number of seeds siliqua^{-1}

The parent BARI Sar-17 exhibited the highest positive (3.39**) and the highly significant GCA effects (Plate 16 C) followed by Brown Special (2.95**) and BARI Sar-14 (2.64**) for this trait. So these parents could be selected as the best general combiner to improve this trait (Table 17). On the other hand, the highest negative and the highly significant GCA values were recorded in Tori-7 (-4.20**) preceded by Brown Special (-3.20**) and BARI Sar-15 (-2.06**). Turi *et al.* (2011) also reported the non-significant GCA effects for this trait. Atikunnaher, *et al.* (2017) reported that based on GCA effects the best general combiners was Nap-9908 for seeds siliqua^{-1}. Singh (2000) and Chowdhury *et al.* (2004) observed the highest number of seeds siliqua^{-1} in *Brassica rapa* and in *Brassica campestris* respectively.

2.2.2.9 Thousand seed weight

The significant and the highest positive GCA effects were observed in the parent Brown Special (Plate 16 B) (0.11*) followed by BARI Sar-6 (0.10*) for thousand seed weight. So these parents could be used to improve this traits while Tori-7 showed the highest negative and the highly significant GCA values (-0.16**). Rest of the parents showed the non-significant GCA effects (Table 17). Thus there was no opportunity to improve this trait by using these parents due to their poor GCA effects. Chowdhury *et al.* (2004) also reported the highest seed weight in *Brassica rapa*. Aghao *et al.* (2010), Azizinia (2011), Gupta *et al.* (2011), Nasrin *et al.* (2011), Turi *et al.* (2011) and Azizinia (2012) observed that thousand seed weight showed the significant positive GCA effects.

2.2.2.10 Seed yield plant^{-1}

The highly significant and the highest positive GCA effects was observed in Brown Special (2.39**) (Plate 16 B) followed by Tori-7 (1.58**). Therefore, these parents could be selected as promising general combiner for high yield potential for this trait. However, the parent Yellow Special (0.05^{NS}) showed the non-significant but positive GCA effects. On the

other side, three parents BARI Sar-14 (-1.75**), BARI Sar-17 (-0.96**) and BARI Sar-6 (-0.75**) showed the highly significant but negative GCA effects while BARI Sar-15 (-0.55*) showed the significant but negative GCA effect for this trait (Table 17) indicated these parents were not good general combiner for improving this traits. Singh *et al*. (2010), Azizinia (2011), Gupta *et al.* (2011), Nasrin *et al.* (2011), Rameeh (2011d), Turi *et al.* (2011), Vaghela *et al.* (2011) and Azizinia (2012) also reported that seed yield plant^{-1} showed the significant GCA effects. Arifullah *et al.* (2012), Atikunnaher, *et al.* (2017), Channa *et al.* (2018) and Singh *et al*. (2019) reported that the seed yield plant^{-1} in Indian mustard also showed the significant and positive GCA effects.

2.2.3 Specific combining ability (SCA) effects

The SCA effects significant the role of non-additive i.e. dominance and/or epistatic gene action in the expression of the characters. The high SCA effects leading to the high performance of some specific cross combinations. For this reason, it relates to a particular cross. The high SCA effects might arise not only on cross involving high × high combinations, but also in those involving low × high and also from low × low. Thus in practice, some of the low combiners should also be accommodated in hybridization program. The SCA effects represent mainly dominance, additive × dominance, dominance × dominance effects. The crosses showing SCA effects involving parents with good GCA could be exploited. Therefore the magnitude and direction of the significant effects for seven selected parents provide meaningful comparisons and would give a clue to the future breeding program. The SCA effects for ten yield and related characters of the parental lines were presented in Table 18.

2.2.3.1 Days to 50% flowering

The negative estimates are desirable for days to 50% flowering, as they are associated with earliness. The highly significant and the highest negative SCA effect was observed in reciprocal F_1- BARI Sar-6 × Brown Special (-12.29**) preceded by F_1- BARI Sar-6 × Tori-7 (-9.79**), F_1- BARI Sar-6 × BARI Sar-14 (-6.29**) and F_1- BARI Sar-17 × BARI Sar-14 (-6.04**) for this trait (Table 18). Therefore, F_1- BARI Sar-6 × Brown Special was considered as best combination for early flowering. Singh *et al.* (2000) also observed earliness in *Brassica campestris*. Gupta *et al.* (2011) showed the significant SCA effects in hybrids for this trait.

Table 18. Specific combining ability (SCA) effects of F_1s obtained from 7 × 7 full diallel crosses among seven *Brassica rapa* genotypes for yield and yield contributing traits

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length	Number of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
	Crosses										
1.	$P_1 \times P_2$	-0.38	-0.58	13.18**	1.71**	7.74**	212.48**	-0.04	-10.27**	-0.16*	5.41**
2.	$P_1 \times P_3$	0.78**	0.92*	3.84**	-0.19	-0.02	19.71**	0.20*	1.49**	0.73**	1.17**
3.	**$P_1 \times P_4$**	1.87**	2.04**	14.52**	2.59**	8.26**	290.16**	-0.04	-10.98**	0.24**	5.00**
4.	$P_1 \times P_5$	3.12**	2.92**	-6.11**	-1.73**	0.78*	-26.56**	0.55**	9.89**	0.09	1.29**
5.	$P_1 \times P_6$	2.12**	2.42**	3.59**	0.72	0.33	40.00**	0.00	-5.86**	0.09	0.48
6.	$P_1 \times P_7$	5.62**	5.92**	16.31**	3.34**	1.84**	96.29**	-0.09	-6.68**	-0.41**	3.44**
7.	$P_2 \times P_3$	3.25**	3.57**	1.80	-0.31	-7.58**	-138.19**	0.18*	5.66**	0.03	-0.95*
8.	$P_2 \times P_4$	1.25**	1.57**	-7.48**	0.60	-1.32**	-95.19**	-0.09	1.20*	-0.49**	-3.52**
9.	$P_2 \times P_5$	9.75**	10.07**	0.26	-1.70**	-3.17**	-81.23**	-0.98**	1.13*	-0.50**	-0.66
10.	**$P_2 \times P_6$**	6.97**	7.51**	12.49**	2.77**	9.85**	361.48**	-0.66**	0.11	0.63**	6.17**
11.	$P_2 \times P_7$	4.25**	4.23**	4.00**	-1.00*	-7.53**	-181.18**	0.71**	7.06**	0.56**	-4.77**
12.	**$P_3 \times P_4$**	0.63*	0.47	5.97**	2.14**	12.36**	365.22**	-0.70**	-10.60**	0.39**	8.01**
13.	$P_3 \times P_5$	0.97**	0.97*	-0.34	0.86*	1.54**	-1.69	-0.05	0.24	-0.18*	-0.60
14.	$P_3 \times P_6$	1.97**	2.09**	5.35**	1.44**	-0.09	22.30**	-0.62**	-5.06**	-0.45**	-2.45**
15.	$P_3 \times P_7$	5.59**	6.30**	9.05**	0.41	0.97**	14.96**	0.33**	1.04*	-1.39**	-1.30**

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15 and P_7 = BARI Sarisha-6. * and ** significant at 5% and 1% level of probability, respectively.

Table 18 (Cont'd).

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length	Number of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
	Crosses										
16.	$P_4 \times P_5$	6.58**	7.57**	-1.69	-2.00**	-3.84**	-85.39**	0.42**	6.54**	1.27**	-0.11
17.	$P_4 \times P_6$	5.74**	5.32**	15.66**	2.16**	0.39	101.65**	-0.28**	0.35	-0.70**	1.17**
18.	$P_4 \times P_7$	3.08**	3.16**	10.31**	0.16	-9.41**	-195.78**	0.79**	7.19**	0.00	-1.34**
19.	$P_5 \times P_6$	-2.38**	-2.41**	9.88**	1.27**	-1.72**	15.03**	-0.17*	-8.58**	-1.43**	-2.13**
20.	$P_5 \times P_7$	-0.04	0.61	20.95**	2.41**	-0.66	36.33**	0.00	-9.56**	0.76**	0.13
21.	$P_6 \times P_7$	3.72**	3.96**	5.31**	-1.98**	-3.91**	-125.24**	0.39**	-1.35**	0.52**	-1.13*
	Reciprocal crosses										
22.	$P_2 \times P_1$	4.25**	4.57**	8.26**	-1.55**	-3.72**	-98.82**	-0.19*	1.42**	-0.50**	-2.88**
23.	$P_3 \times P_1$	-2.36**	-2.03**	1.55	-0.24	-0.06	-9.07**	-0.31**	0.89	0.52**	-2.44**
24.	$P_3 \times P_2$	-4.53**	-4.53**	4.42**	2.91**	3.84**	144.33**	-0.18*	-6.64**	0.15*	3.73**
25.	**$P_4 \times P_1$**	2.83**	3.45**	10.57**	-1.57**	-8.98**	-192.92**	0.17*	2.73**	0.45**	-1.68**
26.	$P_4 \times P_2$	-2.42**	-2.18**	-6.52**	-0.30	-7.11**	-266.98**	0.28**	3.21**	0.06	-1.91**
27.	**$P_4 \times P_3$**	4.74**	4.82**	4.30**	-1.97**	-4.86**	-89.08**	0.03	3.71**	0.82**	4.94**
28.	$P_5 \times P_1$	-6.04**	-6.08**	-2.79**	-0.80*	-1.05**	-48.95**	0.54**	8.39**	-0.02	-0.29
29.	$P_5 \times P_2$	-4.04**	-4.08**	8.50**	2.49**	6.46**	207.68**	-0.83**	-12.06**	-0.27**	6.04**
30.	$P_5 \times P_3$	-5.04**	-5.08**	5.28**	1.84**	-0.26	4.70	0.45**	-0.65	-0.07	1.43**
31.	$P_5 \times P_4$	-3.54**	-2.83**	5.59**	3.09**	11.57**	375.31**	0.20*	-8.67**	0.95**	5.00**

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15 and P_7 = BARI Sarisha-6. * and ** significant at 5% and 1% level of probability, respectively.

Table 18 (Cont'd).

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length	Number of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
	Reciprocal crosses										
32.	$P_6 \times P_1$	-3.77**	-3.04**	-9.21**	-2.71**	-6.37**	-238.56**	0.51**	3.57**	0.10	-1.91**
33.	**$P_6 \times P_2$**	-3.55**	-3.10**	4.61**	2.60**	14.62**	394.21**	-0.00	-2.17**	0.98**	12.06**
34.	$P_6 \times P_3$	-0.77**	-0.42	-5.16**	-1.94**	-6.75**	-227.50**	0.40**	4.97**	-0.23**	-1.23**
35.	$P_6 \times P_4$	-1.11**	-1.54**	6.82**	2.89**	10.95**	306.17**	0.01	-3.93**	-0.91**	5.46**
36.	$P_6 \times P_5$	0.89**	1.13**	-6.24**	-3.09**	-6.58**	-241.15**	0.34**	2.34**	-1.31**	-2.94**
37.	$P_7 \times P_1$	-6.29**	-7.34**	-10.59**	0.79*	1.64**	35.58**	-0.76**	-2.34**	-0.72**	1.44**
38.	$P_7 \times P_2$	-12.29**	-14.17**	-17.98**	-0.29	3.73**	69.41**	0.19*	-0.30	0.59**	1.51**
39.	$P_7 \times P_3$	-3.17**	-4.00**	-15.56**	-2.09**	0.81*	-16.97**	0.17*	5.98**	-1.48**	0.31
40.	$P_7 \times P_4$	-9.79**	-11.50**	-12.63**	1.77**	7.64**	226.60**	-0.10	-2.18**	-0.51**	3.34**
41.	$P_7 \times P_5$	-2.79**	-3.65**	-9.27**	-1.07**	0.97**	-2.00	-0.66**	-3.73**	0.56**	-0.29
42.	$P_7 \times P_6$	-2.29**	-3.84**	-8.79**	-1.10**	2.58**	92.62**	-0.79**	-6.43**	0.21**	-0.73
	SE(sij)	0.23	0.38	0.92	0.37	0.34	2.70	0.08	0.46	0.07	0.41
	SED(sij-sik)	0.35	0.57	1.39	0.56	0.51	4.06	0.12	0.70	0.10	0.62
	SED(sij-skl)	0.32	0.52	1.27	0.51	0.47	3.71	0.11	0.64	0.09	0.57

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori -7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15 and P_7 = BARI Sarisha-6. * and ** significant at 5% and 1% level of probability, respectively.

A.

BARI Sarisha-6 × Brown Special
(For dwarfness and earliness)

B.

BARI Sarisha-15 × Brown Special
(For number of secondary branches, siliqua and seed yield plant^{-1})

C.

BARI Sarisha-14 × BARI Sarisha-17
(For more seeds siliqua^{-1})

Plate 17. Siliqua of top three F_1s having good SCA effects for earliness, yield and other yield contributing traits.

2.2.3.2 Days to 80% maturity

For the trait days to 80% maturity, a significant negative SCA effect is desirable for shorter growth duration. The highest significant negative SCA effect was observed in the reciprocal F_1-BARI Sar-6 × Brown Special (-14.17**) preceded by F_1- BARI Sar-6 × Tori-7 (-11.50**), F_1- BARI Sar-6 × BARI Sar-14 (-7.34**) and F_1- BARI Sar-17 × BARI Sar-14 (-6.08**) for this trait (Table 18). Thus these parents could be useful to shorten the duration and F_1- BARI Sar-6 × Brown Special was considered as the best combination for earliness (Plate 17 A). Chowdhury *et al.* (2004) and Singh *et al.* (2000) also observed earliness in M-27 x Din-2 and in SS-3 x SS-1 in *Brassica rapa* respectively. Haung *et al.* (2009) reported the non-significant SCA for this trait.

2.2.3.3 Plant height

Out of forty two F_1s, thirteen showed the highly significant and the negative SCA effects. The reciprocal F_1-BARI Sar-6 × Brown Special (-17.98**) preceded by F_1- BARI Sar-6 × Yellow Special (-15.56**), F_1- BARI Sar-6 × Tori-7 (-12.63**) and F_1- BARI Sar-6 × BARI Sar-14 (-10.59**) showed the highly significant and the highest negative SCA effects for this. So, these F_1s could be used as the suitable combinations for dwarfness and the reciprocal F_1- BARI Sar-6 × Brown Special was found as the best combination for this purpose (Plate 17 A). The highly significant and the highest positive SCA effect was observed in F_1- BARI Sar-14 × BARI Sar-6 (16.31**) (Table 18). Yadav *et al.* (2010) also observed the significant negative SCA effects in different hybrids. Haung *et al.* (2009), Sincik *et al.* (2011) and Inayat *et al.* (2019) reported the significant SCA effects for plant height in different mustard genotypes. Chowdhury *et al.* (2004) and Acharya and Swain (2004) observed dwarfness in *Brassica rapa* and in *Brassica juncea* respectively.

2.2.3.4 Number of primary branches plant^{-1}

Out of forty two F_1s sixteen showed the highly significant and positive SCA effects for this trait. F_1- BARI Sar-14 × BARI Sar-6 (3.34**) was found to be the best to improve this trait as it showed the highly significant and the highest positive SCA effects while the reciprocal F_1-BARI Sar-15 × BARI Sar-17 (-3.09**) showed the highly significant and negative SCA effects (Table 18). Haung *et al.* (2009), Yadav *et al.* (2010), Gupta *et al.* (2011), Nasrin *et al.* (2011) and Inayat *et al.* (2019) also observed the significant SCA effects for this trait in different hybrids. Atikunnaher, *et al.* (2017) and Arifullah *et al.* (2012) reported, Nap-9905×Nap-205 and BRS-2 × UCD-8/4 were the best combiner based on SCA effects for this

trait. Chowdhury *et al.* (2004) and Singh *et al*. (2000) also estimated the more number of primary branches plant^{-1} in *Brassica rapa* and *Brassica campestris* respectively.

2.2.3.5 Number of secondary branches plant^{-1}

Out of forty two F_1s seven produced the non-significant, two produced the significant and rest of thirty three produced the highly significant SCA effects including seventeen positive and sixteen negative values ranged from -9.41** to 14.62**. The reciprocal F_1- BARI Sar-15 × Brown Special possessed the highest positive and the highly significant SCA effect (14.62**) followed by the F_1-Yellow Special × Tori-7 (12.36**). So, they could be selected as the best specific combiner for this trait and could be used in further breeding program for good hybrid combination (Plate 17 B). On the other hand, the reciprocal F_1-Tori-7 × BARI Sar-6 showed the highly significant but negative SCA effects (-9.41**) preceded by F_1-Tori-7 × BARI Sar-14 (-8.98**) thus they were poor specific combiner for this trait and are not suitable for hybrid production (Table 18). Haung *et al.* (2009), Yadav *et al.* (2010), Gupta *et al.* (2011) and Nasrin *et al.* (2011) also observed the significant SCA effects for this trait in different hybrids. Chowdhury *et al.* (2004) and Singh *et al.* (2000) also found the maximum number of secondary branches plants^{-1} in *Brassica rapa* and *Brassica campestris* respectively. Atikunnaher *et al.* (2017) represented that, Nap-9901×Nap-205 was the best specific combiner for this trait based on its SCA effects.

2.2.3.6 Number of siliqua plant^{-1}

Out of forty two F_1s, thirty nine F_1s found to had under the highly significant SCA effects ranged from -266.98** to 394.21** of which twenty one with positive and eighteen with negative values while remaining three crosses showed the non-significant SCA effects. The reciprocal F_1-BARI Sar-15 × Brown Special possessed the highest positive and the highly significant SCA effect (394.21**) followed by F_1-BARI Sar-17 × Tori-7 (375.31**) and the F_1-Yellow Special × Tori-7 (365.22**). Therefore, they could be considered as the best specific combiner for this trait and could be selected for the future breeding program to obtain higher number of siliqua plant^{-1} (Plate 17 B). While the reciprocal F_1-Tori-7 × Brown Special showed the highest negative and the highly significant SCA effect (-266.98**) preceded by F_1-BARI Sar-15 × BARI Sar-17 (-241.15**) and F_1- BARI Sar-15 × BARI Sar-14 (-238.56**) (Table 18). So, they could be avoided for the future breeding program of this trait. Haung *et al.* (2009), Yadav *et al.* (2010), Gupta *et al.* (2011), Nasrin *et al.* (2011), Rameeh (2011d), Sincik *et al.* (2011) also revealed the significant SCA effects for this

trait. Chowdhury *et al.* (2004) and Singh *et al.* (2000) estimated the maximum siliqua in Sampad × Din-2 in *Brassica rapa* and in YSP-842 × SS-3 in *Brassica campestris* respectively. Rameeh (2012) reported that the non-additive genetic effects controlled this trait. Arifullah *et al.* (2012) and Atikunnaher, *et al.* (2017) reported BRS-2 × UCD-8/4 and Nap-9908 × Nap-9901 showed the best desired SCA effects for this trait and could be utilized in future breeding program.

2.2.3.7 Siliqua length

Out of forty two F_1s, twenty two found to be had the highly significant SCA effects ranged from -0.98** to 0.79** of which twelve with positive and ten with negative values. Nine F_1s showed the significant SCA effects ranged from -0.19* to 0.20* out of which six with positive and three with negative values. Remaining eleven F_1s showed the non-significant SCA effects and thus there was no opportunity to improve siliqua length by using these F_1s. The F_1-Tori-7 × BARI Sar-6 possessed the highest positive and the highly significant SCA effect (0.79**) followed by F_1- Brown Special × BARI Ssr-6 (0.71**) and F_1- BARI Sar-14 × BARI Sar-17 (0.55**) (Table 18). So, they could be used as the best specific combiner for this trait. Arifullah *et al.* (2012), Atikunnaher, *et al.* (2017) and Inayat *et al.* (2019) reported the significant SCA effects for this trait in different mustard genotypes while Huq (2006) showed that BINA Sar-6 × Tori-7 was not good for improving this trait in *Brassica rapa*.

2.2.3.8 Number of seeds siliqua^{-1}

For this trait out of forty two F_1s, thirty three showed the highly significant SCA effects ranged from -12.06** to 9.89** of which fifteen with positive and eighteen with negative values. Three F_1s showed the significant and positive SCA effects ranged from 1.04* to 1.20*. Remaining six F_1s showed the non-significant SCA effects and thus they could be avoided to improve this trait. The F_1-BARI Sar-14 × BARI Sar-17 showed the highest positive and the highly significant SCA effects (9.89**) followed by the reciprocal F_1-BARI Sar-17 × BARI Sar-14 (8.39**) and F_1-Tori-7 × BARI Sar-6 (7.19**) (Table 18). So, they could be considered as the best specific combiner for this trait (Plate 17 C). Haung *et al.* (2009), Sincik *et al.* (2011), Arifullah *et al.* (2012), Atikunnaher *et al.* (2017) and Inayat *et al.* (2019) also reported the significant SCA effects for this trait in different mustard genotypes. Chowdhury *et al.* (2004) and Singh *et al.* (2000) revealed the highest number of seeds siliqua^{-1} in *Brassica rapa* and *Brassica campestiris* respectively.

2.2.3.9 Thousand seed weight

In case of thousand seed weight thirty one F_1s showed the highly significant SCA effects ranged from -1.48** to 1.27** of which sixteen with positive and fifteen with negative values. Three F_1s showed the significant SCA effects ranged from -0.18* to 0.15*. Remaining eight F_1s showed the non-significant SCA effects and thus there was no opportunity to improve this trait by using these F_1s due to their poor SCA effects. The F_1-Tori-7 × BARI Sar-17 showed the highest positive and the highly significant SCA effects (1.27**) followed by the reciprocal F_1-BARI Sar-15 × Brown Special (0.98**) and F_1-BARI Sar-17 × Tori-7 (0.95**) (Table 18). So, they could be considered as the best specific combiner for this trait and among these F_1s the F_1-Tori-7 × BARI Sar-17 was selected as the best combination for this purpose. Haung *et al.* (2009), Yadav *et al.* (2010), Azizinia (2011), Gupta *et al.* (2011), Nasrin *et al.* (2011), Azizinia (2012) and Inayat *et al.* (2019) also reported that thousand seed weight showed the significant SCA effects while Huq (2006) and Sincik *et al.* (2011) revealed that SCA effects were non-significant for thousand seed weight. Singh *et al.* (2000), Chowdhury *et al.* (2004) and Arifullah *et al.* (2012) found best desired SCA effects for this trait.

2.2.3.10 Seed yield plant^{-1}

For seed yield plant^{-1} thirty one F_1s showed the highly significant SCA effects ranged from -4.77** to 12.06**. Among them eighteen showed the positive and thirteen showed the negative SCA effects. The reciprocal F_1- BARI Sar-15 × Brown Special represented the highest SCA effects (12.06**) followed by the F_1- Yellow Special × Tori-7 (8.01**), F_1 Brown Special × BARI Sar-15 (6.17**), reciprocal F_1- BARI Sar-17 × Brown Special (6.04**) and F_1- BARI Sar-15 × Tori-7 (5.46**) (Table 18). Therefore, they could be selected as the best specific combiners for this trait and could be incorporated to obtain heterotic hybrid combination (Plate 17 B). However, among the remaining eleven F_1s two showed the significant and negative SCA effects while other nine F_1s showed the non-significant SCA effects thus there was no opportunity to improve the trait by using these F_1s. Haung *et al.* (2009), Yadav *et al.* (2010), Azizinia (2011), Gupta *et al.* (2011), Nasrin *et al.* (2011), Rameeh (2011d), Sincik *et al.* (2011), Vaghela *et al.* (2011), Verma *et al*. (2011), Azizinia (2012) and Rameeh (2012) also reported the significant SCA for seed yield plant^{-1} in some F_1s. Chowdhury *et al.* (2004), Huq (2006), Arifullah *et al.* (2012), Atikunnaher, *et al.* (2017), Channa *et al.* (2018) and Singh *et al*. (2019) showed the good positive SCA for

seed yield plant^{-1} while Inayat *et al.* (2019) found the non-significant SCA effects for seed yield plant^{-1}.

Findings

Out of forty two F_1s, the highly significant and the highest negative heterosis for days to 50% flowering and 80% maturity was provided by the reciprocal F_1- BARI Sar-6 Brown Special (-35.00 %) and (-23.33 %) over the better parents respectively and F_1- BARI Sar-6 × BARI Sar-17 (-22.75 %) and (-13.22 %) over the mid parent respectively thus these could be used for producing genotype with earliness. However, for number of primary branches plant^{-1} reciprocal F_1- BARI Sar-15 × Brown Special and the F_1- Brown Special × Tori-7 showed the highest significant positive heterosis 97.76% and 76.47% over the mid parent and the better parent respectively while the highest significant and positive heterosis for number of secondary branches plant^{-1} was produced by the reciprocal F_1- BARI Sar-17 × Yellow Special over the both parents. The reciprocal F_1- BARI Sar-15 × Brown Special produced the maximum heterosis for number of siliqua plant^{-1}. The F_1-Tori-7 × BARI Sar-17 gave the highest significant and positive heterosis over the both parents for thousand seed weight while the F_1-Yellow Special × Tori-7 represented the highly significant and positive heterosis over the both parents for seed yield plant^{-1}.

The estimates of GCA effects for different characters suggested that the parent Tori-7 was the best general combiner for producing more number of primary branches, secondary branches and siliqua plant^{-1} while Brown Special was the best general combiner for earliness, thousand seed weight and seed yield plant^{-1}. The parent BARI Sar-17 was the best general combiner for plant height and for producing more seeds siliqua^{-1}. For siliqua length BARI Sar-6 was a good general combiner.

The SCA estimates of various traits revealed that the F_1- BARI Sar-6 × Brown Special was the best for plant height (i.e. dwarfness) and earliness while F_1- BARI Sar-14 × BARI Sar-6 was the best for number of primary branches plant^{-1} and F_1- BARI Sar-15 × Brown Special was best for more number of secondary branches plant^{-1}, siliqua plant^{-1} and seed yield plant^{-1} as it represented the highest SCA effects for those traits. The F_1- BARI Sar-14 × BARI Sar-17 showed the highest positive and the highly significant SCA effects for number of seeds siliqua^{-1}. F_1- Tori-7 × BARI Sar-17 was the best for thousand seed weight as it had the highest positive and the highly significant SCA effects.

Experiment 3: Study on the gene actions involved for yield and yield related attributes in *Brassica rapa*

To understand the nature of gene actions for yield and its contributing traits, GMA (Generation Mean Analysis) was conducted using the data recorded for six generations of twenty one crosses obtained from 7 × 7 full diallel crossing among seven *Brassica rapa* genotypes. The mean performance of the six generations including two parents, F_1s, F_2s, BC_1s and BC_2s for ten yield and related traits were represented in Table 19**.** The values of individual scaling tests (Tables 20), estimates of gene effects (Table 21 and 22), components of variation and genetic parameters (Table 23) for different traits in these crosses were estimated. The information on given estimates of various traits are essential for judicious selection of parents and breeding methodology.

3.1 GMA (Generation mean analysis)

Mean performance of the six generations viz., two parents, F_1s, F_2s, BC_1s and BC_2s for all the studied traits of the twenty one cross materials were presented in Table 19. The average performance of the six generations of all the cross materials showed considerable variability in all the traits studied.

The F_1 means for most of the traits over the cross materials had differed from their parental means. In this study most of the F_1s showed better performance than both of their parents in the traits like plant height (except the crosses which involved one parents as BARI Sarisha-6 and the cross $P_4 \times P_5$), number of primary branches plant^{-1} (except the crosses $P_1 \times P_5$, $P_5 \times P_6$ and $P_5 \times P_7$), number of secondary branches plant^{-1}, number of siliqua plant^{-1}, seed yield plant^{-1} (except the cross $P_5 \times P_6$) while all the F_1s had required more time for days to 50% flowering and 80% maturity (except the crosses which involved one parents as BARI Sarisha-6 or/and as BARI Sarisha-17 and the cross $P_4 \times P_5$). For siliqua length, number of seeds siliqua^{-1} and thousand seed weight most of the F_1s showed less siliqua length, less number of seeds siliqua^{-1} and less seed weight than one or both of the parents (except the crosses $P_1 \times P_6$, $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_7$ and $P_4 \times P_6$ for siliqua length, the crosses $P_2 \times P_7$ and $P_4 \times P_6$ for seeds siliqua^{-1} and the crosses $P_1 \times P_2$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_5$, $P_6 \times P_2$ and $P_6 \times P_7$ for thousand seed weight respectively). Superiority of F_1s indicated the presence of dominant genes while the F_1s with the average performance over their parents indicated partial dominance. Elnenny and Shafei Wafaa (2017), Abdelsatar *et al.* (2020) were also reported the similar results.

Table 19. Generation Mean (±SE) of six generations of the cross materials obtained from 7 × 7 diallel crosses among *Brassica rapa* genotypes for yield and contributing traits.

Cross	Gener-ations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_1 \times P_2$	P_1	37.43±0.52	83.33±0.39	90.60±1.91	6.57±0.29	0.07±0.06	84.00±3.70	3.27±0.05	26.35±0.61	3.51±0.05	6.76±0.27
	P_2	35.13±0.20	79.67±0.23	112.33±2.17	6.43±0.34	3.00±0.62	197.77±13.47	4.46±0.08	15.37±0.24	3.57±0.04	11.14±0.28
	F_1	45.00±0.22	91.23±0.30	119.30±1.73	9.93±0.46	12.50±1.11	526.17±29.64	4.08±0.07	19.81±1.17	4.31±0.04	19.47±0.33
	F_2	53.00±0.25	97.53±0.27	115.00±1.62	7.47±0.27	6.73±0.98	390.57±27.05	3.71±0.04	18.93±0.34	4.10±0.02	12.82±0.30
	BC_1	50.10±0.19	95.17±0.25	117.53±1.35	8.37±0.38	14.97±0.70	552.07±26.64	3.44±0.04	15.47±0.31	4.70±0.04	23.20±1.51
	BC_2	47.10±0.27	92.17±0.28	116.50±1.57	7.80±0.36	3.17±0.91	236.63±22.76	4.20±0.04	20.37±0.34	3.50±0.04	11.47±0.46
$P_1 \times P_3$	P_1	37.43±0.52	83.33±0.39	90.60±1.91	6.57±0.29	0.07±0.07	84.00±3.71	3.27±0.05	26.35±0.61	3.51±0.05	6.76±0.27
	P_2	43.70±0.28	88.13±0.32	109.23±2.32	5.80±0.28	0.43±0.22	136.23±8.66	3.93±0.07	21.38±0.26	4.57±0.05	7.77±0.20
	F_1	44.00±0.30	89.23±0.30	111.03±3.17	7.87±0.32	3.23±0.87	202.30±10.19	3.68±0.05	20.76±0.39	3.90±0.03	11.53±0.41
	F_2	43.00±0.24	88.27±0.27	109.20±1.20	7.60±0.36	3.70±0.74	190.97±12.60	3.50±0.05	20.22±0.28	3.80±0.03	10.93±0.40
	BC_1	40.00±0.25	85.33±0.19	114.10±1.35	8.00±0.19	2.67±0.62	235.27±9.32	3.40±0.07	19.33±0.39	4.00±0.03	11.45±0.16
	BC_2	44.00±0.30	89.23±0.30	106.37±1.32	7.03±0.25	0.17±0.10	163.57±8.49	3.31±0.05	21.00±0.35	3.01±0.04	7.42±0.16
$P_1 \times P_5$	P_1	37.43±0.52	83.33±0.39	90.60±1.91	2.47±0.29	0.07±0.07	84.00±3.71	3.27±0.05	26.35±0.61	3.51±0.05	6.76±0.27
	P_2	46.00±0.35	91.13±0.43	99.10±2.11	3.63±0.35	0.10±0.10	85.83±5.88	3.34±0.05	30.13±0.43	4.30±0.06	8.00±0.16
	F_1	42.00±0.35	86.37±0.49	99.87±1.32	1.48±0.22	0.90±0.29	124.27±4.79	3.10±0.03	29.48±0.27	3.40±0.06	9.65±0.19
	F_2	45.00±0.43	90.17±0.53	84.63±1.59	4.94±0.41	1.90±0.35	120.90±3.69	2.96±0.02	28.29±0.29	3.50±0.04	8.04±0.31
	BC_1	43.00±0.35	87.83±0.34	92.00±0.47	3.72±0.35	0.17±0.08	100.10±1.38	3.05±0.08	29.00±0.35	3.09±0.04	7.53±0.20
	BC_2	44.80±0.38	90.03±0.50	95.00±0.59	1.28±0.21	0.73±0.17	114.80±0.97	3.00±0.03	31.00±0.35	2.80±0.03	9.00±0.27

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_5 = BARI Sarisha-17

Table 19 (Cont'd).

Cross	Gener-ations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_1 \times P_6$	P_1	37.43±0.52	83.33±0.39	90.60±1.91	6.57±0.29	0.07±0.06	84.00±3.70	3.27±0.05	26.35±0.61	3.51±0.05	6.76±0.27
	P_2	41.00±0.35	86.00±0.35	108.33±1.74	8.10±0.39	0.67±0.39	148.57±8.53	3.40±0.04	22.00±0.43	4.50±0.06	7.23±0.21
	F_1	44.00±0.35	89.03±0.39	121.63±2.20	8.30±0.55	2.73±0.61	240.97±18.80	4.03±0.07	16.00±0.35	4.30±0.06	13.24±0.22
	F_2	49.00±0.35	94.70±0.36	100.10±1.11	7.93±0.19	2.33±0.48	181.23±7.44	4.00±0.04	20.00±0.35	3.60±0.03	7.93±0.19
	BC_1	42.00±0.35	87.02±0.36	109.13±1.96	8.40±0.18	4.40±0.89	337.10±32.60	3.40±0.04	17.00±0.35	3.50±0.06	9.99±0.22
	BC_2	43.00±0.35	88.03±0.37	106.87±1.08	8.37±0.26	1.87±0.56	216.63±8.91	3.10±0.03	18.00±0.43	4.40±0.03	9.93±0.21
$P_1 \times P_7$	P_1	37.43±0.52	83.33±0.39	90.60±1.91	6.57±0.29	0.07±0.06	84.00±3.70	3.27±0.05	26.35±0.61	3.51±0.05	6.76±0.27
	P_2	60.00±0.35	107.23±0.36	136.10±2.77	8.13±0.59	0.57±0.43	171.13±10.06	4.27±0.05	24.00±0.35	4.70±0.06	10.62±0.20
	F_1	49.00±0.35	94.80±0.35	125.60±1.74	8.40±0.45	1.83±0.60	242.43±15.00	3.80±0.04	17.00±0.35	4.40±0.07	13.52±0.22
	F_2	52.00±0.35	97.63±0.35	111.17±1.29	7.57±0.19	2.03±0.51	196.90±8.25	3.84±0.04	18.00±0.35	4.30±0.03	11.05±0.23
	BC_1	51.00±0.35	96.73±0.36	131.80±2.01	6.90±0.17	0.10±0.07	167.70±4.59	3.40±0.07	23.00±0.35	4.00±0.04	11.67±0.21
	BC_2	51.33±0.32	97.17±0.34	133.30±1.33	7.67±0.35	3.77±0.68	268.63±15.43	4.00±0.08	21.00±0.35	4.08±0.04	12.56±0.25
$P_2 \times P_3$	P_1	35.13±0.20	79.66±0.23	112.33±2.17	6.43±0.34	3.00±0.62	197.77±13.47	4.46±0.08	15.37±0.24	3.57±0.04	11.12±0.28
	P_2	43.70±0.28	88.13±0.32	109.23±2.32	5.80±0.28	0.43±0.22	136.23±8.66	3.93±0.07	21.38±0.26	4.57±0.05	7.76±0.20
	F_1	44.00±0.28	89.13±0.32	123.57±2.41	10.00±0.58	6.97±1.30	400.60±36.63	4.50±0.08	17.33±0.32	4.30±0.06	20.38±0.23
	F_2	56.00±0.43	102.10±0.43	115.00±2.23	7.60±0.21	3.00±0.82	270.67±19.24	2.60±0.07	15.00±0.35	4.28±0.04	9.83±0.21
	BC_1	45.00±0.30	89.53±0.39	114.93±2.24	7.00±0.32	2.70±0.90	265.13±27.58	4.50±0.07	21.00±0.35	4.00±0.04	10.46±0.16
	BC_2	47.00±0.35	92.17±0.35	120.33±1.39	9.07±0.21	7.80±0.23	362.97±14.33	4.03±0.03	20.00±0.35	4.10±0.04	14.28±0.22

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6

Table 19 (Cont'd).

Cross	Gener-ations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_2 \times P_4$	P_1	35.13±0.20	79.66±0.23	112.33±2.17	6.43±0.34	3.00±0.62	197.77±13.47	4.46±0.08	15.37±0.24	3.57±0.04	11.12±0.28
	P_2	33.00±0.35	79.73±0.32	104.97±1.83	5.93±0.28	7.03±0.65	246.10±13.42	4.02±0.03	20.00±0.35	3.10±0.03	5.30±0.18
	F_1	42.00±0.35	87.10±0.35	106.57±2.27	9.00±0.49	9.37±1.15	319.47±15.94	6.37±0.10	19.08±0.33	3.20±0.11	14.90±0.22
	F_2	45.00±0.35	90.23±0.40	98.67±1.19	7.13±0.27	6.47±0.84	325.10±25.80	3.85±0.07	17.00±0.43	3.00±0.03	12.54±0.18
	BC_1	41.33±0.32	86.47±0.32	110.83±0.81	7.10±0.33	3.07±0.61	301.17±19.21	4.18±0.07	19.33±0.32	2.70±0.04	10.66±0.17
	BC_2	41.00±0.35	86.07±0.34	106.67±2.33	8.00±0.30	4.33±0.94	266.97±12.17	4.30±0.06	14.33±0.27	3.00±0.04	10.20±0.18
$P_2 \times P_5$	P_1	35.13±0.20	79.66±0.23	112.33±2.17	6.43±0.34	3.00±0.62	197.77±13.47	4.46±0.08	15.37±0.24	3.57±0.04	11.12±0.28
	P_2	46.00±0.35	91.13±0.43	99.10±2.11	3.63±0.35	0.10±0.10	85.83±5.88	3.34±0.05	30.13±0.43	4.30±0.06	8.00±0.16
	F_1	43.00±0.35	88.00±0.37	126.10±2.54	10.47±0.50	22.97±1.78	819.93±71.11	3.15±0.04	8.00±0.35	3.90±0.04	26.12±0.32
	F_2	55.00±0.35	101.00±0.37	121.67±1.66	9.13±0.31	6.03±0.84	398.60±27.61	3.35±0.06	23.00±0.43	3.30±0.05	10.30±0.29
	BC_1	48.00±0.35	93.10±0.33	112.87±2.44	8.70±0.48	5.00±0.97	332.47±25.57	3.80±0.04	18.97±0.35	3.60±0.04	13.80±0.22
	BC_2	49.00±0.35	94.10±0.32	112.77±1.65	8.50±0.46	11.33±0.44	505.27±13.82	3.10±0.03	22.00±0.35	2.80±0.04	18.38±0.18
$P_2 \times P_7$	P_1	35.13±0.20	79.66±0.23	112.33±2.17	6.43±0.34	3.00±0.62	197.77±13.47	4.46±0.08	15.37±0.24	3.57±0.04	11.12±0.28
	P_2	60.00±0.35	107.23±0.36	136.10±2.77	8.13±0.59	0.57±0.43	171.13±10.06	4.27±0.05	24.00±0.35	4.70±0.06	10.62±0.20
	F_1	43.70±0.35	85.13±0.34	128.97±1.43	9.47±0.36	4.90±1.17	303.73±16.91	4.60±0.07	25.00±0.35	5.00±0.04	13.16±0.22
	F_2	44.00±0.33	88.90±0.34	118.03±3.21	9.10±0.43	2.87±0.59	291.40±21.74	3.90±0.04	19.00±0.43	4.50±0.04	10.40±0.24
	BC_1	43.33±0.32	88.37±0.36	124.00±1.48	7.27±0.33	4.00± 0.51	260.80±13.94	4.34±0.04	19.33±0.32	4.80±0.03	12.33±0.21
	BC_2	51.33±0.32	96.63±0.34	133.10±1.56	7.43±0.35	1.67±0.23	237.77±9.24	4.40±0.04	22.33±0.39	4.77±0.04	12.17±0.28

P_2 = Brown Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_7 = BARI Sarisha-6

Table 19 (Cont'd).

Cross	Generations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_3 \times P_5$	P_1	43.70±0.28	88.13±0.32	109.23±2.32	5.80±0.28	0.43±0.22	136.23±8.66	3.93±0.07	21.38±0.26	4.57±0.05	7.76±0.20
	P_2	46.00±0.35	91.13±0.43	99.10±2.11	3.63±0.35	0.10±0.10	85.83±5.88	3.34±0.05	30.13±0.43	4.30±0.06	8.00±0.16
	F_1	44.00±0.30	88.30±0.39	115.13±2.23	8.27±0.36	1.43±0.48	194.03±11.56	3.90±0.06	22.33±0.32	4.90±0.06	14.19±0.31
	F_2	48.67±0.32	93.90±0.29	106.93±1.18	8.03±0.30	0.87±0.36	199.93±9.93	3.80±0.06	23.00±0.35	4.50±0.04	10.03±0.34
	BC_1	46.33±0.32	91.40±0.41	112.00±1.51	7.30±0.25	0.67±0.28	168.10±8.05	2.63±0.05	11.06±0.33	3.87±0.05	7.41±0.15
	BC_2	50.00±0.35	95.00±0.42	116.87±1.60	7.73±0.29	2.90±1.01	244.30±23.97	3.60±0.04	25.00±0.35	5.01±0.04	11.30±0.31
$P_3 \times P_6$	P_1	43.70±0.28	88.13±0.32	109.23±2.32	5.80±0.28	0.43±0.22	136.23±8.66	3.93±0.07	21.38±0.26	4.57±0.05	7.76±0.20
	P_2	41.00±0.35	86.00±0.35	108.33±1.74	8.10±0.39	0.67±0.39	148.57±8.53	3.40±0.04	22.00±0.43	4.50±0.06	7.23±0.21
	F_1	48.33±0.32	93.50±0.30	112.10±2.65	8.70±0.24	1.90±0.66	228.60±12.56	3.83±0.04	13.65±0.37	4.10±0.04	11.64±0.31
	F_2	50.00±0.35	95.00±0.42	114.70±0.56	8.54±0.24	3.11±0.88	272.80±17.02	3.20±0.04	22.00±0.35	3.70±0.03	11.99±0.31
	BC_1	43.33±0.25	87.30±0.27	112.00±1.41	8.50±0.27	0.00±0.00	205.70±7.29	3.30±0.03	19.33±0.32	4.20±0.04	10.92±0.26
	BC_2	42.00±0.33	86.70±0.32	110.50±0.87	8.10±0.40	0.27±0.17	193.63±7.97	3.80±0.04	22.02±0.34	4.40±0.04	10.18±0.31
$P_3 \times P_7$	P_1	43.70±0.28	88.13±0.32	109.23±2.32	5.80±0.28	0.43±0.22	136.23±8.66	3.93±0.07	21.38±0.26	4.57±0.05	7.76±0.20
	P_2	60.00±0.35	107.23±0.36	136.10±2.77	8.13±0.59	0.57±0.43	171.13±10.06	4.27±0.05	24.00±0.35	4.70±0.06	10.62±0.20
	F_1	51.33±0.32	96.10±0.46	126.63±2.76	9.20±0.49	2.57±0.62	275.13±16.86	3.40±0.04	22.67±0.36	3.30±0.06	14.08±0.33
	F_2	53.00±0.35	98.00±0.35	113.93±2.12	7.07±0.27	0.87±0.18	207.13±7.51	4.90±0.04	21.33±0.39	3.50±0.06	11.27±0.34
	BC_1	46.67±0.36	91.63±0.41	119.43±0.79	7.17±0.26	3.20±0.84	260.43±20.41	3.80±0.03	20.67±0.32	3.00±0.04	10.20±0.35
	BC_2	50.67±0.32	95.43±0.47	121.37±0.72	16.23±0.59	32.83±1.57	1324.07±49.51	3.50±0.04	23.33±0.32	3.50±0.03	42.19±0.39

P_3 = Yellow Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6

Table 19 (Cont'd).

Cross	Gener-ations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_4 \times P_1$	P_1	33.00±0.35	79.73±0.32	104.97±1.83	5.93±0.28	7.03±0.65	246.10±13.42	4.02±0.03	20.00±0.35	3.10±0.03	5.30±0.18
	P_2	37.43±0.52	83.33±0.39	90.60±1.91	6.57±0.29	0.07±0.06	84.00±3.70	3.27±0.05	26.35±0.61	3.51±0.05	6.76±0.27
	F_1	49.67±0.32	94.83±0.39	122.60 ±2.85	9.00±0.56	10.57±1.41	461.60±40.22	3.27±0.05	12.40±0.30	3.97±0.03	15.11±0.35
	F_2	49.33±0.32	94.57±0.34	112.27± 3.86	7.60±0.44	7.57±1.05	349.57±32.88	3.42±0.07	12.00±0.35	3.70±0.04	9.05±0.31
	BC_1	46.67±0.32	91.90±0.41	114.97±1.70	8.77±0.34	15.03±3.54	437.03±30.81	4.13±0.04	16.17±0.36	3.80±0.03	15.67±0.32
	BC_2	48.00±0.35	93.27±0.35	117.73±1.56	7.90±0.35	8.77±1.30	347.03±20.18	4.17±0.05	20.53±0.36	3.52±0.04	17.33±0.32
$P_4 \times P_3$	P_1	33.00±0.35	79.73±0.32	104.97±1.83	5.93±0.28	7.03±0.65	246.10±13.42	4.02±0.03	20.00±0.35	3.10±0.03	5.30±0.18
	P_2	43.70±0.28	88.13±0.32	109.23±2.32	5.80±0.28	0.43±0.22	136.23±8.66	3.93±0.07	21.38±0.26	4.57±0.05	7.76±0.20
	F_1	48.00±0.35	93.27±0.35	128.17±2.16	9.97±0.58	17.60±1.90	667.90±59.04	3.61±0.04	21.50±0.37	5.43±0.05	31.00±0.35
	F_2	46.00±0.35	91.20±0.35	110.60±3.60	8.40±0.56	6.37±1.52	398.97±55.68	3.00±0.03	21.00±0.35	5.42±0.04	15.03±0.35
	BC_1	49.33±0.32	94.57±0.34	112.27±1.74	8.87±0.48	8.73±1.46	472.60±58.80	3.50±0.06	20.71±0.38	4.77±0.04	20.93±0.32
	BC_2	49.00±0.35	94.17±0.37	119.23±1.34	6.97±0.35	5.17±0.99	314.93±29.06	3.40±0.04	18.68±0.32	3.10±0.03	12.00±0.35
$P_4 \times P_5$	P_1	33.00±0.35	79.73±0.32	104.97±1.83	5.93±0.28	7.03±0.65	246.10±13.42	4.02±0.03	20.00±0.35	3.10±0.03	5.30±0.18
	P_2	46.00±0.35	91.13±0.43	99.10±2.11	3.63±0.35	0.10±0.10	85.83±5.88	3.34±0.05	30.13±0.43	4.30±0.06	8.00±0.16
	F_1	49.00±0.35	94.17±0.37	117.90±1.76	9.27±0.42	14.53±1.48	595.03±31.44	3.91±0.04	14.72±0.35	4.42±0.05	18.32±0.34
	F_2	55.77±0.35	100.90±0.36	122.17± 2.57	9.07±0.30	9.63±1.16	466.80±26.41	2.50±0.04	9.33±0.32	3.60±0.04	11.16±0.44
	BC_1	49.33±0.32	94.57±0.34	111.77±1.11	8.87± 0.30	12.53±1.18	580.13±39.00	3.35±0.04	17.42±0.34	4.30±0.05	14.54±0.33
	BC_2	48.33±0.32	93.50±0.30	103.00±1.12	8.03±0.27	4.33±0.24	288.93±5.64	3.50±0.05	21.67±0.32	3.82±0.03	12.33±0.32

P_1 = BARI Sarisha-14, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sarisha-17

Table 19 (Cont'd).

Cross	Generations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_4 \times P_6$	P_1	33.00±0.35	79.73±0.32	104.97±1.83	5.93±0.28	7.03±0.65	246.10±13.42	4.02±0.03	20.00±0.35	3.10±0.03	5.30±0.18
	P_2	41.00±0.35	86.00±0.35	108.33±1.74	8.10±0.39	0.67±0.39	148.57±8.53	3.40±0.04	22.00±0.43	4.50±0.06	7.23±0.21
	F_1	48.33±0.32	93.50±0.30	122.57±2.61	10.27±0.86	13.30±2.06	517.83±67.95	4.12±0.04	10.52±0.29	2.80±0.04	16.25±0.30
	F_2	46.33±0.32	91.67±0.38	120.80±2.11	8.47±0.30	2.63±0.77	320.77±25.60	3.70±0.04	14.20±0.34	3.43±0.04	11.37±0.33
	BC_1	48.00±0.35	93.27±0.35	116.13±1.80	7.30±0.33	11.03±0.95	520.73±37.03	4.23±0.05	17.67±0.32	2.70±0.03	9.48±0.29
	BC_2	46.00±0.35	91.23±0.40	116.53±2.72	9.30±0.24	14.60±1.11	576.90±22.79	3.03±0.03	19.33±0.32	3.07±0.04	9.97±0.26
$P_4 \times P_7$	P_1	33.00±0.35	79.73±0.32	104.97±1.83	5.93±0.28	7.03±0.65	246.10±13.42	4.02±0.03	20.00±0.35	3.10±0.03	5.30±0.18
	P_2	60.00±0.35	107.23±0.36	136.10±2.77	8.13±0.59	0.57±0.43	171.13±10.06	4.27±0.05	24.00±0.35	4.70±0.06	10.62±0.20
	F_1	46.33±0.32	91.47±0.36	115.67±3.08	10.07±0.82	7.13±1.15	340.30±25.89	3.87±0.04	16.00±0.35	4.20±0.04	13.47±0.31
	F_2	54.33±0.32	99.33±0.32	115.17±1.67	9.93±0.42	1.47±0.70	271.77±19.24	4.20±0.06	17.67±0.36	3.50±0.04	10.62±0.32
	BC_1	45.33±0.32	90.33±0.32	105.87±1.12	7.00±0.44	7.00±0.48	282.83±12.39	3.80±0.04	17.50±0.37	3.97±0.04	9.25±0.46
	BC_2	50.00±0.35	95.17±0.37	124.67±1.20	7.70±0.56	3.03±0.39	209.20±12.73	3.70±0.04	20.33±0.32	4.43±0.04	10.23±0.41
$P_5 \times P_6$	P_1	46.00±0.35	91.13±0.43	99.10±2.11	3.63±0.35	0.10±0.10	85.83±5.88	3.34±0.05	30.13±0.43	4.30±0.06	8.00±0.16
	P_2	41.00±0.35	86.00±0.35	108.33±1.74	8.10±0.39	0.67±0.39	148.57±8.53	3.40±0.04	22.00±0.43	4.50±0.06	7.23±0.21
	F_1	49.33±0.32	94.56±0.34	116.47±4.22	7.73±0.55	2.00±0.54	222.50±14.94	2.84±0.06	12.90±0.32	3.22±0.05	10.82±0.29
	F_2	49.67±0.32	94.83±0.39	103.23±1.00	8.57±0.35	0.77±0.21	187.13±8.13	3.35±0.06	14.67±3.72	3.83±0.04	8.82±0.32
	BC_1	43.33±0.32	88.33±0.32	108.97±1.17	6.97±0.26	0.20±0.11	127.10±5.90	3.60±0.05	18.87±0.43	3.50±0.04	7.41±0.38
	BC_2	48.00±0.35	93.27±0.35	118.27±1.31	8.40±0.25	2.87±0.71	249.33±20.33	4.26±0.05	22.17±0.34	4.52±0.04	11.09±0.30

P_4 = Tori-7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6.

Table 19 (Cont'd).

Cross	Gener-ations	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_5 \times P_7$	P_1	46.00±0.35	91.13±0.43	99.10±2.11	3.63±0.35	0.10±0.10	85.83±5.88	3.34±0.05	30.13±0.43	4.30±0.06	8.00±0.16
	P_2	60.00±0.35	107.23±0.36	136.10±2.77	8.13±0.59	0.57±0.43	171.13±10.06	4.27±0.05	24.00±0.35	4.70±0.06	10.62±0.20
	F_1	46.33±0.32	91.47±0.36	129.67±2.82	7.27±0.41	1.07±0.47	192.20±14.99	4.06±0.04	16.92±0.36	3.70±0.04	9.00±0.39
	F_2	52.67±0.32	97.67±0.32	106.10±1.07	6.37±0.24	1.17±0.25	160.77±8.20	3.65±0.04	20.00±0.41	4.33±0.05	8.63±0.32
	BC_1	51.33±0.32	96.33±0.32	95.10±2.43	7.37±0.29	0.93±0.46	116.43±8.27	3.79±0.04	18.50±0.31	4.80±0.03	6.09±0.34
	BC_2	53.67±0.32	98.33±0.47	131.87±0.86	9.07±0.34	0.27±0.16	221.80±9.17	3.65±0.04	21.33±0.39	4.57±0.03	10.52±0.31
$P_6 \times P_2$	P_1	41.00±0.35	86.00±0.35	108.33±1.74	8.10±0.39	0.67±0.39	148.57±8.53	3.40±0.04	22.00±0.43	4.50±0.06	7.23±0.21
	P_2	35.13±0.20	79.66±0.23	112.33±2.17	6.43±0.34	3.00±0.62	197.77±13.47	4.46±0.08	15.37±0.24	3.57±0.04	11.12±0.28
	F_1	47.00±0.35	92.17±0.37	117.37±1.65	12.40±0.54	22.53±1.68	725.60±58.10	4.00±0.04	16.60±0.35	5.62±0.06	25.08±0.31
	F_2	48.00±0.35	93.27±0.35	120.77±2.62	7.50±0.32	8.50±0.90	435.87±35.03	3.30±0.06	12.07±0.34	4.20±0.04	11.80±0.33
	BC_1	50.00±0.35	95.13±0.37	113.43±2.72	8.60±0.23	6.67±1.07	334.93±20.88	5.70±0.04	19.33±0.32	4.70±0.03	11.31±0.31
	BC_2	49.33±0.32	94.57±0.34	112.27±1.37	7.93±0.31	2.87±0.36	157.33±5.66	2.05±0.03	5.05±0.33	5.68±0.17	5.50±0.29
$P_6 \times P_7$	P_1	41.00±0.35	86.00±0.35	108.33±1.74	8.10±0.39	0.67±0.39	148.57±8.53	3.40±0.04	22.00±0.43	4.50±0.06	7.23±0.21
	P_2	60.00±0.35	107.23±0.36	136.10±2.77	8.13±0.59	0.57±0.43	171.13±10.06	4.27±0.05	24.00±0.35	4.70±0.06	10.62±0.20
	F_1	47.33±0.36	92.40±0.35	128.50±2.11	9.87±0.40	4.00±1.09	335.40±38.87	3.50±0.08	11.05±0.34	5.51±0.04	14.67±0.29
	F_2	44.00±0.35	89.00±0.35	117.97±1.88	7.43±0.34	5.03±0.79	278.70±21.90	3.01±0.03	9.33±0.32	4.70±0.03	9.35±0.29
	BC_1	49.67±0.32	94.83±0.39	122.67±2.00	11.43±0.62	1.27±0.34	331.17±17.72	3.92±0.03	18.84±0.36	5.50±0.04	15.33±0.28
	BC_2	55.33±0.32	100.33±0.32	145.13±0.91	10.80±0.60	6.23±1.28	429.87±35.35	3.71±0.05	19.05±0.29	5.47±0.03	12.17±0.30

P_2 = Brown Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6

Majority of the yield components revealed that the F_2 means were lower than their corresponding F_1 means for days to flowering and maturity (except in $P_1 \times P_3$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_6$ and $P_6 \times P_7$), for plant height (except in $P_3 \times P_6$, $P_4 \times P_5$, and $P_6 \times P_2$), for number of primary branches plant^{-1} (except in $P_1 \times P_5$), for number of secondary branches plant^{-1} (except in $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_7$, $P_3 \times P_6$, $P_5 \times P_7$ and $P_6 \times P_7$), for number of siliqua plant^{-1} (except in $P_2 \times P_4$, $P_3 \times P_5$, and $P_3 \times P_6$), for siliqua length (except in $P_1 \times P_7$, $P_2 \times P_5$, $P_3 \times P_7$, $P_4 \times P_1$, $P_4 \times P_7$ and $P_5 \times P_6$), for seeds siliqua^{-1} (except in $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_5$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$), for thousand seed weight (except in $P_1 \times P_5$, $P_3 \times P_7$, $P_4 \times P_6$, $P_5 \times P_6$ and $P_5 \times P_7$) and for yield plant^{-1} (except in $P_3 \times P_6$). Reduced F_2 means in comparison to their F_1 means signified inbreeding depression. The findings of this study matched with Yadav *et al.* (2011) and Singh *et al.* (2012a) who also reported the presence of inbreeding depression in their study.

BC_1 performed better than BC_2 in most of the crosses for the traits days to 50% flowering and 80% maturity (except in $P_1 \times P_2$, $P_2 \times P_4$, $P_3 \times P_6$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_6$ and $P_6 \times P_2$), number of siliqua plant^{-1} and siliqua length (except in $P_1 \times P_2$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_1$, $P_4 \times P_5$ and $P_5 \times P_6$) while BC_2 performed better than BC_1 in most of the crosses for the traits number of primary and secondary branches plant^{-1} and thousand seed weight (except $P_2 \times P_3$, $P_2 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$, $P_3 \times P_7$, $P_4 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_6 \times P_2$) and seed yield plant^{-1} etc. In most of the traits the means of BC_1 were very close towards the parent-1 and the means of BC_2 were resembled towards parent-2. The similar results were reported by Haridy and El-Said (2016) and Abd El-Zaher (2016) for yield and related traits.

3.2 Scaling tests

To determine the gene actions controlling inheritance of the traits in the corresponding crosses, the scaling tests outlined by Mather (1949) and Hayman and Mather (1955) and joint scaling tests ($\chi 2$) proposed by Cavalli (1952) were performed (Table 20).

3.2.1 Adequacy of scaling tests

Significant scaling tests indicated non-allelic inter-actions and inadequacy of additive-dominance model. The existence of non-allelic interactions were observed in most of the traits except plant height (in $P_2 \times P_3$, $P_4 \times P_3$ and $P_4 \times P_6$), number of primary branches plant^{-1} (in $P_1 \times P_2$, $P_1 \times P_7$, $P_2 \times P_4$, $P_4 \times P_3$ and $P_4 \times P_6$), number of secondary branches plant^{-1} (in $P_2 \times P_7$ and $P_5 \times P_7$), siliqua plant^{-1} (in $P_2 \times P_4$ and $P_2 \times P_7$). Due to presence of insignificant scaling tests (A, B, C and D) for some traits in some crosses joint scaling tests were proceeded to

Table 20. Scaling and joint scaling test (χ2) for yield and yield contributing traits in selected *Brassica rapa* materials

Cross	Scaling test factors	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
$P_1 \times P_2$	A	17.77**	15.77**	25.17**	0.23	17.37**	493.97**	-0.47**	-15.22**	1.58**	20.17**
	B	14.07**	13.43**	1.37	-0.77	-9.17**	-250.67**	-0.13	5.55**	-0.87**	-7.66**
	C	49.43**	44.67**	18.47*	-3.00	-1.13	228.17	-1.02**	-5.61*	0.69**	-5.53**
	D	8.80**	7.73**	-4.03	-1.23	-4.67*	-7.57	-0.21*	2.03*	-0.01	-9.02**
	(χ2)	11.00	5.39	12.09*	3.07	41.38	1045.29	0.10	17.11*	0.93	132.06
$P_1 \times P_3$	A	-1.43	-1.90*	26.57**	1.57*	2.03	184.23**	-0.15	-8.44**	0.59**	4.61**
	B	0.00	1.10	-7.53	0.40	-3.33**	-11.40	-0.99**	-0.14	-2.45**	-4.45**
	C	2.57	3.13*	14.90	2.30	7.83*	139.03*	-0.54*	-8.36**	-0.68**	6.17**
	D	2.00*	1.97*	-2.07	0.17	4.57*	-16.90	0.30*	0.11	0.59**	3.01**
	(χ2)	0.35	0.23	9.21	0.90	22.60**	204.94	0.30	4.61	2.48	5.36
$P_1 \times P_5$	A	6.57**	5.97**	-6.47*	-1.60*	-0.63	-8.07	-0.26	2.17*	-0.73**	-1.35*
	B	1.60	2.57*	-8.97*	1.63*	0.47	19.50*	-0.35**	2.39*	-2.10**	0.35
	C	12.57**	13.47**	-50.90**	4.03*	5.63**	65.23**	37.58	-2.29	-0.61*	-1.89
	D	2.20*	2.47*	-17.73**	2.00*	2.90**	26.90**	19.09	-3.42**	1.11**	-0.44
	(χ2)	0.96	0.47	13.95*	12.49*	9.08	27.03	39.51	2.15	10.66	1.10
$P_1 \times P_6$	A	2.57*	1.68	6.03	1.93*	6.00*	349.23**	-0.50**	-8.35**	-0.81**	-0.03
	B	1.00	1.03	-16.23**	0.33	0.33	43.73	-1.24**	-2.00	0.00	-0.61
	C	29.57**	31.40**	-41.80**	0.47	3.13	10.43	1.26**	-0.35	-2.21**	-8.74**
	D	13.00**	14.34**	-15.80**	-0.90	-1.60	-191.27**	1.50**	5.00**	-0.70**	-4.05**
	(χ2)	17.23**	9.47	20.60**	1.18	12.36*	839.78	19.02**	128.14	0.70	10.82

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15. Significance of any one of these scales indicated the presence of epistasis, (*P < 0.05 and **P < 0.01).

Table 20 (Cont'd).

Cross	Scaling test factors	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
$P_1 \times P_7$	A	15.57**	15.33**	47.40**	-1.17	-1.70*	8.97	-0.27	2.65*	0.09	3.06**
	B	-6.33**	-7.70**	4.90	-1.20	5.13*	123.70**	-0.07	1.00	-1.10**	0.99
	C	12.57**	10.37**	-33.23**	-1.23	3.83	47.60	0.23	-12.35**	0.19	-0.21
	D	1.67	1.37	-42.77**	0.57	0.20	-42.53	0.28*	-8.00**	0.60**	-2.13**
	(χ2)	5.11	2.88	65.83	0.14	7.46	192.10	0.11	9.73	0.54	6.32
$P_2 \times P_3$	A	10.87**	11.27**	-6.03	-2.43*	-4.57	-68.10	0.04	9.29**	0.13	-10.60**
	B	6.00**	8.07**	7.87	2.33*	8.20**	189.10**	-0.36*	1.28	-0.67**	0.43
	C	56.87**	64.33**	-8.70	-1.83	-5.37	-52.53	-6.99**	-11.42**	0.47*	-20.32**
	D	20.00**	22.50**	-5.27	-0.87	-4.50*	-86.77	-3.33**	-11.00**	0.50**	-5.08**
	(χ2)	48.62	25.42**	5.04	4.33	23.80**	460.12	7.92	19.82**	0.32	22.28**
$P_2 \times P_4$	A	5.53**	6.17**	2.77	-1.23	-6.23**	85.10	-2.46	4.21**	-1.37**	-4.71**
	B	7.00**	5.30**	1.80	1.07	-7.73*	-31.63	-1.79	-10.41**	-0.30*	0.20
	C	27.87**	27.33**	-35.77**	-1.83	-2.90	217.60	-5.82	-5.53*	-1.07**	3.94**
	D	7.67**	7.93**	-20.17**	-0.83	5.53*	82.07	-0.78**	0.33	0.30*	4.22**
	(χ2)	6.19	3.02	13.26*	2.39	337.56	98.11	1.68	7.48	0.76	5.97
$P_2 \times P_5$	A	17.87**	18.53**	-12.70*	0.50	-15.97**	-352.77**	-0.01	14.56**	-0.27*	-9.66**
	B	9.00**	9.07**	0.33	0.93	-0.40	104.77	-0.29*	5.87**	-2.60**	2.64**
	C	52.87**	57.20**	23.03*	3.57*	-24.90**	-329.07	-0.70*	30.49**	-2.47**	-30.18**
	D	13.00**	14.80**	17.70**	1.07	-4.27*	-40.53	-0.20	5.03**	0.20	-11.58**
	(χ2)	17.15**	10.87	8.96	2.91	67.90	1035.85	0.29	56.11	1.76	45.98

P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_7 = BARI Sarisha-6. Significance of any one of these scales indicated the presence of epistasis, (*P < 0.05 and **P < 0.01).

Table 20 (Cont'd).

Cross	Scaling test factors	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
$P_2 \times P_7$	A	11.53**	11.93**	6.70	-1.37	0.10	20.10	-0.38*	-0.71	1.03**	0.36
	B	2.67*	0.90	1.13	-2.73*	-2.13	0.67	-0.07	-3.33**	-0.17	0.55
	C	0.87	-1.57	-34.23*	2.90	-1.90	189.23	-2.31**	-11.37**	-0.27	-6.48**
	D	-6.67**	-7.20**	-21.03*	3.50**	0.07	84.23	-0.93**	-3.67**	-0.57**	-3.69**
	(χ2)	3.36	2.18	14.77*	8.13	2.74	98.71	0.82	4.31	0.93	5.13
$P_3 \times P_5$	A	4.67**	6.37**	-0.37	0.53	-0.53	5.93	-2.56**	-21.59**	-1.73**	-7.13**
	B	10.00**	10.57**	19.50**	1.60*	4.27*	208.73**	-0.04	-2.47*	0.81**	0.41
	C	16.67**	19.73**	-10.87	4.20*	0.07	189.60**	0.13	-4.18*	-0.67*	-4.02*
	D	1.00	1.40	-15.00**	1.03	-1.83	-12.53	1.37**	9.94**	0.12	1.35
	(χ2)	0.94	0.58	15.15**	1.55	10.06	204.46	6.66	1660.31**	0.78	4.31
$P_3 \times P_6$	A	-5.67**	-7.03**	2.67	2.50**	-2.33*	46.57*	-1.16**	3.63**	-0.27*	2.45**
	B	-5.33**	-6.10**	0.57	-0.60	-2.03*	10.10	0.37**	8.38**	0.20	1.49*
	C	18.33**	18.87**	17.03*	2.85*	7.54	349.20**	-2.20**	17.31**	-2.47**	9.70**
	D	14.67**	16.00**	6.90**	0.47	5.95*	146.27**	-0.70**	2.65*	-1.20**	2.88**
	(χ2)	24.87**	12.22*	1.53	1.26	12.60*	594.65	1.02	10.04	1.12	3.66
$P_3 \times P_7$	A	-2.00*	-0.97	3.00	-0.67	3.40	109.50*	0.27*	-2.72**	-1.87**	-1.44
	B	-10.00**	-12.47**	-20.00**	15.13**	62.53**	2201.87**	-0.67**	0.00	-1.00**	59.68**
	C	5.33*	4.43*	-42.87**	-4.07*	-2.67	-29.10	4.60**	-5.38*	-1.87**	-1.46
	D	8.67**	8.93**	-12.93*	-9.27**	-34.30**	-1170.23**	2.50**	-1.33	0.50**	-29.85**
	(χ2)	11.12*	6.30	8.48	33.92	180.21	5430.06**	15.26**	0.58	6.13	123.00

P_2 = Brown Special, P_3 = Yellow Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6. Significance of any one of these indicated the presence of epistasis, (*P < 0.05 and **P < 0.01).

Table 20 (Cont'd).

Cross	Scaling test factors	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
$P_4 \times P_1$	A	10.67**	9.23**	2.37	2.60*	12.47	166.37*	0.98**	-0.07	0.53**	10.92**
	B	8.90**	8.37**	22.27 **	0.23	6.90*	148.47*	1.80**	2.32*	-0.45**	12.80**
	C	27.57**	25.53**	8.30	-0.10	2.03	144.97	-0.14	-23.15**	0.26	-6.08**
	D	4.00**	3.97**	-8.17	-1.47	-8.67	-84.93	-1.46**	-12.70**	0.08	-14.90**
	(χ2)	10.05	4.39	18.85**	3.77	32.70	576.76	1.81	36.61	0.26	47.89
$P_4 \times P_3$	A	17.67**	16.13**	-8.60	1.83	-7.17*	31.20	-0.63**	-0.08	1.00**	5.57**
	B	6.00**	6.93**	1.07	-1.83	-7.70*	-174.27*	-0.74**	-5.55**	-3.80**	-14.76**
	C	19.00**	18.67**	-28.13	1.93	-17.20*	-122.27	-3.17**	-0.38	3.14**	-14.94**
	D	-2.33*	-2.20*	-10.30	0.97	-1.17	10.40	-0.90**	2.62*	2.97**	-2.87**
	(χ2)	10.56	5.21	11.47*	2.61	16.42**	519.02	0.97	2.54	21.70**	39.73
$P_4 \times P_5$	A	16.67**	15.23**	0.67	2.53*	3.50	319.13**	-1.23**	0.12	1.08**	5.46**
	B	1.67*	1.70*	-11.00*	1.20	-5.97**	-103.00*	-0.25	-1.52	-1.09**	-1.65*
	C	46.07**	44.40**	48.80**	6.20**	2.33	345.20*	-5.18**	-42.24**	-1.84**	-5.30*
	D	13.87**	13.73**	29.57**	1.23	2.40	64.53	-1.85**	-20.42**	-0.92**	-4.55**
	(χ2)	16.84**	8.46	31.82	2.80	11.85*	580.63	3.70	91.34	1.77	21.92**
$P_4 \times P_6$	A	14.67**	13.30**	-361.83	-1.60	1.73	277.53*	0.32*	4.82**	-0.50**	-2.58**
	B	2.67*	2.97*	-364.40	0.23	15.23**	487.40**	-1.47**	6.15**	-1.17**	-3.53**
	C	14.67**	13.93**	-708.37	-0.70	-23.77**	-147.27	-0.87**	-6.23**	0.53*	0.44
	D	-1.33	-1.17	8.93	0.33	-20.37**	-456.10**	0.14	-8.60**	1.10**	3.28**
	(χ2)	9.92	101.13	614.57	1.25	112.75	1557.54**	0.52	12.74*	31.47	6.76

P_1 = BARI Sarisha-14, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15. Significance of any one of these scales indicated the presence of epistasis, (*P < 0.05 and **P < 0.01).

Table 20 (Cont'd).

Cross	Scaling test factors	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
$P_4 \times P_7$	A	11.33**	9.47**	-8.90*	-2.00`	-0.17	-20.73	-0.29*	-1.00	0.63**	-0.27
	B	-6.33**	-8.37**	-2.43	-2.80	-1.63	-93.03*	-0.54**	0.67	-0.03	-3.62**
	C	31.67**	27.43**	-11.73	5.53*	-16.00**	-10.77	0.77*	-5.33*	-2.20**	-0.37
	D	13.33**	13.17**	-0.20	5.17**	-7.10**	51.50	0.80**	-2.50*	-1.40**	1.76
	(χ2)	25.13**	12.03*	1.17	25.30**	22.41**	49.66	1.47	2.79	1.77	2.78
$P_5 \times P_6$	A	-8.67**	-9.03**	2.37	0.60	-1.70*	-54.13*	1.02**	-5.30**	-0.52**	-4.00**
	B	5.67**	5.97**	11.73*	0.97	3.07	127.60*	2.27**	9.43**	1.33**	4.14**
	C	13.00**	13.07**	-27.43*	5.10*	-1.70	69.13	0.99**	-19.27	0.09	-1.58
	D	8.00**	8.07**	-20.77**	1.77*	-1.53	-2.17	-1.15**	-11.70	-0.36**	-0.86
	(χ2)	6.38	3.37	21.09**	1.54	9.84	146.81	1.49	39.02	0.93	5.73
$P_5 \times P_7$	A	10.33**	10.07**	-38.57**	1.87*	0.70	-45.17	0.17	-10.06**	1.60**	-4.81**
	B	1.00	-2.03	-2.03	2.73*	-1.10	80.27*	-1.03**	1.74	0.73**	1.42
	C	12.00**	9.37**	-70.13**	-2.80	1.87	1.70	-1.14**	-7.98**	0.93**	-2.09
	D	0.33	0.67	-14.77**	-3.70**	1.13	-16.70	-0.14	0.17	-0.70**	0.65
	(χ2)	1.62	1.48	21.61**	5.85	5.12	95.13	0.26	21.09**	0.43	4.61
$P_6 \times P_2$	A	12.00**	12.10**	1.17	-3.30**	-9.87**	-204.30*	3.99**	0.07	-0.72**	-9.69**
	B	16.53**	17.30**	-5.17	-2.97*	-19.80**	-608.70**	-4.36**	-21.87**	2.18**	-25.21**
	C	21.87**	23.07**	27.67*	-9.33**	-14.73*	-54.07	-2.66**	-22.31**	-2.51**	-21.32**
	D	-3.33**	-3.17**	15.83*	-1.53*	7.47**	379.47**	-1.15**	-0.25	-1.98**	6.79**
	(χ2)	11.13*	6.45	8.40	4.09	25.03**	1520.53**	51.07	82.94	4.78	22.54**

P_2 = Brown Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6. Significance of any one of these scales indicated the presence of epistasis, (*P < 0.05 and **P < 0.01).

Table 20 (Cont'd).

Cross	Scaling test factors	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	Thousand seed weight	Seed yield plant^{-1}
$P_6 \times P_7$	A	11.00**	11.27**	8.50	4.90**	-2.13	178.37*	0.93**	4.63**	0.99**	8.75**
	B	3.33**	1.03	25.67**	3.60*	7.90*	353.20**	-0.35*	3.05**	0.79**	-0.94
	C	-19.67**	-22.03**	-29.57*	-6.23**	10.90*	124.30	-2.63**	-30.76**	-1.42**	-9.77**
	D	-17.00**	-17.17**	-31.87**	-7.37**	2.57	-203.63**	-1.61**	-19.22**	-1.60**	-8.79**
	(χ2)	18.05**	10.77	33.48	15.49*	15.56**	715.52	2.40	66.17	2.34	26.82

P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6. Significance of any one of these scales indicated the presence of epistasis, (*P < 0.05 and **P < 0.01).

evaluate the adequacy of simple additive-dominance model (Cavalii 1952). The $\chi 2$ test was conducted to assess the goodness of fit of this model. Non-significant $\chi 2$ values indicated the absence of non-allelic interaction and so, additive-dominance model was adequate enough to explain the effects. In general, such cases the genetic model of Jinks and Jones (1958) were usually suggested while significance of one or more scaling tests, (i.e. A, B, C and D) indicated the presence of epistasis and six parameters model was used to estimate the type of gene effects for these traits. In this study the $\chi 2$ values of joint scaling tests were found to be non-significant in most of the traits over the crosses except plant height (in the crosses $P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_6$, $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_1$, $P_4 \times P_3$, $P_5 \times P_6$ and $P_5 \times P_7$), days to 50 % flowering (in the crosses $P_1 \times P_6$, $P_2 \times P_5$, $P_3 \times P_6$, $P_3 \times P_7$, $P_4 \times P_5$, $P_4 \times P_7$, $P_6 \times P_2$ and $P_6 \times P_7$), days to 80 % maturity (in the crosses $P_2 \times P_3$, $P_3 \times P_6$ and $P_4 \times P_7$), number of primary branches plant^{-1} (in the crosses $P_1 \times P_5$, $P_4 \times P_7$ and $P_6 \times P_7$), number of secondary branches plant^{-1} (in the crosses $P_1 \times P_3$, $P_1 \times P_6$, $P_2 \times P_3$, $P_3 \times P_6$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_7$, $P_6 \times P_2$ and $P_6 \times P_7$), number of siliqua plant^{-1} (in the crosses $P_3 \times P_7$, $P_4 \times P_6$ and $P_6 \times P_2$), siliqua length (in the crosses $P_1 \times P_6$ and $P_3 \times P_7$) and number of seeds siliqua^{-1} (in the crosses $P_1 \times P_2$, $P_2 \times P_3$, $P_3 \times P_5$, $P_4 \times P_6$ and $P_5 \times P_7$), thousand seed weight (in the cross $P_4 \times P_3$) and Seed yield plant^{-1} (in the crosses $P_2 \times P_3$, $P_4 \times P_5$ and $P_6 \times P_2$). Therefore, Jinks and Jones (1958) and six parameters both models were performed here to understand the gene effects. The findings of the present study matched with Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al*. (2020) in most of the cases, who observed that epistasis gene actions governed the inheritance of all the studied traits. Sharma and Rastogi (2001) and Parihar *et al.* (2016), Lal *et al.* (2013) also reported similar trends for yield and related traits.

3.3 Estimation of gene effects

Significant values of scaling tests (Table 20) in most of the traits over the crosses indicated the presence of non-allelic interactions. Hence six parameter models were used to explain the nature of gene actions and types of epistasis for the expression of that traits (Table 21) but those showed non-significant values, genetic model of Jinks and Jones (1958) were performed to estimate the gene actions (Table 22).

In most of the crosses the additive effects were found to be significant for most of the traits (Table 20) except days to 50% flowering (in the crosses $P_1 \times P_7$, $P_2 \times P_4$, $P_4 \times P_3$ and $P_6 \times P_2$), days to 80% maturity (in the crosses $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_3 \times P_6$, $P_4 \times P_3$ and $P_6 \times P_2$), plant

Table 21. Estimation of gene effects and epistasis for yield and yield contributing traits in different cross materials of different *Brassica rapa* genotypes [Hayman (1958)]

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_1 \times P_2$	M (Mean)	53.00**	97.53**	115.00**	7.47**	6.73**	390.57**	3.71**	18.93**	4.10**	12.82**
	D (additive)	3.00**	3.00**	1.03	0.57	11.80**	315.43**	-0.76**	-4.90**	1.20**	11.73**
	H (dominance)	-8.88**	-5.73**	25.90*	5.90**	20.30**	400.42*	0.63*	-5.11*	0.78**	28.56**
	I (add × add)	-17.60**	-15.47**	8.07	2.47	9.33*	15.13	0.42*	-4.06*	0.01	18.04**
	J (add × dom)	1.85**	1.17*	11.90**	0.50	13.27**	372.32**	-0.17*	-10.38**	1.23**	13.92**
	L (dom × dom)	-14.23**	-13.73**	-34.60*	-1.93	-17.53*	-258.43	0.18	13.73**	-0.72*	-30.55**
Type of epistasis		C	C	D	D	D	D	C	D	D	D
$P_1 \times P_3$	M (Mean)	43.00**	88.27**	109.20**	7.60**	3.70**	190.97**	3.50**	20.22**	3.80**	10.93**
	D (additive)	-4.00**	-3.90**	7.73**	0.97*	2.50**	71.70**	0.09	-1.67*	0.99**	4.03**
	H (dominance)	-0.72	-0.43	15.25*	1.35	-6.15	125.98*	-0.52	-3.33*	-1.32**	-1.74
	I (add × add)	-4.00*	-3.93*	4.13	-0.33	-9.13*	33.80	-0.59*	-0.22	-1.18**	-6.01**
	J (add × dom)	-0.72	-1.50**	17.05**	0.58	2.68**	97.82**	0.42**	-4.15**	1.52**	4.53**
	L (dom × dom)	5.43*	4.73*	-23.17*	-1.63	10.43*	-206.63*	1.73**	8.81**	3.04**	5.85*
Type of epistasis		D	D	D	D	D	D	D	D	D	D
$P_1 \times P_5$	M (Mean)	45.00**	90.17**	84.63**	7.57**	1.90**	120.90**	12.60**	28.29**	3.50**	8.04**
	D (additive)	-1.80**	-2.20**	-3.00**	-1.13*	-0.57*	-14.70**	0.01	-2.00**	0.29**	-1.47**
	H (dominance)	-4.12	-5.80*	40.48**	-3.06	-4.98**	-14.45	-38.40	8.08**	-2.72**	3.16*
	I (add × add)	-4.40*	-4.93*	35.47**	-4.01*	-5.80**	-53.80**	-38.18	6.84**	-2.21**	0.89
	J (add × dom)	2.48**	1.70*	1.25	-1.61**	-0.55*	-13.78**	0.05	-0.11	0.69**	-0.85*
	L (dom × dom)	-3.77	-3.60	-20.03*	3.98	5.97**	42.37*	38.79	-11.40**	5.04**	0.11
Type of epistasis		C	C	D	D	D	D	D	D	D	C

Where, P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_5 = BARI Sarisha-17; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 21 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_1 \times P_6$	M (Mean)	49.00**	94.70**	100.10**	7.93**	2.33**	181.23**	6.34**	20.00**	3.60**	7.93**
	D (additive)	-1.00*	-1.01	2.27	0.03	2.53*	120.47**	-0.07**	-1.00	-0.90**	0.05
	H (dominance)	-21.22**	-24.32**	53.77**	2.77*	5.57	507.22**	-7.05**	-18.17**	1.69**	14.35**
	I (add × add)	-26.00**	-28.69**	31.60**	1.80	3.20	382.53**	-3.00**	-10.00**	1.40**	8.11**
	J (add × dom)	0.78	0.32	11.13**	0.80	2.83*	152.75**	0.37**	-3.17**	-0.41**	0.29
	L (dom × dom)	22.43**	25.97**	-21.40	-4.07*	-9.53	-775.50**	4.74**	20.35**	-0.59	-7.47**
Type of epistasis		D	D	D	D	D	D	D	D	D	D
$P_1 \times P_7$	M (Mean)	52.00**	97.63**	111.17**	7.57**	2.03**	196.90**	3.84**	18.00**	4.30**	11.05**
	D (additive)	-0.33	-0.43	-1.50	-0.77	-3.67**	-100.93**	-0.60**	2.00**	-0.02	-0.90*
	H (dominance)	-3.05	-3.22	97.78**	-0.08	1.12	199.93**	-0.54	7.83**	-0.90**	9.08**
	I (add × add)	-3.33	-2.73	85.53**	-1.13	-0.40	85.07	-0.57*	16.00**	-1.20**	4.26**
	J (add × dom)	10.95**	11.52**	21.25**	0.02	-3.42**	-57.36**	-0.10	0.83	0.59**	1.04*
	L (dom × dom)	-5.90*	-4.90	-137.83**	3.50	-3.03	-217.73*	0.91	-19.65**	2.21**	-8.30**
Type of epistasis		C	C	D	D	D	D	D	D	D	D
$P_2 \times P_3$	M (Mean)	56.00**	102.10**	115.00**	7.60**	3.00**	270.67**	2.60**	15.00**	4.30**	9.83**
	D (additive)	-2.00**	-2.63**	-5.40*	-2.07**	-5.10**	-97.83*	0.47**	1.00*	-0.10	-3.82**
	H (dominance)	-35.57**	-40.77**	23.32*	5.62**	14.25**	407.13**	6.97**	20.96**	-0.77**	21.09**
	I (add × add)	-40.00**	-45.00**	10.53	1.73	9.00*	173.53	6.67**	22.00**	-1.00**	10.15**
	J (add × dom)	2.43**	1.60*	-6.95*	-2.38**	-6.38**	-128.60**	0.20*	4.01**	0.40**	-5.51**
	L (dom × dom)	23.13**	25.67**	-12.37	-1.63	-12.63*	-294.53	-6.35**	-32.58**	1.53**	0.01
Type of epistasis		D	D	D	D	D	D	D	D	D	C

Where, P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 21 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_2 \times P_4$	M (Mean)	45.00**	90.23**	98.67**	7.13**	6.47**	325.10**	3.85**	17.00**	3.00**	12.54**
	D (additive)	0.33	0.40	4.17	-0.90*	-1.27	34.20	-0.12	5.00**	-0.30**	0.46
	H (dominance)	-7.40**	-8.47**	38.25**	4.48*	-6.72	-66.60	3.70*	0.73	-0.73**	-1.76
	I (add × add)	-15.33**	-15.87**	40.33**	1.67	-11.07*	-164.13	1.57**	-0.67	-0.60*	-8.45**
	J (add × dom)	-0.73	0.43	0.48	-1.15*	0.75	58.37*	-0.33*	7.31**	-0.53**	-2.45**
	L (dom × dom)	2.80	4.40	-44.90**	-1.50	25.03**	110.67	2.68	6.87*	2.27**	12.96**
Type of epistasis		D	D	D	D	D	D	C	C	D	D
$P_2 \times P_5$	M (Mean)	55.00**	101.00**	121.67**	9.13**	6.03**	398.60**	3.35**	23.00**	3.30**	10.30**
	D (additive)	-1.00*	-1.00*	0.10	0.20	-6.33**	-172.80**	0.70**	-3.03**	0.80**	-4.58**
	H (dominance)	-23.57**	-27.00**	-15.02	2.32	29.95**	759.20**	-0.35	-24.82**	-0.43	39.71**
	I (add × add)	-26.00**	-29.60**	-35.40**	-2.13	8.53*	81.07	0.40	-10.07**	-0.40	23.16**
	J (add × dom)	4.43**	4.73**	-6.52	-0.22	-7.78**	-228.77**	0.14	4.35**	1.17**	-6.15**
	L (dom × dom)	-0.87	2.00	47.77*	0.70	7.83	166.93	-0.10	-10.36**	3.27**	-16.14**
Type of epistasis		C	D	D	C	C	C	C	C	D	D
$P_2 \times P_7$	M (Mean)	44.00**	88.90**	118.03**	9.10**	2.87**	291.40**	3.90**	19.00**	4.50**	10.40**
	D (additive)	-8.00**	-8.27**	-9.10**	-0.17	2.33**	23.03	-0.06	-3.00**	0.03	0.16
	H (dominance)	5.77**	6.08**	46.82**	-4.82*	2.98	-49.18	2.11**	11.65**	2.00**	9.67**
	I (add × add)	13.33**	14.40**	42.07*	-7.00**	-0.13	-168.47	1.87**	7.33**	1.13**	7.39 **
	J (add × dom)	4.43**	5.52**	2.78	0.68	1.12	9.72	-0.15*	1.31*	0.60**	-0.10
	L (dom × dom)	-27.53**	-27.23**	-49.90*	11.10**	2.17	147.70	-1.43**	-3.29	-2.00**	-8.30**
Type of epistasis		D	D	D	D	C	D	D	D	D	D

Where, P_2 = Brown Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 21 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_3 \times P_5$	M (Mean)	48.67**	93.90**	106.93**	8.03*	0.87*	199.93**	3.80**	23.00**	4.50**	10.03**
	D (additive)	-3.67**	-3.60**	-4.87*	-0.43	-2.23*	-76.20*	-0.97**	-13.94**	-1.14**	-3.89**
	H (dominance)	-3.00	-4.13*	40.97**	0.50	4.83	108.07	-2.47**	-23.30**	0.22	3.61*
	I (add × add)	-2.00	-2.80	30.00**	-2.07	3.67	25.07	-2.73**	-19.87**	-0.25	-2.70
	J (add × dom)	-2.67**	-2.10**	-9.93**	-0.53	-2.40*	-101.40**	-1.26**	-9.56**	-1.27**	-3.77**
	L (dom × dom)	-12.67**	-14.13**	-49.13**	-0.07	-7.40	-239.73*	5.34**	43.93**	1.16**	9.43**
Type of epistasis		C	C	D	D	D	D	D	D	C	C
$P_3 \times P_6$	M (Mean)	50.00**	95.00**	114.70**	8.54**	3.11**	272.80**	3.20**	22.00**	3.70**	11.99**
	D (additive)	1.33*	0.60	1.50	0.40	-0.27	12.07	-0.50**	-2.68**	-0.20*	0.74
	H (dominance)	-23.50**	-25.57**	-10.48*	0.80	-10.56*	-206.33*	1.57**	-13.34**	1.97**	-1.61
	I (add × add)	-29.33**	-32.00**	-13.80**	-0.95	-11.91*	-292.53**	1.40**	-5.30*	2.40**	-5.76**
	J (add × dom)	-0.17	-0.47	1.05	1.55*	-0.15	18.23	-0.76**	-2.37**	-0.23 *	0.48
	L (dom × dom)	40.33**	45.13**	10.57	-0.95	16.27**	235.87*	-0.60	-6.71*	-2.33**	1.83
Type of epistasis		D	D	D	D	D	D	D	C	D	D
$P_3 \times P_7$	M (Mean)	53.00**	98.00**	113.93**	7.07**	0.87**	207.13**	4.90**	21.33**	3.50**	11.27**
	D (additive)	-4.00**	-3.80**	-1.93	-9.07**	-29.63**	-1063.63**	0.30**	-2.67**	-0.50**	-31.99**
	H (dominance)	-18.00**	-19.45**	29.83*	20.77**	70.67**	2461.92**	-5.70**	2.64	-2.33**	64.59**
	I (add × add)	-17.33**	-17.87**	25.87*	18.53**	68.60**	2340.47**	-5.00**	2.67	-1.00**	59.70**
	J (add × dom)	4.00**	5.75**	11.50**	-7.90**	-29.57**	-1046.18**	0.47**	-1.36*	-0.43**	-30.56**
	L (dom × dom)	29.33**	31.30**	-8.87	-33.00**	-134.53**	-4651.83**	5.40**	0.05	3.87**	-117.95**
Type of epistasis		D	D	D	D	D	D	D	C	D	D

Where, P_3 = Yellow Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 21 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_4 \times P_1$	M (Mean)	49.33**	94.57**	112.27**	7.60**	7.57**	349.57**	3.42**	12.00**	3.70**	9.05**
	D (additive)	-1.33*	-1.37*	-2.77	0.87	6.27	90.00*	-0.03	-4.37**	0.28**	-1.67**
	H (dominance)	6.45**	5.37*	41.15*	5.68*	24.35*	466.42*	2.54**	14.63**	0.49*	38.88**
	I (add × add)	-8.00**	-7.93**	16.33	2.93	17.33	169.87	2.92**	25.40**	-0.17	29.80**
	J (add × dom)	0.88	0.43	-9.95**	1.18*	2.78	8.95	-0.41**	-1.19	0.49**	-0.94
	L (dom × dom)	-11.57**	-9.67**	-40.97*	-5.77	-36.70*	-484.70*	-5.70**	-27.65**	0.08	-53.52**
Type of epistasis		D	D	D	D	D	D	D	D	C	D
$P_4 \times P_3$	M (Mean)	48.00**	93.27**	110.60**	8.40**	6.37**	398.97**	3.00**	21.00**	5.42**	15.03**
	D (additive)	0.33	0.40	-6.97*	1.90*	3.57*	157.67*	0.10	2.04**	1.67**	8.93**
	H (dominance)	14.17**	13.73**	41.67*	2.17	16.20*	455.93	1.43**	-4.44*	-4.34**	30.22**
	I (add × add)	4.67*	4.40*	20.60	-1.93	2.33	-20.80	1.80**	-5.25*	-5.94**	5.75**
	J (add × dom)	5.83**	4.60**	-4.83	1.83*	0.27	102.73	0.05	2.74**	2.40**	10.16**
	L (dom × dom)	-28.33**	-27.46**	-13.07	1.93	12.53	163.87	-0.43	10.88**	8.74**	3.45
Type of epistasis		D	D	D	C	C	C	D	D	D	C
$P_4 \times P_5$	M (Mean)	55.77**	100.90**	122.17**	9.07**	9.63**	466.80**	2.50**	9.33**	3.60**	11.16**
	D (additive)	1.00*	1.07*	8.77**	0.83*	8.20**	291.20**	-0.15*	-4.25**	0.48**	2.21**
	H (dominance)	-18.23**	-18.73**	-43.27**	1.03	6.17	300.00*	3.93**	30.49**	2.55**	20.78**
	I (add × add)	-27.73**	-27.47**	-59.13**	-2.47	-4.80	-129.07	3.70**	40.84**	1.83**	9.11**
	J (add × dom)	7.50**	6.77**	5.83*	0.67	4.73**	211.07**	-0.49**	0.82	1.08**	3.56**
	L (dom × dom)	9.40**	10.53**	69.47**	-1.27	7.27	-87.07	-2.22**	-39.44**	-1.83**	-12.91**
Type of epistasis		D	D	D	D	C	D	D	D	D	D

Where, P_1 = BARI Sarisha-14, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sarisha-17; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 21 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_4 \times P_6$	M (Mean)	46.33**	91.67**	120.80**	8.47**	2.63**	320.77**	3.70**	14.20**	3.43**	11.37**
	D (additive)	2.00**	2.03**	-0.40	-2.00**	-3.57*	-56.17	1.20**	-1.67**	-0.37**	-0.49
	H (dominance)	14.00**	12.97**	364.62	2.58	50.18**	1232.70**	0.13	6.72**	-3.20**	3.43*
	I (add × add)	2.67	2.33	-17.87	-0.67	40.73**	912.20**	-0.28	17.20**	-2.20**	-6.55**
	J (add × dom)	6.00**	5.17**	1.28	-0.92	-6.75**	-104.93*	0.89**	-0.67	0.33**	0.48
	L (dom × dom)	-20.00**	-18.60**	744.10	2.03	-57.70**	-1677.13**	1.42**	-28.17**	3.87**	12.66**
Type of epistasis		D	D	C	C	D	D	C	D	D	C
$P_4 \times P_7$	M (Mean)	54.33**	99.33**	115.17**	9.93**	1.47*	271.77**	4.20**	17.67**	3.50**	10.62**
	D (additive)	-4.67**	-4.83**	-18.80**	-0.70	3.97**	73.63**	0.01	-2.83**	-0.47**	-0.99
	H (dominance)	-26.83**	-28.35**	-4.47	-7.30*	17.53**	28.68	-1.87**	-1.00	3.10**	1.99
	I (add × add)	-26.67**	-26.33**	0.40	-10.33**	14.20**	-103.00	-1.60**	5.00*	2.80**	-3.52
	J (add × dom)	8.83**	8.92**	-3.23	0.40	0.73	36.15	0.12	-0.83	0.33**	1.67*
	L (dom × dom)	21.67**	25.23**	10.93	15.13**	-12.40*	216.77	2.43**	-4.67	-3.40**	7.41*
Type of epistasis		D	D	D	D	D	C	D	C	D	C
$P_5 \times P_6$	M (Mean)	49.67**	94.83**	103.23**	8.57**	0.77**	187.13**	3.35**	14.67**	3.83**	8.82**
	D (additive)	-4.67**	-4.93**	-9.30**	-1.43**	-2.67**	-122.23**	-0.66**	-3.30**	-1.02 **	-3.68**
	H (dominance)	-10.17**	-10.13**	54.28**	-2.65	4.68*	109.63	1.77**	10.23	-0.47*	4.93*
	I (add × add)	-16.00**	-16.13**	41.53**	-3.53*	3.07	4.33	2.30**	23.40	0.71**	1.72
	J (add × dom)	-7.17**	-7.50**	-4.68*	-0.18	-2.38*	-90.87**	-0.63**	-7.37**	-0.92**	-4.07**
	L (dom × dom)	19.00**	19.20**	-55.63**	1.97	-4.43	-77.80	-5.59**	-27.53	-1.52**	-1.87
Type of epistasis		D	D	D	D	D	D	D	D	C	D

Where, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 21 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_5 \times P_7$	M (Mean)	52.67**	97.67 **	106.10**	6.37**	1.17**	160.77**	3.65**	20.00**	4.33**	8.63**
	D (additive)	-2.33**	-2.00**	-36.77**	-1.70**	0.67	-105.37**	0.14*	-2.83**	0.23**	-4.43**
	H (dominance)	-7.33**	-9.05**	41.60**	7.80**	-1.53	97.12*	0.54*	-10.48**	0.60*	-1.62
	I (add × add)	-0.67	-1.33	29.53**	7.40**	-2.27	33.40	0.29	-0.33	1.40**	-1.31
	J (add × dom)	4.67**	6.05**	-18.27**	-0.43	0.90	-62.72**	0.60**	-5.90**	0.43**	-3.12**
	L (dom × dom)	-10.67**	-6.70*	11.07	-12.00**	2.67	-68.50	0.57	8.65*	-3.73**	4.70
Type of epistasis		C	C	C	D	D	D	C	D	D	D
$P_6 \times P_2$	M (Mean)	48.00**	93.27**	120.77**	7.50**	8.50**	435.87**	3.30**	12.07**	4.20**	11.80**
	D (additive)	0.67	0.57	1.17	0.67	3.80**	177.60**	3.65**	14.28**	-0.98**	5.81**
	H (dominance)	15.60**	15.67**	-24.63	8.20**	5.77	-206.50	2.37**	-1.58	5.55**	2.31
	I (add × add)	6.67**	6.33**	-31.67*	3.07*	-14.93**	-758.93**	2.30**	0.51	3.97**	-13.59**
	J (add × dom)	-2.27**	-2.60**	3.17	-0.17	4.97**	202.20**	4.17**	10.97**	-1.45**	7.76**
	L (dom × dom)	-35.20**	-35.73**	35.67*	3.20	44.60**	1571.93**	-1.94**	21.29**	-5.43**	48.49**
Type of epistasis		D	D	D	C	C	D	D	D	D	C
$P_6 \times P_7$	M (Mean)	44.00**	89.00**	117.97**	7.43**	5.03**	278.70**	3.01**	9.33**	4.70**	9.36**
	D (additive)	-5.67**	-5.50**	-22.47**	0.63	-4.97**	-98.70*	0.21**	-0.21	-0.09	3.15**
	H (dominance)	30.83**	30.12**	70.02**	16.48**	-1.75	582.82**	2.88**	26.49**	4.11**	23.32**
	I (add × add)	34.00**	34.33**	63.73**	14.73**	-5.13	407.27**	3.22**	38.44**	3.20**	17.58**
	J (add × dom)	3.83**	5.12**	-8.58*	0.65	-5.02**	-87.42*	0.64**	0.79	0.10	4.85**
	L (dom × dom)	-48.33**	-46.63**	-97.90**	-23.23**	-0.63	-938.83**	-3.80**	-46.13**	-4.98**	-25.39**
Type of epistasis		D	D	D	D	C	D	D	D	D	D

Where, P_2 = Brown Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively; D and C denoted, duplicate and complementary epistasis, respectively.

Table 22. Estimation of gene effects for yield and yield contributing traits in different cross materials of selected *Brassica rapa* genotypes [3 Parameter Model in the absence of epistasis; Jinks and Jones (1958)]

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_1 \times P_2$	M (Mean)	53.88**	96.97**	93.40**	4.03*	-7.80	125.75	3.44**	24.92**	3.53**	-9.10*
	D (additive)	1.15**	1.83**	-10.87**	0.07	-1.47**	-56.88**	-0.59**	5.49**	-0.03	-2.19**
	H (dominance)	5.35	8.00*	60.50*	7.83	37.83**	658.85*	0.46	-18.84**	1.50**	59.12**
$P_1 \times P_3$	M (Mean)	44.72**	89.67**	95.78**	6.52**	9.38*	76.32	4.19**	24.09**	5.22**	13.27 **
	D (additive)	-3.28**	-2.40**	-9.32**	0.38	-0.18	-26.12**	-0.33**	2.48**	-0.53**	-0.50*
	H (dominance)	-6.15	-5.17	38.42*	2.98	-16.58*	332.62*	-2.24*	-12.14*	-4.36**	-7.60*
$P_1 \times P_5$	M (Mean)	46.12**	92.17**	59.38**	10.09**	5.88**	138.72**	41.49	21.40**	6.12**	6.49**
	D (additive)	-4.28**	-3.90**	-4.25*	0.48*	-0.02	-0.92	-0.04	-1.89**	-0.39**	-0.62**
	H (dominance)	-0.35	-2.20	60.52**	-7.04	-10.95**	-56.82	-77.19	19.48**	-7.76**	3.05
$P_1 \times P_6$	M (Mean)	65.22**	113.35**	67.87**	5.53**	-2.83	-266.25**	4.00**	34.17**	2.60**	-1.11
	D (additive)	-1.78**	-1.33**	-8.87**	-0.77**	-0.30	-32.28**	0.30*	2.17**	-0.49**	-0.24
	H (dominance)	-43.65**	-50.29**	75.17**	6.83*	15.10*	1282.72**	-2.30**	-38.52**	2.28**	21.83**
$P_1 \times P_7$	M (Mean)	52.05**	98.02**	27.82**	8.48**	0.72	42.50	4.34**	9.17**	5.31**	4.43**
	D (additive)	-11.28**	-11.95**	-22.75**	-0.78*	-0.25	-43.57**	-0.50**	1.17*	-0.59**	-1.93**
	H (dominance)	2.85	1.68	235.62**	-3.58	4.15	417.67**	-1.45*	27.48**	-3.12**	17.39**

Where, P_1 = BARI Sarisha-14, P_2 = Brown Special, P_3 = Yellow Special, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively.

Table 22 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_2 \times P_3$	M (Mean)	79.57**	128.90**	100.25**	4.38**	-7.28	-6.53	-2.47**	-3.62*	5.07**	-0.71
	D (additive)	-4.43**	-4.23**	1.55	0.32	1.28**	30.77**	0.26**	-3.00**	-0.50**	1.69**
	H (dominance)	-58.70**	-66.43**	35.68	7.25*	26.88*	701.67*	13.32**	53.53**	-2.30**	21.07**
$P_2 \times P_4$	M (Mean)	49.40**	95.57**	68.32**	4.52*	16.08**	386.07**	2.67**	18.35**	3.93**	16.66**
	D (additive)	1.07**	-0.03	3.68*	0.25	-2.02**	-24.17*	0.22**	-2.31**	0.23**	2.92**
	H (dominance)	-10.20*	-12.87*	83.15**	5.98	-31.75*	-177.27	1.02	-6.14	-3.00**	-14.72**
$P_2 \times P_5$	M (Mean)	66.57**	115.00**	141.12**	8.15**	-6.98	60.73	3.50**	32.84**	4.33**	-13.59**
	D (additive)	-5.43**	-5.73**	6.62**	0.42	1.45**	55.97**	0.56**	-7.38**	-0.37**	1.57**
	H (dominance)	-22.70**	-29.00**	-62.78*	1.62	22.12*	592.27*	-0.25	-14.46*	-3.70**	55.85**
$P_2 \times P_7$	M (Mean)	34.23**	79.05**	82.15**	14.28**	1.92	352.92**	2.49**	12.35**	3.00**	3.49*
	D (additive)	-12.43**	-13.78**	-11.88**	-0.85*	1.22*	13.32	0.09	-4.31**	-0.57**	0.26
	H (dominance)	33.30**	33.32**	96.72*	-15.92**	0.82	-196.88	3.53**	14.94*	4.00**	17.98**
$P_3 \times P_5$	M (Mean)	47.00**	92.43**	74.17**	7.77**	-3.40	85.97	6.37**	45.63**	4.68**	10.58**
	D (additive)	-1.00**	-1.50**	5.07*	0.10	0.17	25.20**	0.29**	-4.38**	0.13**	-0.12
	H (dominance)	9.67*	10.00*	90.10**	0.57	12.23	347.80*	-7.81**	-67.23**	-0.94	-5.82

Where, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively.

Table 22 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_3 \times P_6$	M (Mean)	71.83**	119.07**	122.58**	7.90**	12.46**	434.93**	2.26**	26.99**	2.13**	13.26**
	D (additive)	1.50**	1.07**	0.45	-1.15**	-0.12	-6.17	0.26**	-0.31	0.03	0.26
	H (dominance)	-63.83**	-70.70**	-21.05	1.76	-26.83**	-442.20*	2.17**	-6.63	4.30**	-3.44
$P_3 \times P_7$	M (Mean)	69.33**	115.55**	96.80**	-11.57**	-68.10**	-2186.78**	9.10**	20.03**	5.63**	-50.51**
	D (additive)	-8.00**	-9.55**	-13.43**	-1.17**	-0.07	-17.45*	-0.17**	-1.31**	-0.07	-1.43**
	H (dominance)	-47.33**	-50.75**	38.70*	53.77**	205.20**	7113.75**	-11.09**	2.59	-6.20**	182.54**
$P_4 \times P_1$	M (Mean)	43.22**	89.47**	81.45**	3.32	-13.78	-4.82	0.72*	-2.23	3.47**	-23.77**
	D (additive)	-2.22**	-1.80**	7.18**	-0.32	3.48**	81.05**	0.38**	-3.17**	-0.21**	-0.73**
	H (dominance)	18.02**	15.03**	82.12*	11.45*	61.05*	951.12*	8.24**	42.28**	0.42	92.40**
$P_4 \times P_3$	M (Mean)	33.83**	79.53**	86.50**	7.80*	1.40	211.97	2.17**	25.94**	9.77**	0.78
	D (additive)	-5.50**	-4.20**	-2.13	0.07	3.30**	54.93**	0.05	-0.69*	-0.73**	-1.23**
	H (dominance)	42.50**	41.20**	54.73	0.23	3.67	292.07	1.87**	-15.32**	-13.08**	26.77**
$P_4 \times P_5$	M (Mean)	67.23**	112.90**	161.17**	8.23**	8.37	295.03*	-0.02	-15.77**	1.87**	-2.46
	D (additive)	-6.50**	-5.70**	2.93*	0.17	3.47**	80.13**	0.34**	-5.07**	-0.60**	-1.35**
	H (dominance)	-27.63**	-29.27**	-112.73**	2.30	-1.10	387.07	6.14**	69.93**	4.38**	33.69**
$P_4 \times P_6$	M (Mean)	34.33**	80.53**	124.52**	7.68**	-36.88**	-714.87**	3.99**	3.80*	6.00**	12.82**
	D (additive)	-4.00**	-3.13**	-1.68	-1.08**	3.18**	48.77**	0.31**	-1.00**	-0.70**	-0.97**
	H (dominance)	34.00**	31.57**	-379.48	0.55	107.88**	2909.83**	-1.30*	34.88**	-7.07**	-9.24*

Where, P_1 = BARI Sarisha-14, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively.

Table 22 (Cont'd).

Crosses	Gene effects	Days to 50% flowering	Days to 80% maturity	Plant height	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length	No. of seeds siliqua^{-1}	1000 seed weight	Seed yield plant^{-1}
$P_4 \times P_7$	M (Mean)	73.17**	119.82**	120.13**	17.37**	-10.40*	311.62**	5.74**	17.00**	1.10**	11.48**
	D (additive)	-13.50**	-13.75**	-15.57**	-1.10**	3.23**	37.48**	-0.12**	-2.00**	-0.80**	-2.66**
	H (dominance)	-48.50**	-53.58**	-15.40	-22.43**	29.93**	-188.08	-4.30**	3.67	6.50**	-5.43
$P_5 \times P_6$	M (Mean)	59.50**	104.70**	62.18**	10.38**	-2.68	112.87*	1.07**	2.67	3.69**	5.89**
	D (additive)	2.50**	2.57**	-4.62**	-1.25**	-0.28	-31.37**	-0.03	4.07**	-0.10*	0.39*
	H (dominance)	-29.16**	-29.33**	109.92**	-4.62	9.12	187.43	7.36**	37.76	1.06*	6.79
$P_5 \times P_7$	M (Mean)	53.67 **	100.52**	88.07**	-0.53	2.60	95.08*	3.52**	27.40**	3.10**	10.62**
	D (additive)	-7.00**	-8.05**	-18.50**	-1.27**	-0.23	-42.65**	-0.46**	3.07**	-0.20**	-1.31**
	H (dominance)	3.33	-2.35	30.53	19.80**	-4.20	165.62	-0.02	-19.12**	4.33**	-6.32
$P_6 \times P_2$	M (Mean)	31.40**	76.50**	142.00**	4.20*	16.77**	932.10**	1.63**	18.18**	0.07	22.77**
	D (additive)	2.93**	3.17**	-2.00	0.83*	-1.17*	-24.60*	-0.52**	3.31**	0.47**	-1.95**
	H (dominance)	50.80**	51.40**	-60.30*	5.00	-38.83**	-1778.43**	4.31**	-22.87**	10.98**	-46.18**
$P_6 \times P_7$	M (Mean)	16.50**	62.28**	58.48**	-6.62*	5.75	-247.42*	0.62**	-15.44**	1.40**	-8.65**
	D (additive)	-9.50**	-10.62**	-13.88**	-0.02	0.05	-11.28	-0.43**	-1.00**	-0.10*	-1.70**
	H (dominance)	79.17**	76.75**	167.92**	39.72**	-1.12	1521.65**	6.68**	72.62**	9.09**	48.71**

Where, P_2 = Brown Special, P_4 = Tori-7, P_5 = BARI Sarisha-17, P_6 = BARI Sarisha-15, P_7 = BARI Sarisha-6; * and ** means significant at 0.05 and 0.01 level of probability, respectively.

height (in the crosses $P_1 \times P_2$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_6$, $P_3 \times P_7$, $P_4 \times P_1$, $P_4 \times P_6$ and $P_6 \times P_2$), number of primary branches plant^{-1} (in the crosses P_1XP_6, $P_1 \times P_7$, $P_2 \times P_5$, $P_2 \times P_7$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_1$, $P_4 \times P_7$, $P_6 \times P_2$ and $P_6 \times P_7$), number of secondary branches plant^{-1} (in the crosses $P_1 \times P_5$, $P_2 \times P_4$, $P_2 \times P_7$, $P_4 \times P_1$, $P_4 \times P_3$ and $P_4 \times P_7$), number of siliqua plant^{-1} (in the crosses $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_6$ and $P_4 \times P_6$), siliqua length (in the crosses $P_2 \times P_4$, $P_3 \times P_6$, $P_4 \times P_1$ and $P_5 \times P_7$), number of seeds siliqua^{-1} (in the crosses $P_1 \times P_6$ and $P_6 \times P_7$), thousand seed weight (in the crosses $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_7$ and $P_6 \times P_7$) and seed yield plant^{-1} (in the crosses $P_1 \times P_6$, $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_6$, $P_4 \times P_6$ and $P_4 \times P_7$). Non-significant additive effects (D) indicated the involvement of several genes with small effects and different expressions (Mathews *et al.* 2008). Sridhar and Raut (2003), Singh, *et al.* (2010) and Mishra (2010) reported only additive gene actions were important for different traits.

The dominance effects (H) were also found to be significant in most of the crosses for most of the traits except for days to 50% flowering (in the crosses $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_7$ and $P_3 \times P_5$), days to 80% maturity (in the crosses $P_1 \times P_3$ and $P_1 \times P_7$), plant height (in the crosses $P_2 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_6 \times P_2$), number of primary branches plant^{-1} (in the crosses $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_5$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_6$ and $P_5 \times P_6$), number of secondary branches plant^{-1} (in the crosses $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_5$, $P_5 \times P_7$, $P_6 \times P_2$ and $P_6 \times P_7$), number of siliqua plant^{-1} (in the crosses $P_1 \times P_5$, $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_3$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_6 \times P_2$), siliqua length (in the crosses $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_7$, $P_2 \times P_5$ and $P_4 \times P_6$), number of seeds siliqua^{-1} (in the crosses $P_2 \times P_4$, $P_3 \times P_7$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_6 \times P_2$), thousand seed weight (in the crosses $P_2 \times P_5$ and $P_3 \times P_5$) and seed yield plant^{-1} (in the crosses $P_1 \times P_3$, $P_2 \times P_4$, $P_3 \times P_6$, $P_4 \times P_7$, $P_5 \times P_7$ and $P_6 \times P_2$).

Dominance gene effects (H) were higher than the additive gene effects (D) in most of the traits across the crosses. Therefore, heterosis breeding was suggested. The sign of D and H indicated which parent concentrated the highest number of genes or positive alleles for increasing the traits. The significant positive D indicated predominant additive effects while the significant negative D indicated the inheritance of these traits was not controlled by additive gene actions. Similarly, the significant positive H indicated predominant dominant effect and selection should be delayed until heterozygosity is reduced while negative H indicated that dominance effects were to be contributed by the parents having alleles responsible for low values for the traits. In this study, most of the traits in most of the crosses showed positive H indicated direct dominance. Significant but similar sign of D

and H indicated the predominant role of additive and dominant gene effects. Significant additive and dominance gene with greater magnitude of non-additive gene action indicated the presence of both additive and non-additive genes with greater magnitude of non-additive genes for the inheritance of the traits. Mishra (2010), Gupta (2011), Peerasak and Supapan (2014) also reported additive and dominance gene actions with greater magnitude of non-additive gene actions for the inheritance of the studied traits. The high magnitude of dominance effects than the additive effects can be improved through conventional breeding (pedigree/bulk/single seed descent method) if selection delayed to later generation when dominance effect would have diminished (Sirohi and Gupta1993).

The additive × additive (I) effects were found to be significant in the maximum traits over the crosses except for days to 50% flowering and 80% maturity (in the crosses $P_1 \times P_7$, $P_3 \times P_5$, $P_4 \times P_6$ and $P_5 \times P_7$), for plant height (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_2 \times P_3$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_6$ and $P_4 \times P_7$), for number of primary branches plant^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_5$ and $P_4 \times P_6$), for number of secondary branches plant^{-1} (in the crosses $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_5$, $P_5 \times P_6$, $P_5 \times P_7$ and $P_6 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$), for siliqua length (in the crosses $P_1 \times P_5$, $P_2 \times P_5$, $P_4 \times P_6$ and $P_5 \times P_7$), for of seeds siliqua^{-1} (in the crosses $P_1 \times P_3$, $P_2 \times P_4$, $P_3 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$ and $P_6 \times P_2$), for 1000 seed weight (in the crosses $P_1 \times P_2$, $P_2 \times P_5$, $P_3 \times P_5$ and $P_4 \times P_1$) and for seed yield plant^{-1} (in the crosses $P_1 \times P_5$, $P_3 \times P_5$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$). Positive additive × additive interaction showed association and negative form showed dispersion of alleles in parents. Therefore, in this study positive significant values of I in most of the traits across the crosses indicated alleles association in the parents.

Additive × dominance effects were also found to be significant in most of the traits for most of the crosses except for days to 50% flowering and 80% maturity (in the crosses $P_1 \times P_6$, $P_2 \times P_4$, $P_3 \times P_6$ and $P_4 \times P_1$), for plant height (in the crosses $P_1 \times P_5$, $P_2 \times P_4$, $P_2 \times P_5$, $P_2 \times P_7$, $P_3 \times P_6$, $P_4 \times P_3$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_6 \times P_2$), for number of primary branches plant^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_5$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$, $P_6 \times P_2$ and $P_6 \times P_7$), for number of secondary branches plant^{-1} (in the crosses $P_2 \times P_4$, $P_2 \times P_7$, $P_3 \times P_6$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_7$ and $P_5 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_2 \times P_7$, $P_3 \times P_6$, $P_4 \times P_1$, $P_4 \times P_3$ and $P_4 \times P_7$), for siliqua length (in the crosses $P_1 \times P_5$, $P_1 \times P_7$,

$P_2 \times P_5$, $P_4 \times P_3$ and $P_4 \times P_7$), for number of seeds siliqua^{-1} (in the crosses $P_1 \times P_5$, $P_1 \times P_7$, $P_4 \times P_1$, $P_4 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_6 \times P_7$), for 1000 seed weight (in the cross $P_6 \times P_7$) and for seed yield plant^{-1} (in the crosses $P_1 \times P_6$, $P_2 \times P_7$, $P_3 \times P_6$, $P_4 \times P_1$ and $P_4 \times P_6$). Non-significant additive × dominance epistasis (J) with negative sign indicated this type of epistasis were not contributing in the inheritance of any trait in the crosses.

While for dominance × dominance (L) effects, significant result was observed in most of the traits across the crosses except for days to 50% flowering and 80% maturity (in the crosses $P_1 \times P_5$, $P_1 \times P_7$, $P_2 \times P_4$ and $P_2 \times P_5$), for plant height (in the crosses $P_1 \times P_6$, $P_2 \times P_3$, $P_3 \times P_6$, $P_3 \times P_7$, $P_4 \times P_3$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_5 \times P_7$), for number of primary branches plant^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_6$, $P_5 \times P_6$ and $P_6 \times P_2$), for number of secondary branches plant^{-1} (in the crosses $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_5$, $P_2 \times P_7$, $P_3 \times P_5$, $P_4 \times P_3$, $P_4 \times P_5$, $P_5 \times P_6$, $P_5 \times P_7$ and $P_6 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_1 \times P_2$, $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_2 \times P_7$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$), for siliqua length (in the crosses $P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_6$, $P_4 \times P_3$ and $P_5 \times P_7$), for number of seeds siliqua^{-1} (in the crosses $P_2 \times P_7$, $P_3 \times P_7$, $P_4 \times P_7$ and $P_5 \times P_6$), for 1000 seed weight (in the crosses $P_1 \times P_6$ and $P_4 \times P_1$) and for seed yield plant^{-1} (in the crosses $P_1 \times P_5$, $P_2 \times P_3$, $P_3 \times P_6$, $P_4 \times P_3$, $P_5 \times P_6$ and $P_5 \times P_7$). Significant dominance × dominance (L) interaction indicated that it had major role in the genetic control of these traits. The positive sign of L show unidirectional dominant and negative sign of L show ambi-directional dominant. In this study, most of the traits showed negetive sign of L so ambi-directional dominant was present.

Therefore, the traits in different crosses with significant and negative estimates of H, I and L gene effects suggested that selection should be delayed to later generation until negative alleles removed. Hence, improvement of these traits could be achieved through recurrent selection procedure (Singh and Narayanan 2000a). Selection should be delayed up to 6th segregating generation for highly significant genotypic mean square and pre-dominant role of non-additive type of gene action while selection in early generations would be suitable due to prominance of additive gene action (Arifullah *et al.* 2012).

3.3.1 Types of epistasis

In addition to additive gene effects, dominance (H) and dominance × dominance (L) gene effects had also high contributions in the genetic control of different traits. The gene interaction was considered to be complementary when the dominance (H) and dominance

× dominance (L) had the same signs and was duplicate when the signs differed (Mather and Jinks, 1982). Duplicate-type epistasis indicated predominant dispersed alleles at the interacting loci and leading to reduced heterosis (Shashikumar *et al.* 2010). In this study duplicate epistasis were to be found in the maximum crosses for most of the traits except for days to 50% flowering and 80% maturity (in the crosses $P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_7$, $P_2 \times P_5$, $P_3 \times P_5$ and $P_5 \times P_7$), for plant height (in the crosses $P_4 \times P_6$ and $P_5 \times P_7$), for number of primary branches plant^{-1} (in the crosses $P_2 \times P_5$, $P_4 \times P_3$, $P_4 \times P_6$ and $P_6 \times P_2$), for number of secondary branches plant^{-1} (in the crosses $P_2 \times P_5$, $P_2 \times P_7$, $P_4 \times P_3$, $P_4 \times P_5$, $P_6 \times P_2$ and $P_6 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_2 \times P_5$, $P_4 \times P_3$ and $P_4 \times P_7$), for siliqua length (in the crosses $P_1 \times P_2$, $P_2 \times P_4$, $P_2 \times P_5$, $P_4 \times P_6$ and $P_5 \times P_7$), for number of seeds siliqua^{-1} (in the crosses $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_6$, $P_3 \times P_7$ and $P_4 \times P_7$), for 1000 seed weight (in the crosses $P_3 \times P_5$, $P_4 \times P_1$ and $P_5 \times P_6$) and for seed yield plant^{-1} (in the crosses $P_1 \times P_5$, $P_2 \times P_3$, $P_3 \times P_5$, $P_4 \times P_3$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_6 \times P_2$) while the cross materials that showed complementary epistasis, their respective parents could be identified as the best parents as gene actions for this epistasis acts in favour of heterosis. Similar result was observed by Ajay *et al.* (2012).

In duplicated type epistasis variability in segregating generations might be reduced which hindered the selection process (Kumar and Patra 2010), hence it was difficult to utilize them in breeding programme (Sameer *et al.* 2009). Therefore, selection with duplicate type epistasis must be delayed to advanced generations. Duplicate type non-allelic interactions were also reported for different yield contributing characters by Singh *et al.* (2007), Dashti *et al*. (2010), Kabdal and Singh (2010) and Singh *et al.* (2012 b). The results also matched with Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al*. (2019) and Abdelsatar *et al.* (2020).

3.4 Components of variance

The additive gene effects or interaction effects related to additive effects, are subjected to increasing the degree of gene dispersion of the traits between the parents, while dominance gene effect is pure multiple of dominance direct effect in each locus. Therefore, additive gene effect may be little because of gene dispersion and also dominance gene effect can be little because of ambi-directional dominant. But, genetic variances are mean squares of each locus effects and are not affected by gene dispersion and dominance direct effect. Thus, data of generation variances could be used to complete genetic information. The variation estimation using values from six generations showed that the variations due to

dominance effect were predominant for most of the studied traits over majority of the crosses except for days to 50% flowering (in the crosses $P_2 \times P_3$, $P_4 \times P_3$, $P_4 \times P_7$ and $P_5 \times P_6$), for days to 80% maturity (in the crosses $P_2 \times P_3$ and $P_2 \times P_4$), for plant height (in the crosses $P_1 \times P_2$, $P_2 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_6 \times P_2$), for number of primary branches plant^{-1} (in the crosses $P_2 \times P_4$, $P_3 \times P_7$, $P_4 \times P_3$ and $P_4 \times P_7$), for number of secondary branches plant^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_7$, $P_4 \times P_3$, $P_4 \times P_6$ and $P_5 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_1 \times P_3$, $P_1 \times P_6$, $P_2 \times P_3$, $P_2 \times P_4$, $P_4 \times P_1$ and $P_4 \times P_3$), for siliqua length (in the crosses $P_1 \times P_5$, $P_4 \times P_1$, $P_4 \times P_3$, $P_4 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_6 \times P_7$), for number of seeds siliqua^{-1} (in the crosses $P_1 \times P_3$, $P_2 \times P_7$ and $P_4 \times P_7$), for 1000 seed weight (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_6$, $P_3 \times P_6$ and $P_4 \times P_5$) and for seed yield plant^{-1} (in the crosses $P_1 \times P_5$, $P_1 \times P_6$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_3$, $P_4 \times P_5$, $P_4 \times P_6$ and $P_6 \times P_2$) (Table 22). In these crosses additive gene action was predominant which indicated that the gene action was fixable and selection would be very effective for improving the traits with predominant additive variance. Predominance of dominance gene action for most of the traits across the crosses revealed that the gene action was non-fixable in nature and selection for these traits would be postponed to later generations (Ajay *et al.* 2012 and Pathak *et al.* 2014). Negative dominance variances was found in many crosses for different traits which might be due to sampling error and/or genotypes and environmental interactions (Mather, 1949 and Robinson *et al.* 1955). Deb and Khaleque (2009) and Ajay *et al*. (2012) also reported negative dominance variances for different traits. Ajay *et al*. (2012) and Parihar *et al.* (2015) reported that both additive and dominance variances were important for the inheritance of the traits.

The phenotypic variances were found to be higher than the genotypic variances for most of the traits across the crosses except for days to 50% flowering (in the crosses $P_1 \times P_2$ and $P_1 \times P_3$), for plant height (in the crosses $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$), for number of primary branches plant^{-1} (in the crosses $P_1 \times P_6$, $P_3 \times P_7$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_5 \times P_7$), for number of secondary branches plant^{-1} (in the crosses $P_3 \times P_7$, $P_4 \times P_6$, $P_5 \times P_6$ and $P_5 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_1 \times P_6$, $P_2 \times P_5$, $P_3 \times P_7$, $P_4 \times P_6$ and $P_6 \times P_2$), for siliqua length (in the crosses $P_1 \times P_2$, $P_1 \times P_5$, $P_2 \times P_4$, $P_2 \times P_7$, $P_4 \times P_3$ and $P_6 \times P_7$), for number of seeds siliqua^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_3$ and $P_1 \times P_5$) and for 1000 seed weight (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_3 \times P_6$ and $P_6 \times P_7$) (Table 23 and Plate 18-22). The higher phenotypic variance over the genotypic

Table 23. Estimation of components of variation and genetic parameters for yield and yield contributing traits in different cross materials of *Brassica rapa* genotypes

Days to 50% flowering									Days to 80%maturity								
Crosses	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**	**Crosses**	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**
$P_1 \times P_2$	-1.00	0.17	-0.51	-7.57	1.01	-8.58	7.57	-2.92	**$P_1 \times P_2$**	-0.21	0.25	-0.12	-3.60	0.73	-4.33	17.14	-2.43
$P_1 \times P_3$	-1.44	-0.50	-0.73	-8.06	-2.48	-5.58	5.60	1.50	**$P_1 \times P_3$**	-0.62	0.14	-0.34	-6.37	0.94	-7.31	10.27	-2.78
$P_1 \times P_5$	0.11	0.58	0.09	-4.28	6.70	-10.99	-38.91	-1.28	**$P_1 \times P_5$**	0.31	0.71	0.34	-1.31	12.22	-13.53	-4.23	-1.05
$P_1 \times P_6$	-0.42	0.01	-0.30	-0.85	5.01	-5.86	2.02	-1.17	**$P_1 \times P_6$**	-0.10	-0.08	-0.08	-1.35	-0.33	-1.02	13.50	1.74
$P_1 \times P_7$	-0.42	0.17	-0.30	-6.78	0.92	-7.70	16.14	-2.89	**$P_1 \times P_7$**	-0.14	-0.08	-0.10	-1.69	-0.14	-1.55	12.07	3.27
$P_2 \times P_3$	0.65	0.89	0.58	4.67	10.07	-5.40	7.18	-0.73	**$P_2 \times P_3$**	0.54	0.50	0.47	6.15	5.36	0.79	11.39	0.38
$P_2 \times P_4$	0.22	0.17	0.16	2.23	0.92	1.31	10.14	1.19	**$P_2 \times P_4$**	0.44	0.69	0.36	1.64	6.03	-4.38	3.73	-0.85
$P_2 \times P_5$	0.22	0.01	0.16	6.14	2.99	3.15	27.91	1.00	**$P_2 \times P_5$**	0.03	0.38	0.02	-2.30	3.21	-5.51	-76.67	-1.31
$P_2 \times P_7$	0.15	0.18	0.10	1.31	0.46	0.85	8.73	1.36	**$P_2 \times P_7$**	0.19	-0.05	0.14	2.91	-0.59	3.50	15.32	-2.44
$P_3 \times P_5$	0.03	-0.20	0.02	1.93	-0.92	2.85	64.33	-1.76	**$P_3 \times P_5$**	-0.63	-1.78	-0.39	2.88	-10.19	13.07	-4.57	-1.13
$P_3 \times P_6$	0.16	0.58	0.12	-1.82	4.09	-5.92	-11.38	-1.20	**$P_3 \times P_6$**	0.39	1.00	0.33	-1.89	10.03	-11.92	-4.85	-1.09
$P_3 \times P_7$	0.17	0.08	0.12	1.81	0.46	1.35	10.65	1.71	**$P_3 \times P_7$**	-0.22	-1.25	-0.16	5.56	-8.85	14.41	-25.27	-1.28
$P_4 \times P_1$	-0.63	-0.20	-0.41	-6.16	-0.92	-5.24	9.78	2.39	**$P_4 \times P_1$**	-0.21	-0.64	-0.15	0.79	-3.57	4.36	-3.76	-1.10
$P_4 \times P_3$	0.11	0.17	0.08	0.74	0.92	-0.18	6.73	-0.45	**$P_4 \times P_3$**	0.11	-0.08	0.08	2.03	-0.54	2.57	18.45	-2.18
$P_4 \times P_5$	0.03	-0.20	0.02	-1.84	2.30	-4.14	-61.33	-1.34	**$P_4 \times P_5$**	-0.10	0.46	-0.08	-4.74	3.49	-8.23	47.40	-1.54
$P_4 \times P_6$	-0.05	-0.40	-0.07	0.61	-1.84	2.45	-12.20	-1.15	**$P_4 \times P_6$**	0.51	0.13	0.41	4.21	0.70	3.51	8.25	2.24
$P_4 \times P_7$	-0.10	-0.15	-0.09	-0.31	-0.92	0.61	3.10	-0.82	**$P_4 \times P_7$**	-0.20	-0.40	-0.13	0.16	-2.03	2.20	-0.80	-1.04
$P_5 \times P_6$	-0.13	-0.20	-0.09	-0.31	-0.92	0.61	2.38	-0.82	**$P_5 \times P_6$**	0.07	0.53	0.05	-3.22	4.95	-8.17	-46.00	-1.28
$P_5 \times P_7$	-0.10	-0.29	-0.06	-1.17	1.03	-2.20	11.70	-2.14	**$P_5 \times P_7$**	-0.50	-1.20	-0.33	1.73	-6.90	8.63	-3.46	-1.12
$P_6 \times P_2$	0.22	0.17	0.16	2.23	0.92	1.31	10.14	1.19	**$P_6 \times P_2$**	0.14	-0.08	0.10	2.59	-0.35	2.95	18.50	-2.89
$P_6 \times P_7$	-0.03	0.33	-0.02	-2.15	1.84	-3.98	71.67	-1.47	**$P_6 \times P_7$**	-0.03	-0.08	-0.02	0.68	-1.16	1.84	-22.67	-1.26

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6; H_{BS} = heritability in broad sense, H_{NS} = heritability in narrow sense; GA = genetic advance; V_G = genotypic variance; V_D = additive variance; V_H = dominance variance; V_P = phenotypic variance; h/d = Degree of dominance (H/D).

Table 23 (Cont'd).

	Plant height								Number of primary branches plant^{-1}							
Crosses	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**
$P_1 \times P_2$	-0.45	0.37	-1.49	-197.87	57.45	-255.32	439.71	-2.11	-0.67	-1.38	-0.39	0.09	-7.37	7.46	-0.13	-1.01
$P_1 \times P_3$	-3.39	-0.46	-8.42	-549.10	-40.00	-509.10	161.98	3.57	0.33	1.31	0.25	-4.51	9.48	-13.99	-13.67	-1.22
$P_1 \times P_5$	-0.30	1.78	-0.98	-359.92	269.24	-629.16	1199.73	-1.53	0.48	1.00	0.40	-0.08	9.76	-9.84	-0.17	-1.00
$P_1 \times P_6$	-2.13	-2.06	-4.88	-163.01	-151.14	-11.87	76.53	0.28	-3.42	-0.50	-1.41	-15.45	-1.69	-13.77	4.52	2.86
$P_1 \times P_7$	-1.89	-1.49	-5.02	-227.93	-148.74	-79.19	120.60	0.73	-4.08	-1.75	-1.68	-16.09	-4.60	-11.50	3.94	1.58
$P_2 \times P_3$	-0.07	0.60	-0.32	-218.79	177.62	-396.40	3125.57	-1.49	-2.47	-1.00	-1.14	-12.15	-3.41	-8.74	4.92	1.60
$P_2 \times P_4$	-2.13	-2.33	-5.21	-163.21	-196.38	33.17	76.62	-0.41	-0.79	-0.50	-0.46	-5.39	-2.74	-2.65	6.82	0.98
$P_2 \times P_5$	-0.89	-1.16	-3.06	-103.12	-191.14	88.02	115.87	-0.68	-0.60	-2.50	-0.39	7.48	-15.09	22.57	-12.47	-1.22
$P_2 \times P_7$	0.53	1.55	3.53	-300.29	960.64	-1260.93	-566.58	-1.15	0.98	1.97	6.12	-9.63	7.87	-17.50	-9.83	-1.49
$P_3 \times P_5$	-2.55	-1.47	-6.19	-301.63	-123.57	-178.06	118.29	1.20	-0.22	0.44	-0.14	-4.26	2.19	-6.45	19.36	-1.72
$P_3 \times P_6$	-15.60	-6.81	-17.92	-453.26	-126.96	-326.31	29.06	1.60	-0.61	-1.83	-0.31	2.32	-6.97	9.29	-3.80	-1.15
$P_3 \times P_7$	-0.53	1.74	-2.33	-758.88	470.72	-1229.59	1431.85	-1.62	-2.14	-4.00	-1.17	-1.41	-16.40	14.99	0.66	-0.96
$P_4 \times P_1$	0.66	1.64	5.27	-287.36	1471.10	-1758.46	-435.39	-1.09	0.18	0.79	0.16	-4.74	9.26	-14.01	-26.33	-1.23
$P_4 \times P_3$	0.65	1.63	4.84	-246.14	1261.46	-1507.60	-378.68	-1.09	0.49	0.91	0.57	1.29	17.10	-15.81	2.63	-0.96
$P_4 \times P_5$	0.45	1.62	2.37	-286.36	640.20	-926.56	-636.36	-1.20	-0.37	0.22	-0.23	-4.98	1.06	-6.03	13.46	-2.39
$P_4 \times P_6$	0.02	-0.40	0.09	41.59	-106.30	64.71	2079.50	-0.61	-2.59	0.11	-1.60	-29.08	0.85	-29.93	11.23	-5.93
$P_4 \times P_7$	-1.45	1.03	-5.00	-658.53	172.01	-830.55	454.16	-2.20	-1.14	-0.94	-0.97	-13.18	-9.42	-3.77	11.56	0.63
$P_5 \times P_6$	-7.53	-1.13	-15.45	-826.79	-66.77	-760.02	109.80	3.37	-0.46	1.00	-0.34	-15.01	7.21	-22.22	32.63	-1.76
$P_5 \times P_7$	-4.83	-3.78	-10.68	-405.28	-260.74	-144.54	83.91	0.74	-2.50	-1.17	-1.26	-13.39	-4.89	-8.50	5.36	1.32
$P_6 \times P_2$	0.49	0.65	2.66	138.23	266.72	-128.49	282.10	-0.69	-0.83	0.50	-0.54	-13.04	3.17	-16.21	15.71	-2.26
$P_6 \times P_7$	-0.42	0.65	-1.65	-318.79	138.19	-456.98	759.02	-1.82	-0.97	-4.73	-0.66	17.78	-30.44	48.22	-18.33	-1.26

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3=Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6; H_{BS} = heritability in broad sense, H_{NS} = heritability in narrow sense; GA = genetic advance; V_G = genotypic variance; V_D = additive variance; V_H = dominance variance; V_P = phenotypic variance; h/d = Degree of dominance (H/D).

Table 23 (Cont'd).

Number of secondary branches plant^{-1}									Number of siliqua plant^{-1}							
Cross	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**
$P_1 \times P_2$	0.43	0.63	0.88	13.99	36.32	-22.32	32.53	-0.78	0.51	0.32	28.51	30716.6	14138.3	16578.3	60228.6	1.08
$P_1 \times P_3$	0.52	1.29	0.79	-8.75	42.33	-51.08	-16.83	-1.10	0.60	1.00	15.49	1831.7	9523.8	-7692.1	3052.8	-0.90
$P_1 \times P_5$	0.72	1.67	0.52	-1.80	12.23	-14.04	-2.50	-1.07	-0.75	1.79	-5.68	-2679.9	1464.1	-4144.1	3573.3	-1.68
$P_1 \times P_6$	0.25	-2.83	0.24	45.09	-38.30	83.38	180.36	-1.48	-1.65	-18.63	-25.31	50933.0	-61888.0	112821.1	-30868.5	-1.35
$P_1 \times P_7$	0.31	0.19	0.32	5.92	3.44	2.48	19.10	0.85	-0.66	-1.81	-11.31	1960.05	-7388.4	9348.5	-2969.8	-1.12
$P_2 \times P_3$	-0.05	0.72	-0.08	-33.27	29.03	-62.30	665.40	-1.47	-0.44	-0.61	-17.45	-5985.5	-13537.0	7551.5	13603.5	-0.75
$P_2 \times P_4$	-0.19	0.23	-0.01	-9.89	9.82	-19.71	52.05	-1.42	0.69	1.22	36.83	6408.1	48878.6	-42470.6	9287.1	-0.93
$P_2 \times P_5$	-0.67	0.38	-1.17	-73.69	16.91	-90.60	109.99	-2.31	-1.31	0.89	-74.37	241721.5	40766.4	200955.1	-184520.2	-2.22
$P_2 \times P_7$	-0.86	1.11	-1.05	-59.59	23.47	-83.06	69.29	-1.88	0.60	1.41	26.85	-5949.4	39896.1	-45845.52	-9915.6	-1.07
$P_3 \times P_5$	0.26	-6.46	0.19	54.47	-50.65	105.12	209.50	-1.44	0.18	-4.49	3.63	28628.4	-26533.0	55161.42	159046.5	-1.44
$P_3 \times P_6$	0.73	1.96	1.32	-23.63	92.19	-115.82	-32.37	-1.12	0.65	1.60	22.78	-5221.8	27776.3	-32998.09	-8033.5	-1.09
$P_3 \times P_7$	-5.78	-98.72	-2.06	166.59	-187.17	353.77	-28.82	-1.37	-1.72	-48.83	-26.68	153628.2	-165285.0	318913.19	-89318.7	-1.39
$P_4 \times P_1$	0.27	-10.81	0.59	756.15	-720.11	1476.26	2800.56	-1.43	0.44	0.75	29.93	8916.5	48312.7	-39396.2	20264.8	-0.90
$P_4 \times P_3$	0.41	0.65	1.28	23.66	89.79	-66.13	57.71	-0.86	0.60	0.61	68.68	108458.9	113967.8	-5508.91	180764.9	-0.22
$P_4 \times P_5$	0.35	0.93	0.83	-18.89	74.88	-93.78	-53.97	-1.12	0.43	-0.23	23.17	45016.8	-9422.47	54439.3	104690.2	-2.40
$P_4 \times P_6$	-1.73	-1.59	-2.75	-66.15	-56.29	-9.85	38.24	0.42	-1.48	-0.89	-78.02	-81320.9	-34837.4	-46483.5	54946.5	1.16
$P_4 \times P_7$	-0.31	1.22	-0.44	-54.50	36.69	-91.19	175.81	-1.58	0.14	1.15	5.69	-19120.2	25484.0	-44604.21	-136573.1	-1.32
$P_5 \times P_6$	-2.00	-8.20	-0.92	12.69	-25.35	38.04	-6.35	-1.23	-0.67	-4.78	-11.19	13655.5	-18946.4	32601.9	-20381.3	-1.31
$P_5 \times P_7$	-1.33	-2.17	-0.67	-2.27	-6.72	4.45	1.71	-0.81	-0.79	-0.27	-13.31	-5275.1	-1073.75	-4201.4	6677.4	1.98
$P_6 \times P_2$	-0.37	0.45	-0.68	-57.93	21.71	-79.64	156.57	-1.92	0.01	1.62	0.99	-117130.8	119150.1	-236280.9	-117130.0	-1.41
$P_6 \times P_7$	0.20	-0.79	0.32	44.87	-30.30	75.16	224.35	-1.58	-0.17	-1.26	-7.74	26409.2	-36273.0	62682.3	-155348.6	-1.31

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3=Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6; H_{BS} = heritability in broad sense, H_{NS} = heritability in narrow sense; GA = genetic advance; V_G = genotypic variance; V_D = additive variance; V_H = dominance variance; V_P = phenotypic variance; h/d = Degree of dominance (H/D).

Table 23 (Cont'd).

	Siliqua length								Number of seeds siliqua^{-1}							
Crosses	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**
$P_1 \times P_2$	-1.74	-0.11	-0.15	-0.36	-0.02	-0.35	0.21	-1.74	-4.42	0.09	-3.03	-59.13	1.28	-60.41	13.38	-6.87
$P_1 \times P_3$	-0.11	-0.66	-0.01	0.08	-0.11	0.19	-0.70	-0.11	-1.46	-1.38	-0.85	-7.55	-6.63	-0.93	5.17	0.37
$P_1 \times P_5$	-3.92	-14.50	-0.16	0.16	138.76	-138.59	-0.04	-3.92	-1.58	-1.00	-0.92	-10.81	-4.24	-6.57	6.84	1.24
$P_1 \times P_6$	-0.58	0.37	-0.05	-0.18	0.04	-0.22	0.30	-0.58	-0.89	-0.58	-0.64	-8.77	-4.14	-4.63	9.85	1.06
$P_1 \times P_7$	-0.56	-5.47	-0.04	0.40	-0.50	0.89	-0.71	-0.56	-0.69	0.03	-0.50	-0.13	10.02	-10.15	0.19	-1.00
$P_2 \times P_3$	-0.33	0.78	-0.05	-0.39	0.22	-0.60	1.17	-0.33	0.36	0.03	0.26	9.86	4.87	4.99	27.39	1.02
$P_2 \times P_4$	-2.04	-2.32	-0.18	-86.29	-0.27	-86.02	42.30	-2.04	0.49	1.05	0.44	-0.79	11.85	-12.64	-1.61	-1.03
$P_2 \times P_5$	0.09	1.21	0.01	-0.24	0.28	-0.51	-2.62	0.09	0.37	0.74	0.33	-0.01	8.07	-8.08	-0.03	-1.00
$P_2 \times P_7$	-1.40	0.26	-0.13	-0.36	0.03	-0.39	0.26	-1.40	0.47	0.68	0.43	3.31	7.36	-4.04	7.04	-0.74
$P_3 \times P_5$	-0.14	0.57	-0.02	-0.15	0.11	-0.26	1.09	-0.14	0.03	0.08	0.02	-0.48	0.47	-0.95	-16.00	-1.42
$P_3 \times P_6$	-0.46	0.37	-0.04	-0.14	0.04	-0.19	0.31	-0.46	-0.11	0.17	-0.08	-2.54	1.05	-3.59	23.09	-1.85
$P_3 \times P_7$	-0.61	0.37	-0.06	-0.18	0.04	-0.22	0.30	-0.61	0.29	0.67	0.23	-0.16	5.52	-5.68	-0.55	-1.01
$P_4 \times P_1$	0.53	0.98	0.07	0.02	0.25	-0.23	0.04	0.53	-0.61	-0.17	-0.44	-7.94	-1.14	-6.80	13.02	2.44
$P_4 \times P_3$	-1.17	-2.08	-0.08	-0.01	-0.15	0.14	0.01	-1.17	0.08	0.01	0.06	1.58	-0.42	1.99	19.75	-2.18
$P_4 \times P_5$	0.07	-0.58	0.01	0.09	-0.07	0.15	1.22	0.07	-0.40	-0.10	-0.26	-4.06	-0.57	-3.49	10.15	2.47
$P_4 \times P_6$	0.28	0.37	0.03	0.02	0.04	-0.03	0.07	0.28	-0.21	0.18	-0.15	-3.26	1.12	-4.38	15.52	-1.98
$P_4 \times P_7$	0.42	0.73	0.05	0.02	0.14	-0.12	0.05	0.42	0.08	0.15	0.06	0.29	0.63	-0.34	3.63	-0.74
$P_5 \times P_6$	0.38	0.74	0.05	0.04	0.19	-0.15	0.11	0.38	0.99	1.98	7.58	-1.07	1639.98	-1641.05	-1.08	-1.00
$P_5 \times P_7$	-0.13	0.06	-0.01	-0.03	0.01	-0.04	0.24	-0.13	0.16	0.53	0.13	-2.43	5.23	-7.66	-15.19	-1.21
$P_6 \times P_2$	-0.16	1.03	-0.02	-0.24	0.19	-0.43	1.51	-0.16	-0.12	0.09	-0.08	-1.85	0.79	-2.63	15.42	-1.83
$P_6 \times P_7$	-3.04	-2.22	-0.19	-0.21	-0.12	-0.09	0.07	-3.04	-0.40	-0.10	-0.26	-4.00	-0.34	-3.66	10.00	3.27

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3=Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6; H_{BS} = heritability in broad sense, H_{NS} = heritability in narrow sense; GA = genetic advance; V_G = genotypic variance; V_D = additive variance; V_H = dominance variance; V_P = phenotypic variance; h/d = Degree of dominance (H/D).

Table 23 (Cont'd).

	1000 seed weight								Seed yield plant^{-1}							
Crosses	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**	**H_{BS}**	**H_{NS}**	**GA**	**V_G**	**V_D**	**V_H**	**V_P**	**h/d**
$P_1 \times P_2$	-2.11	-3.33	-0.11	-0.03	-0.12	0.09	0.01	-0.87	0.04	-25.78	0.02	139.86	-139.64	279.50	3496.50	-1.41
$P_1 \times P_3$	-0.93	-0.90	-0.06	-0.06	-0.06	0.00	0.06	-0.14	0.42	1.63	0.34	-8.19	16.09	-24.28	-19.50	-1.23
$P_1 \times P_5$	-0.51	0.68	-0.05	-0.20	0.08	-0.28	0.39	-1.87	0.57	0.90	0.37	1.49	4.82	-3.34	2.61	-0.83
$P_1 \times P_6$	-1.28	-1.50	-0.09	-0.08	-0.11	0.03	0.06	-0.55	-0.33	-0.50	-0.14	-0.97	-1.31	0.34	2.94	-0.51
$P_1 \times P_7$	-1.72	-1.17	-0.12	-0.17	-0.08	-0.09	0.10	1.02	-0.07	0.03	-0.03	-0.15	0.19	-0.35	2.14	-1.33
$P_2 \times P_3$	-0.23	1.58	-0.02	-0.02	0.04	-0.06	0.09	-0.16	-0.13	0.40	-0.06	-2.33	0.97	-3.29	17.92	-1.85
$P_2 \times P_4$	-3.17	-1.17	-0.23	-0.37	-0.08	-0.29	0.12	1.88	-0.78	0.03	-0.28	-2.64	0.35	-3.00	3.38	-2.91
$P_2 \times P_5$	0.21	0.72	0.02	-0.05	0.13	-0.19	-0.24	-1.19	0.13	1.00	0.07	-3.50	5.40	-8.90	-26.92	-1.28
$P_2 \times P_7$	-0.05	0.58	0.02	-0.08	0.06	-0.14	1.60	-1.49	0.06	0.02	0.03	0.78	-0.75	1.53	13.00	-1.43
$P_3 \times P_5$	-0.54	-0.32	-0.05	-0.09	-0.04	-0.05	0.17	1.19	0.48	0.91	0.33	0.57	6.60	-6.03	1.19	-0.96
$P_3 \times P_6$	-0.97	-1.17	-0.07	-0.06	-0.08	0.02	0.06	-0.54	0.37	0.11	0.23	2.70	1.51	1.19	7.30	0.89
$P_3 \times P_7$	0.07	0.97	0.01	-0.15	0.18	-0.33	-2.14	-1.37	0.42	-0.45	0.29	8.75	-2.78	11.53	20.83	-2.04
$P_4 \times P_1$	0.23	0.68	0.02	-0.03	0.07	-0.10	-0.13	-1.16	0.27	0.01	0.17	3.52	-0.99	4.51	13.04	-2.14
$P_4 \times P_3$	-0.43	0.07	-0.03	-0.08	0.00	-0.08	0.19	-6.69	0.47	0.17	0.34	5.60	1.01	4.59	11.91	2.13
$P_4 \times P_5$	-0.49	-0.47	-0.04	-0.05	-0.04	0.00	0.10	0.27	0.72	0.95	0.66	6.01	10.82	-4.81	8.35	-0.67
$P_4 \times P_6$	-0.38	0.33	-0.03	-0.10	0.03	-0.13	0.26	-2.04	0.52	0.55	0.35	2.34	3.72	-1.38	4.50	-0.61
$P_4 \times P_7$	-0.07	0.42	-0.02	-0.06	0.05	-0.11	0.86	-1.55	0.47	-1.80	0.30	16.37	-10.53	26.90	34.83	-1.60
$P_5 \times P_6$	-0.89	-0.13	-0.07	-0.15	-0.01	-0.14	0.17	3.64	0.47	-0.40	0.30	8.06	-1.97	10.03	17.15	-2.26
$P_5 \times P_7$	0.05	1.24	0.01	-0.20	0.21	-0.41	-4.00	-1.39	0.27	-0.20	0.17	4.16	-0.01	4.17	15.41	-17.70
$P_6 \times P_2$	-0.54	-13.37	-0.05	1.40	-1.53	2.93	-2.59	-1.38	0.36	0.36	0.25	2.07	2.72	-0.65	5.75	-0.49
$P_6 \times P_7$	-1.14	-0.58	-0.08	-0.13	-0.04	-0.08	0.11	1.42	0.41	0.11	0.25	3.33	0.35	2.98	8.12	2.92

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3=Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6; H_{BS} = heritability in broad sense, H_{NS} = heritability in narrow sense; GA = genetic advance; V_G = genotypic variance; V_D = additive variance; V_H = dominance variance; V_P = phenotypic variance; h/d = Degree of dominance (H/D).

BARI Sar-14 (P_1)

(P_1×P_2) F_1

(P_1×P_2) BC_1

(BARI Sar-9 × BARI Sar-6) (P_2)

(P_1×P_2) F_2

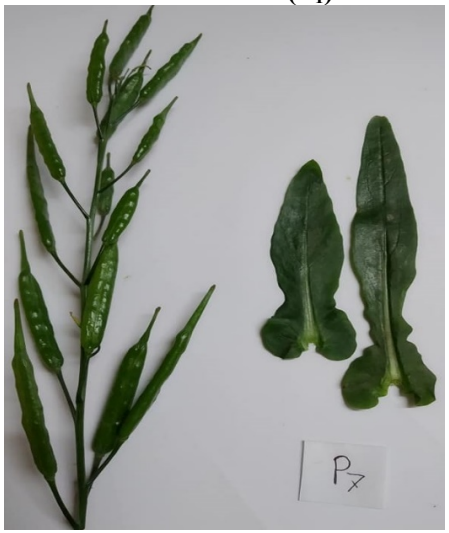
(P_1×P_2) BC_2

Plate 18. Phenotypic variation among different generations of cross P_1 × P_2 (P_1 = BARI Sar-14 and P_2 = Brown Special)

BARI Sar-14 (P_1)

(P_1×P_7) F_1

(P_1×P_7) BC_1

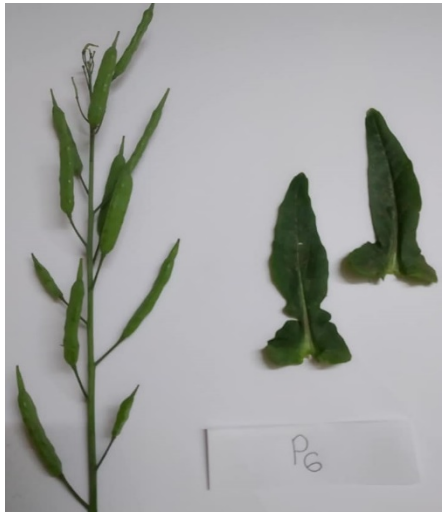


BARI Sar-6 (P_7)

(P_1×P_7) F_2

(P_1×P_7) BC_2

Plate 19. Phenotypic variation among different generations of cross P_1 × P_7 (P_1= BARI Sar-14 and P_7 = BARI Sar-6)



BARI Sar-15 (P_6)

(P_6×P_2) F_1

(P_6×P_2) BC_1

(BARI Sar-9 × BARI Sar-6) (P_2)

(P_6×P_2) F_2

(P_6×P_2) BC_2

Plate 20. Phenotypic variation among different generations of cross P_6 × P_2 (P_6 = BARI Sar-15 and P_2 = Brown Special)

(BARI Sar-9 × BARI Sar-6) (P_2)

(P_2×P_4) F_1

(P_2×P_4) BC_1

Local Tori-7 (P_4)

(P_2×P_4) F_2

(P_2×P_4) BC_2

Plate 21. Phenotypic variation among different generations of cross P_2 × P_4 (P_2 = Brown Special and P_4= Tori-7)

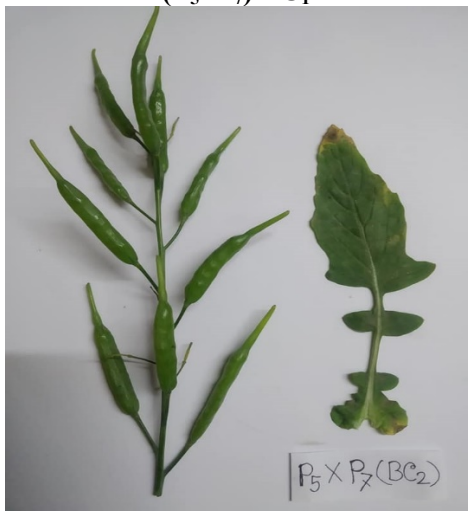
BARI Sar-17 (P_5)

(P_5×P_7) F_1

(P_5×P_7) BC_1

BARI Sar-6 (P_7)

(P_5×P_7) F_2



(P_5×P_7) BC_2

Plate 22. Phenotypic variation among different generations of cross P_5 × P_7 (P_5= BARI Sar-17 and P_7 = BARI Sar-6)

variance indicated predominance of environmental component of variance over the genotypic components of variances.

The degree of dominance (h/d) was higher than one for most of the studied traits across the crosses, indicated over dominance effects in the inheritance of traits. Abo Mostafa *et al.* (2014) also found over dominance effect for most traits. On the other hand, the values of this parameter were less than one for days to 50% flowering (in the crosses $P_2 \times P_3$, $P_4 \times P_3$, $P_4 \times P_7$ and $P_5 \times P_6$), for days to 80% maturity (in the crosses $P_2 \times P_3$ and $P_2 \times P_4$), for plant height (in the crosses $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_5$, $P_4 \times P_6$, $P_5 \times P_7$ and $P_6 \times P_2$), for number of primary branches plant^{-1} (in the crosses $P_2 \times P_4$, $P_3 \times P_7$, $P_4 \times P_3$ and $P_4 \times P_7$), for number of secondary branches plant^{-1} (in the crosses $P_1 \times P_2$, $P_1 \times P_7$, $P_4 \times P_3$, $P_4 \times P_6$ and $P_5 \times P_7$), for number of siliqua plant^{-1} (in the crosses $P_1 \times P_3$, $P_2 \times P_3$, $P_2 \times P_4$, $P_4 \times P_1$ and $P_4 \times P_3$), for number of seeds siliqua^{-1} (in the crosses $P_1 \times P_3$, $P_2 \times P_7$ and $P_4 \times P_7$), for 1000 seed weight (in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_6$, $P_2 \times P_3$, $P_3 \times P_6$ and $P_4 \times P_5$) and for seed yield plant^{-1} (in the crosses $P_1 \times P_5$, $P_1 \times P_6$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$, $P_4 \times P_6$ and $P_6 \times P_2$) indicated partial dominance effect in control of inheritance of these traits.

3.5 Heritability and genetic advance

The highest broad sense heritability for days to 50% flowering was exhibited by the cross $P_1 \times P_3$ followed by the cross $P_1 \times P_2$ while it was the lowest in $P_3 \times P_5$, $P_4 \times P_5$ and $P_6 \times P_7$. For days to 80% maturity it was the highest in cross $P_3 \times P_5$ followed by $P_1 \times P_3$ and the lowest in $P_4 \times P_5$ and $P_6 \times P_7$. For plant height it was the highest in cross $P_3 \times P_6$ followed by $P_5 \times P_6$ and the lowest in $P_4 \times P_6$. For number of primary branches plant^{-1} it was the highest in cross $P_1 \times P_7$ followed by $P_1 \times P_6$ and the lowest in $P_4 \times P_1$. For number of secondary branches plant^{-1} it was the highest in cross $P_3 \times P_7$ followed by $P_5 \times P_6$ and the lowest in $P_2 \times P_3$. For number of siliqua plant^{-1} it was the highest in cross $P_3 \times P_7$ followed by $P_1 \times P_6$ and the lowest in $P_6 \times P_2$. For siliqua length it was the highest in cross $P_1 \times P_5$ followed by $P_6 \times P_7$ and the lowest in $P_4 \times P_5$. For number of seeds siliqua^{-1} it was the highest in cross $P_1 \times P_2$ followed by $P_1 \times P_5$ and the lowest in $P_3 \times P_5$. For 1000 seed weight it was the highest in cross $P_2 \times P_4$ followed by $P_1 \times P_2$ and the lowest in $P_2 \times P_7$ and $P_5 \times P_7$. For seed yield plant^{-1} it was the highest in cross $P_2 \times P_4$ followed by $P_4 \times P_5$ and the lowest in $P_1 \times P_2$ (Table 23).

In case of narrow sense heritability the highest heritability was exhibited for days to 50% flowering by the cross $P_2 \times P_3$ followed by $P_1 \times P_5$ and $P_3 \times P_5$ while it was the lowest in $P_1 \times P_6$ and $P_2 \times P_5$. For days to 80% maturity it was the highest in cross $P_3 \times P_5$ followed by $P_3 \times P_7$

and the lowest in $P_2 \times P_7$. For plant height it was the highest in cross $P_3 \times P_6$ followed by $P_5 \times P_7$ and the lowest in $P_1 \times P_2$. For number of primary branches plant^{-1} it was the highest in cross $P_6 \times P_7$ followed by $P_3 \times P_7$ and the lowest in $P_4 \times P_6$. For number of secondary branches plant^{-1} it was the highest in cross $P_3 \times P_7$ followed by $P_4 \times P_1$ and the lowest in $P_1 \times P_7$. For number of siliqua plant^{-1} it was the highest in cross $P_3 \times P_7$ followed by $P_1 \times P_6$ and the lowest in $P_4 \times P_5$. For siliqua length it was the highest in cross $P_1 \times P_5$ followed by $P_1 \times P_7$ and the lowest in $P_5 \times P_7$. For number of seeds siliqua^{-1} it was the highest in cross $P_5 \times P_6$ followed by $P_1 \times P_3$ and the lowest in $P_4 \times P_3$. For 1000 seed weight it was the highest in cross $P_6 \times P_2$ followed by $P_1 \times P_2$ and the lowest in $P_4 \times P_3$. For seed yield plant^{-1} it was the highest in cross $P_1 \times P_2$ followed by $P_4 \times P_7$ and the lowest in $P_4 \times P_1$ (Table 23).

The highest genetic advance was exhibited in days to 50% flowering by the cross $P_1 \times P_3$ followed by $P_2 \times P_3$ while it was the lowest in $P_3 \times P_5$, $P_4 \times P_5$ and $P_6 \times P_7$. For days to 80% maturity it was the highest in cross $P_2 \times P_3$ followed by $P_4 \times P_6$ and the lowest in $P_2 \times P_5$ and $P_6 \times P_7$. For plant height it was the highest in cross $P_3 \times P_6$ followed by $P_5 \times P_6$ and the lowest in $P_4 \times P_6$. For number of primary branches plant^{-1} it was the highest in cross $P_2 \times P_7$ followed by $P_1 \times P_7$ and the lowest in $P_3 \times P_5$. For number of secondary branches plant^{-1} it was the highest in cross $P_4 \times P_6$ followed by $P_3 \times P_7$ and the lowest in $P_2 \times P_4$. For number of siliqua plant^{-1} it was the highest in cross $P_4 \times P_6$ followed by $P_2 \times P_5$ and the lowest in $P_6 \times P_2$. For siliqua length it was the highest in cross $P_6 \times P_7$ followed by $P_2 \times P_4$ and the lowest in $P_5 \times P_7$, $P_4 \times P_5$, $P_2 \times P_5$ and $P_1 \times P_3$. For number of seeds siliqua^{-1} it was the highest in cross $P_5 \times P_6$ followed by $P_1 \times P_2$ and the lowest in $P_3 \times P_5$. For 1000 seed weight it was the highest in cross $P_2 \times P_4$ followed by $P_1 \times P_7$ and the lowest in $P_3 \times P_7$ and $P_5 \times P_7$. For seed yield plant^{-1} it was the highest in $P_4 \times P_5$ followed by $P_1 \times P_5$ and the lowest in $P_1 \times P_2$ (Table 23).

The high heritability and the high genetic advance indicated that the trait was under the additive gene control and selection for the improvement of this trait would be effective. In this study in most of the cases both heritability and genetic advance were found to be very low due to opposite direction of additive and dominance variance. Apraku *et al*. (2004) also mentioned that the necessary condition for the higher magnitude of narrow sense heritability and genetic advance appeared to be dependent on the direction of additive and dominance effects. Estimated narrow sense heritability and genetic advance varied for different crosses and traits but none of the trait had shown good estimates of narrow sense heritability and genetic advance. An increase in error variance had been reported to cause the decrease in the

heritability estimates (Hulmel *et al.,* 2005). Divya *et al.* (2014) and Naveed *et al.* (2009) also reported very low narrow sense heritability and genetic advance. Sikarwar *et al.* (2017), Salam *et al.* (2017), Singh *et al.* (2018), Aktar *et al*. (2019) and Gupta *et al.* (2019) reported days to 50% flowering and 80% maturity and plant height showed the high heritability with the high genetic advance but Afrin *et al.* (2011) reported days to 80% maturity showed the lowest heritability. Rauf and Rahim (2018), and Rout *et al.* (2019) observed the high heritability and the high genetic advance for number of primary and secondary branches plant^{-1}, 1000 seed weight and seed yield plant^{-1}. Kumar *et al.* (2017) and Mansour (2017) reported the high broad sense heritability than narrow sense heritability for all the studied traits and the differences between broad sense and narrow sense heritability were closest.

3.6 Heterosis and inbreeding depression

The heterosis based on better parents (H_{BP}) and mid parents (H_{MP}) were found to be significant for most of the studied traits in most of the crosses except H_{MP} in the crosses $P_1 \times P_5$, $P_1 \times P_7$ and $P_4 \times P_7$ and H_{BP} in the crosses $P_1 \times P_3$ and $P_2 \times P_3$ for days to 50% flowering, H_{BP} in the cross $P_1 \times P_5$ for plant height, H_{BP} in the crosses $P_1 \times P_6$, $P_1 \times P_7$, $P_3 \times P_6$ and $P_5 \times P_6$ for number of primary branches plant^{-1}, H_{MP} in the cross $P_5 \times P_7$ and H_{BP} in the crosses $P_1 \times P_5$, $P_4 \times P_7$ and $P_5 \times P_7$ for number of secondary branches plant^{-1}, H_{MP} in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_7$, $P_3 \times P_6$ and $P_6 \times P_2$ and H_{BP} in the crosses $P_1 \times P_3$, $P_1 \times P_5$, $P_2 \times P_3$, $P_2 \times P_7$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$, $P_4 \times P_6$ and $P_5 \times P_7$ for siliqua length, H_{MP} in the cross $P_3 \times P_7$ and H_{BP} in the cross $P_4 \times P_3$ for number of seeds siliqua^{-1}, H_{MP} in the crosses $P_1 \times P_3$, $P_2 \times P_3$, $P_2 \times P_4$ and $P_2 \times P_5$ and H_{BP} in the crosses $P_1 \times P_6$, $P_2 \times P_3$ and $P_4 \times P_5$ for thousand seed weight and H_{MP} in the cross $P_5 \times P_7$ for seed yield plant^{-1} (Table 24).

Inbreeding depression (ID) was also highly significant for most of the studied traits in most of all crosses except for days to 50% flowering and 80% maturity in the crosses $P_4 \times P_1$ and $P_5 \times P_6$) (Figure 1), for plant height in the cross $P_4 \times P_7$, for number of primary branches plant^{-1} in the crosses $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_7$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$ and $P_4 \times P_7$, for number of secondary branches plant^{-1} in the crosses $P_1 \times P_3$, $P_1 \times P_6$, $P_1 \times P_7$, $P_3 \times P_5$, $P_3 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$, for number of siliqua plant^{-1} in the crosses $P_1 \times P_5$, $P_2 \times P_4$ and $P_3 \times P_5$, for the siliqua length in the crosses $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_5$, $P_3 \times P_5$ and $P_4 \times P_1$, for number of seeds siliqua^{-1} in the crosses $P_1 \times P_2$, $P_1 \times P_3$, $P_3 \times P_5$, $P_4 \times P_1$ and $P_4 \times P_3$, for 1000 seed weight in the crosses $P_1 \times P_2$,$P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_4$, $P_3 \times P_7$ and $P_4 \times P_3$ and for seed yield

Table 24. Estimation of heterosis and inbreeding depression for yield and yield contributing traits in different cross materials of *Brassica rapa* genotypes

Crosses	Days to 50% flowering			Plant height			Number of primary branches plant^{-1}			Number of secondary branches plant^{-1}		
	H_{MP}	H_{BP}	ID	H_{MP}	H_{BP}	ID	H_{MP}	H_{BP}	ID	H_{MP}	H_{BP}	ID
$P_1 \times P_2$	24.04**	20.22**	-17.78**	17.58**	6.20**	3.60**	52.77**	51.14**	24.77**	714.33**	316.67**	46.16**
$P_1 \times P_3$	8.47**	0.69	2.27**	11.12**	1.65**	1.65**	27.24**	19.79**	3.43	1192.00**	651.16**	-14.55
$P_1 \times P_5$	0.68	-8.70**	-7.14**	5.29**	0.78	15.26**	-70.98**	-77.47**	-233.78**	958.82*	800.00	-111.11**
$P_1 \times P_6$	12.20**	7.32**	-11.36**	22.28**	12.28**	17.70**	13.16*	2.47	4.46	637.84**	307.46**	14.65
$P_1 \times P_7$	0.59	-18.33**	-6.12**	10.81**	-7.71**	11.49**	14.29**	3.32	9.88	471.88**	221.05*	-10.93
$P_2 \times P_3$	11.63**	0.69	-27.27**	11.55**	10.01**	6.94**	63.53**	55.52**	24.00**	306.41**	132.33**	56.96**
$P_2 \times P_4$	23.29**	19.56**	-7.14**	-1.91**	-5.13**	7.41**	45.63**	39.97**	20.78**	86.84**	33.29**	30.95**
$P_2 \times P_5$	6.00**	-6.52**	-27.91**	19.28**	12.26**	3.51**	108.15**	62.83**	12.80**	1381.94**	665.67**	73.75**
$P_2 \times P_7$	-15.90**	-33.33**	-10.00**	3.83**	-5.24**	8.48**	30.08**	16.48**	3.91	174.51**	63.33**	41.43**
$P_3 \times P_5$	-1.90**	-4.35**	-10.61**	10.53**	5.40**	7.12**	75.40**	42.59**	2.90	439.62**	232.56*	39.16
$P_3 \times P_6$	14.12**	10.59**	-3.46**	3.05**	2.63**	-2.32**	25.18**	7.41	1.84	245.45**	183.58*	-63.68**
$P_3 \times P_7$	-1.00*	-14.45**	-3.25**	3.23**	-6.96**	10.03**	32.09**	13.16*	23.15**	414.00**	350.88**	66.15
$P_4 \times P_1$	41.05**	32.70**	0.68	25.38**	16.80**	8.43**	44.00**	36.99**	15.56**	197.75**	50.36**	28.38**
$P_4 \times P_3$	25.16**	9.84**	4.16**	19.67**	17.34**	13.71**	69.99**	68.13**	15.75**	371.85**	150.36**	63.81**
$P_4 \times P_5$	24.05**	6.52**	-13.82**	15.55**	12.32**	-3.62**	93.93**	56.32**	2.16	307.57**	106.69**	33.72**
$P_4 \times P_6$	30.62**	17.88**	4.14**	14.83**	13.05**	1.36**	46.40**	26.79**	17.53**	245.45**	89.19**	80.23**
$P_4 \times P_7$	-0.37	-21.78**	-17.27**	-4.04**	-15.01**	0.43	43.24**	23.86**	1.39	87.63**	1.42	79.38**
$P_5 \times P_6$	13.40**	7.24**	-0.69	12.30**	7.51**	11.37**	31.80**	-4.57	-10.87*	419.48**	198.51**	61.50
$P_5 \times P_7$	-12.58**	-22.78**	-13.68**	10.26**	-4.72**	18.18**	23.64**	-10.58*	12.38*	219.40	87.72	-9.35
$P_6 \times P_2$	23.47**	14.63**	-2.13**	6.38**	4.49**	-2.90**	70.68**	53.09**	39.52**	1127.79**	651.00**	62.27**
$P_6 \times P_7$	-6.28**	-21.12**	7.04**	5.14**	-5.58**	8.19**	21.63**	21.40**	24.72**	545.16**	497.01**	-25.75**

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6; H_{BP} = Heterosis over better parent, H_{MP} = Heterosis over mid parent; ID = Inbreeding depression.

Table 24 (Cont'd).

Crosses	Number of siliqua plant^{-1}			Siliqua length			Number of seeds siliqua^{-1}			1000 seed weight		
	H_{MP}	H_{BP}	H_{MP}	H_{BP}	H_{MP}	H_{BP}	H_{MP}	H_{BP}	ID	H_{MP}	H_{BP}	ID
$P_1 \times P_2$	273.47**	166.05**	273.47**	166.05**	273.47**	166.05**	-5.03**	-24.82**	4.44	21.75**	20.73**	4.87
$P_1 \times P_3$	83.72**	48.50**	83.72**	48.50**	83.72**	48.50**	-13.01**	-21.21**	2.60	-3.47	-14.66**	2.56
$P_1 \times P_5$	46.35**	44.79**	46.35**	44.79**	46.35**	44.79**	4.39**	-2.16*	4.04*	-12.93**	-20.93**	-2.94
$P_1 \times P_6$	107.22**	62.19**	107.22**	62.19**	107.22**	62.19**	-33.82**	-39.28**	-25.00**	7.37*	-4.44	16.28**
$P_1 \times P_7$	90.04**	41.66**	90.04**	41.66**	90.04**	41.66**	-32.47**	-35.48**	-5.88*	7.19*	-6.38*	2.27
$P_2 \times P_3$	139.88**	102.56**	139.88**	102.56**	139.88**	102.56**	-5.69**	-18.94**	13.44**	5.65	-5.91	0.00
$P_2 \times P_4$	43.95**	29.81**	43.95**	29.81**	43.95**	29.81**	7.89**	-4.60**	10.90**	-4.05	-10.36*	6.25
$P_2 \times P_5$	478.23**	314.59**	478.23**	314.59**	478.23**	314.59**	-64.84**	-73.45**	-187.50**	-0.89	-9.30*	15.38**
$P_2 \times P_7$	64.67**	53.58**	64.67**	53.58**	64.67**	53.58**	27.00**	4.17**	20.83**	20.92**	6.38*	10.00**
$P_3 \times P_5$	74.75**	42.43**	74.75**	42.43**	74.75**	42.43**	-13.30**	-25.89**	-3.00	10.48**	7.22*	8.16**
$P_3 \times P_6$	60.53**	53.87**	60.53**	53.87**	60.53**	53.87**	-37.07**	-37.95**	-61.17**	-9.59**	-10.28**	9.76**
$P_3 \times P_7$	79.03**	60.77**	79.03**	60.77**	79.03**	60.77**	-0.09	-5.54**	5.91*	-28.80**	-29.79**	-6.06
$P_4 \times P_1$	179.67**	87.57**	179.67**	87.57**	179.67**	87.57**	-46.49**	-52.94**	3.23	20.12**	13.11**	6.80*
$P_4 \times P_3$	249.38**	171.39**	249.38**	171.39**	249.38**	171.39**	3.91**	0.56	2.33	41.59**	18.82**	0.18
$P_4 \times P_5$	258.53**	141.78**	258.53**	141.78**	258.53**	141.78**	-41.27**	-51.15**	36.62**	19.46**	2.79	18.55**
$P_4 \times P_6$	162.41**	110.41**	162.41**	110.41**	162.41**	110.41**	-49.90**	-52.18**	-34.98**	-26.32**	-37.78**	-22.50**
$P_4 \times P_7$	63.12**	38.28**	63.12**	38.28**	63.12**	38.28**	-27.27**	-33.33**	-10.44**	7.69*	-10.64**	16.67**
$P_5 \times P_6$	89.85**	49.76**	89.85**	49.76**	89.85**	49.76**	-50.51**	-57.19**	-13.72**	-26.82**	-28.44**	-18.94**
$P_5 \times P_7$	49.60**	12.31**	49.60**	12.31**	49.60**	12.31**	-37.48**	-43.84**	-18.20**	-17.78**	-21.28**	-17.03**
$P_6 \times P_2$	319.01**	266.89**	319.01**	266.89**	319.01**	266.89**	-11.16**	-24.55**	27.29**	39.28**	57.42**	25.27**
$P_6 \times P_7$	109.82**	95.99**	109.82**	95.99**	109.82**	95.99**	-51.96**	-53.96**	15.57**	19.78**	17.23**	14.70**

Where, P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 = Tori-7, P_5 = BARI Sar-17, P_6 = BARI Sar -15, P_7 = BARI Sar-6; H_{BP} = Heterosis over better parent, H_{MP} = Heterosis over mid parent; ID = Inbreeding depression.

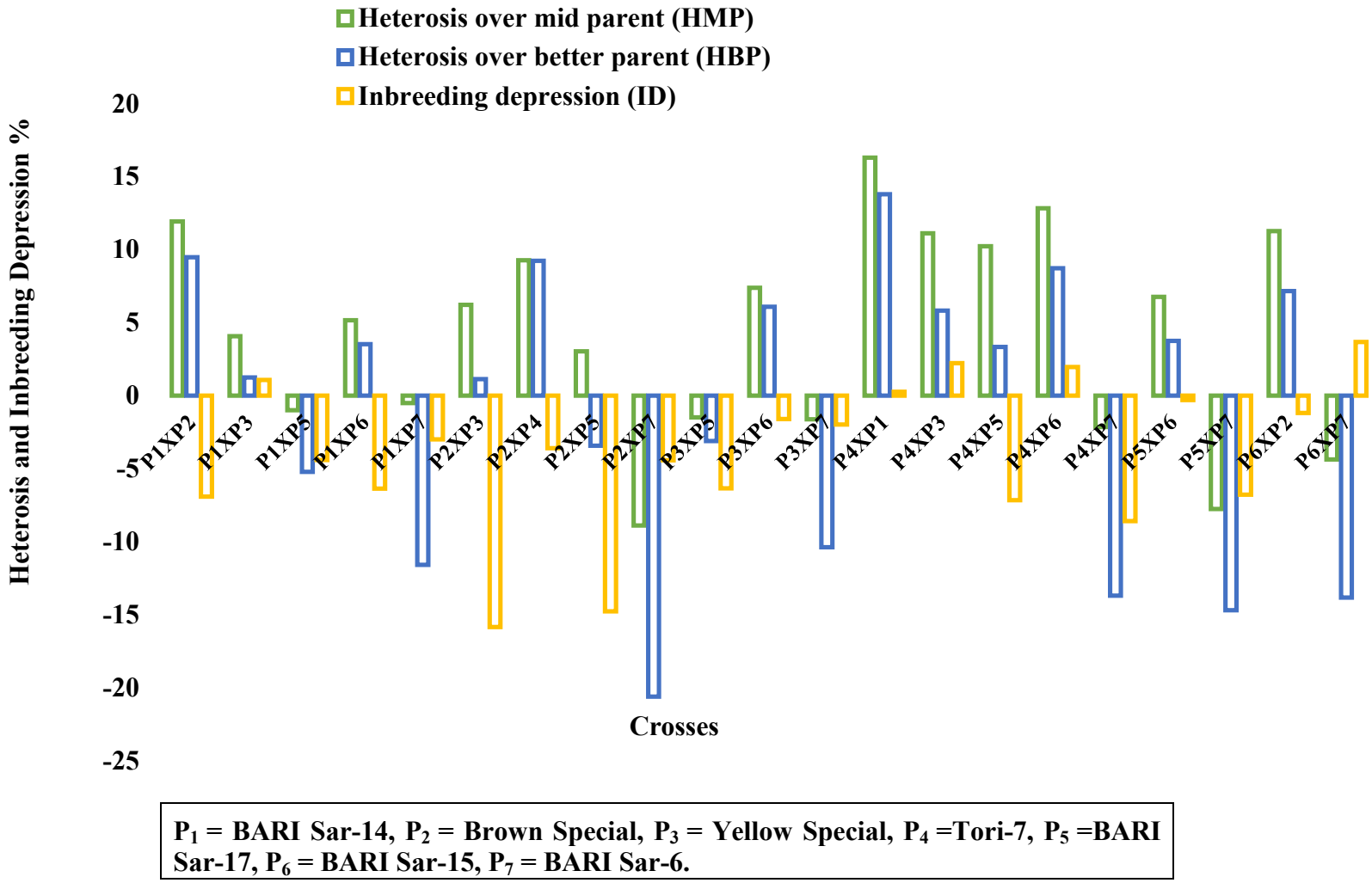
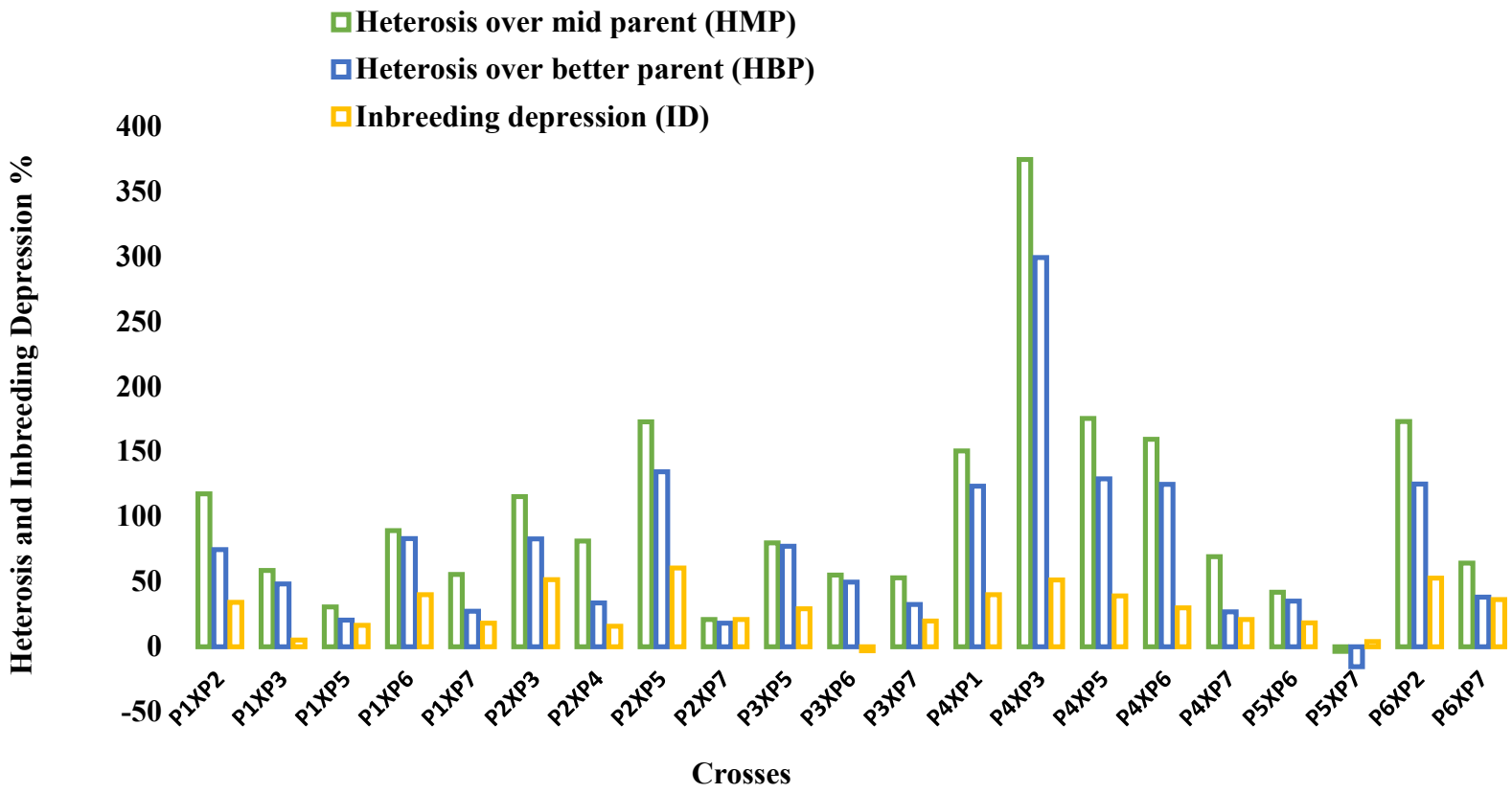


Figure 1. Heterosis and inbreeding depression for days to 80% maturity in different cross materials of *Brassica rapa.*



P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6.

Figure 2. Heterosis and inbreeding depression for seed yield plant^{-1} in different cross materials of selected *Brassica rapa*

plant^{-1} in cross $P_1 \times P_3$, $P_3 \times P_6$ and $P_5 \times P_7$ (Figure 2). Positive ID (Inbreeding depression) indicated that the values of F_2 progenies had reduced in comparison to their respective F_1s and vice versa. Abdalla *et al.* (2015) and Haridy and El-Said (2016) also observed the high positive heterosis over mid and better parent and inbreeding depression for different yield related traits. Similar result was also observed by Singh *et al.* (2017), Bharti *et al.* (2018), Ferdous (2019) and Rameeh (2019).

Findings

In this study most of the F_1s performed better than their both parents in most of the traits across the crosses. Superiority of F_1s indicated the presence of dominant gene effects while the F_1's with average performance over their two parents indicated partial dominance. However, most of the yield components revealed that the F_2 means were lower than their corresponding F_1 means signifying the presence of inbreeding depression. In general, BC_1s performed better than BC_2s in most of the crosses for the characters such as days to 50% flowering and 80% maturity, number of siliqua plant^{-1} and siliqua length while BC_2s performed better than BC_1s in most of the crosses for the characters viz., number of primary and secondary branches plant^{-1}, 1000 seed weight and seed yield plant^{-1}.

Out of twenty one crosses, the highly significant and the highest negative heterosis for days to 50% flowering (-15.90 %) and for 80% maturity (-8.90 %) were recorded by the cross $P_1 \times P_7$ over the mid parents and (-33.33 %) and (-20.61 %) over the better parents respectively. For thousand seed weight the cross $P_4 \times P_3$ gave the highest significant and the positive heterosis (41.59 %) over the mid parent and in the cross $P_6 \times P_2$ (57.42 %) over the better parent. The highest significant positive heterosis (374.37 %) and (298.97 %) over the mid and better parents respectively were recorded in the cross $P_4 \times P_3$ for seed yield plant^{-1}. Therefore, selection could be effective for these crosses. The highly significant and the highest negative ID (Inbreeding depression) for days to 50% flowering was represented by the cross $P_2 \times P_5$ (-27.91 %) and for 80% maturity by the cross $P_2 \times P_3$ (-15.85 %). The highest negative and significant ID for thousand seed weight was observed in the cross $P_4 \times P_6$ (-22.50 %) and for seed yield plant^{-1} in the cross $P_3 \times P_6$ (-3.01 %) while it was the highly significant and positive for the cross $P_6 \times P_2$ (25.27 %) and the cross $P_2 \times P_5$ (60.57 %) respectively. The positive ID indicated that the mean values of F_2 progenies were reduced compared to their F_1 generations and vice versa.

The highest broad sense heritability for days to 50% flowering and 80% maturity were exhibited by the cross $P_1 \times P_3$ and $P_3 \times P_5$ respectively while for 1000 seed weight and seed yield plant^{-1} it was highest in $P_2 \times P_4$. In case of narrow sense heritability the highest heritability for days to 50% flowering and 80% maturity were exhibited by the cross $P_2 \times P_3$ and $P_3 \times P_5$ respectively while for 1000 seed weight and seed yield plant^{-1} it was the highest in $P_6 \times P_2$ and $P_1 \times P_2$ respectively. The highest genetic advance for days to 50% flowering and 80% maturity was exhibited by the cross $P_1 \times P_3$ and $P_2 \times P_3$ respectively while for 1000 seed weight and seed yield plant^{-1} it was the highest in $P_2 \times P_4$ and $P_4 \times P_5$ respectively. In this study in most of the cases both heritability and genetic advance were found to be very low due to opposite direction of additive and dominance variance.

The phenotypic variance was higher than the genotypic variance for most of the traits across the crosses indicated the predominance of the environmental variance over the genotypic variance. The dominance (H) values were higher than the additive (D) values. Degree of dominance (h/d) was higher than one for most of the traits across the crosses, indicated over dominance effects. If magnitude of D was less, then we could move for heterosis breeding but the significant and the negative estimates of H, I and L gene effects in different traits across the crosses suggested that the selection could be delayed to later generation, so that negative alleles are removed. Hence, improvement of these traits could be achieved through the recurrent selection procedure. The duplicate type epistasis in most of the crosses for majority of the traits also indicated in decreased heterosis and also hindered the rate of progress through selection. Therefore, selection might be delayed to advanced generations for the reduction of di-genic epistasis variation, utilization of both additive and non-additive gene effects and exploit transgressive segregants. But where non-additive effects hold considerable importance in traits expression, recurrent selection for specific combining ability could be used as a suitable breeding procedure.

Experiment 4: Study on the oil content and quality characteristics of selected *Brassica rapa* materials

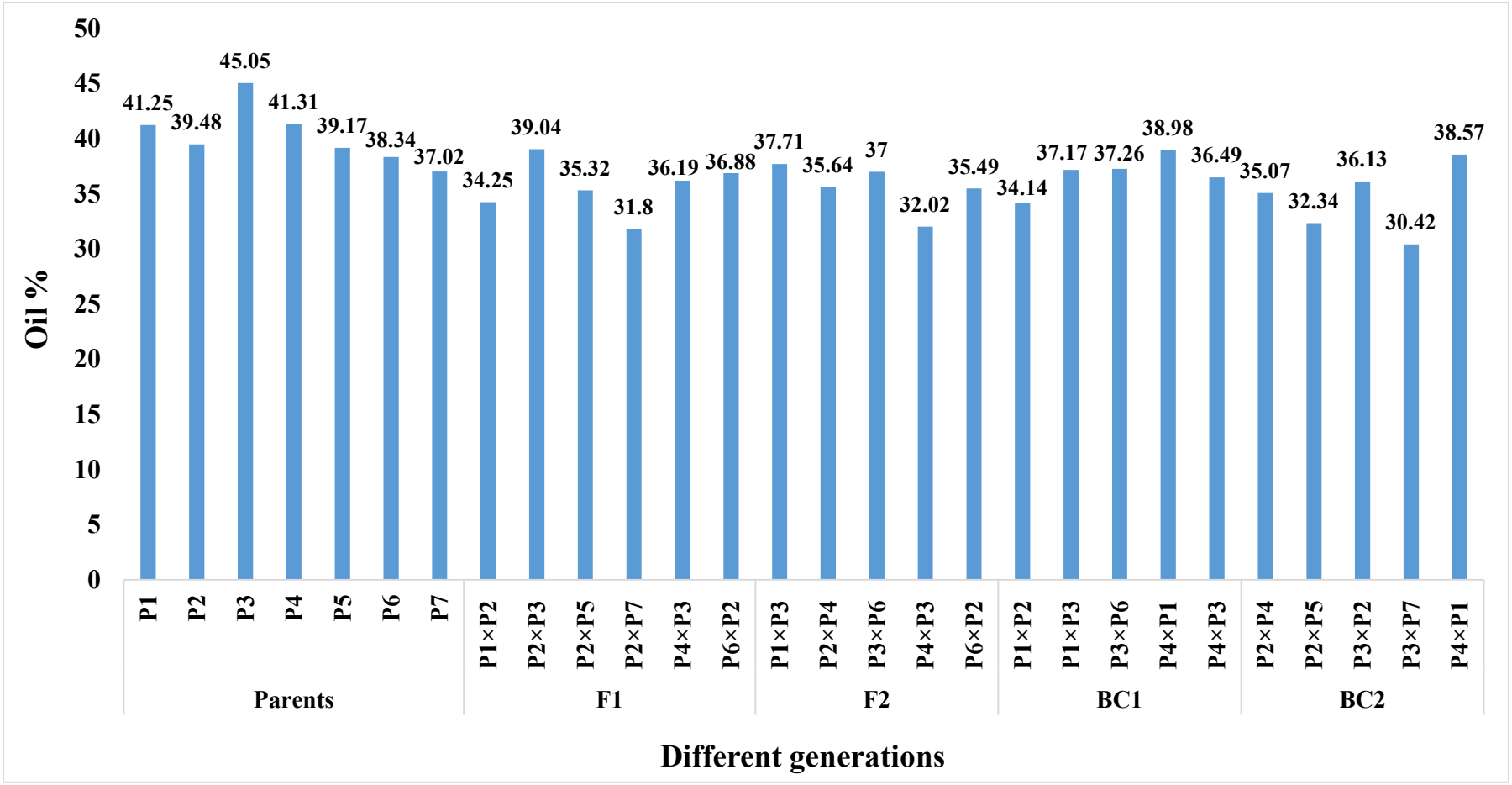
Besides developing a short duration high yielding materials, the quality seed production was also a major objective of this study. Oil quality is usually determined by the constituent of fatty acids composition which is highly influenced by the variety / genotype type. Therefore, seven parents, six F_1s, five F_2s, five BC_1s and five BC_2s were selected on the basis of their yield performance and duration mentioned in the previous experiment to study their oil content and quality and the results obtained had been presented here.

4.1 Oil content

The oil contents ranged from 30.42-45.05%. Among the parents Yellow Special contained the highest (45.05%) and BARI Sar-6 contained the lowest (37.02%) oils. In the F_1 generations Brown Special × Yellow Special contained the highest (39.04%) and Brown Special × BARI Sar-6 contained the lowest (31.80%) oil while among the F_2 generations it was the highest (37.71%) in BARI Sar-14 × Yellow Special and the lowest (32.02%) in Tori-7 × Yellow Special. In the BC_1 and BC_2 generations the highest (38.98%) and (38.57%) both in Tori-7 × BARI Sar-14 BC_1 and BC_2 while the lowest (34.14%) and (30.42%) in BARI Sar-14 × Brown Special BC_1 and in Yellow Special × BARI Sar-6 BC_2 respectively were recorded (Figure 3). Therefore, the parents, F_1s, F_2s, BC_1s and BC_2s with the high oil contents could be selected for the further improvement of this trait. The result exceeded the findings of Gadei *et al*. (2012) and Islam *et al.* (2020) who reported that the oil content ranged from 28.00 - 32.00% and 38.74 - 40.55% respectively while more or less similar result was reported by Arif *et al.* (2012) and Sharafi *et al*. (2015) who found 35.67 - 45.87% and 21.00 - 45.00% oils respectively in different rapeseed and mustard variety. These variations might be due to biological and environmental factor or for soil and crop management practices.

4.2 Fatty acids composition

The significant variations were observed in different saturated and unsaturated fatty acids (SFA and USFA) contents among the parents and their different generations. The SFA and USFA contents ranged from 3.92 - 5.96% and 92.14 - 93.89% respectively. Here the most common and important SFA and USFA were counted and other remaining SFA and USFA were found in very negligible amounts (1.08 - 3.64%). Among the parents BARI Sar-6



P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. F_1 = First Filial Generation, F_2 = Second Filial Generation, BC_1= Back Cross 1 and BC_2= Back Cross 2.
Minimum = 44.97, Maximum = 54.82, Mean = 36.77, CV% = 0.06 and LSD = 0.04

Figure 3. Oil contents of selected cross materials of *Brassica rapa* genotypes in different generations

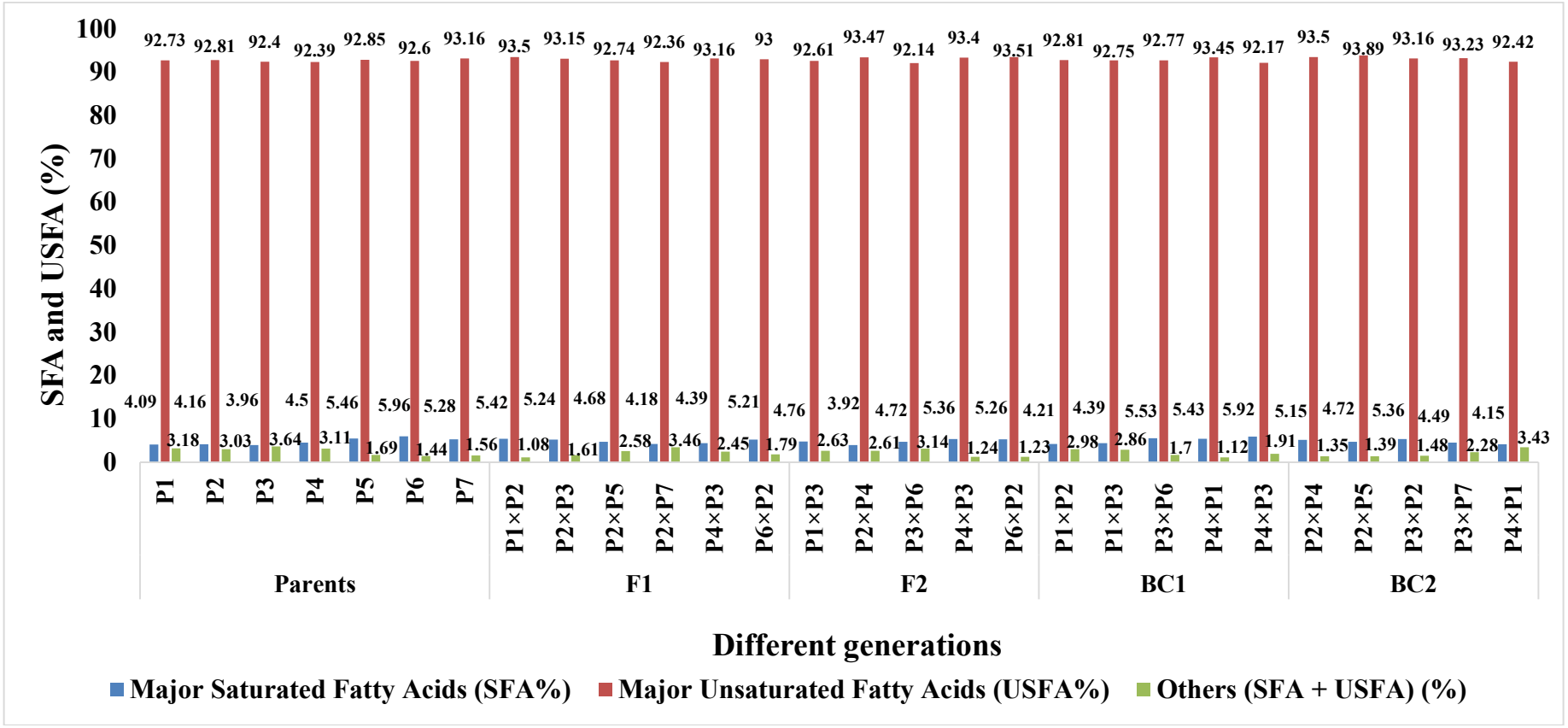
contained the highest (93.16%) USFA of which 79.61% was monounsaturated (MUSFA) and 13.55% polyunsaturated (PUSFA) and Tori-7 contained the lowest (92.39%) USFA of which 75.41% MUSFA and 16.98 % PUSFA while Yellow Special contained the lowest (3.96%) and BARI Sar-15 contained the highest (5.96%) SFA. In F_1 generations the highest (93.50%) USFA was recorded in BARI Sar-14 × Brown Special of which 79.04% MUSFA and 14.46% PUSFA followed by (93.16%) in Tori-7 × Yellow Special of which 73.89% MUSFA and 19.27% PUSFA while the lowest (4.18%) SFA was in Brown Special × BARI Sar-6. In F_2 generations the highest (93.51%) USFA was recorded in BARI Sar-15 × Brown Special of which 77.83% MUSFA and 15.68% PUSFA while the lowest (3.92%) SFA was in Brown Special × Tori-7. In the BC_1 generations the highest (93.45%) USFA was estimated in Tori-7 × BARI Sar-14 of which 76.80% MUSFA and 16.65% PUSFA and in BC_2 generations the highest (93.89%) USFA was recorded in Brown Special × BARI Sar-17 of which 79.14% MUSFA and 14.75% PUSFA respectively and the lowest (4.21%) and (4.15%) SFA were recorded in BARI Sar-14 × Brown Special and Tori-7 × BARI Sar-14 in BC_1 and BC_2 generations respectively (Figure 4 and 5).

Therefore, the parents, F_1s, F_2s, BC_1s and BC_2s with the high amount of USFA and the low amount of SFA could be used for further improvement of this trait according to the breeding purposes. Similar result was reported by Fadl *et al.* (2011) and Karmokar (2018) for USFA where it ranged from 91.06 - 91.55% and 90.79 - 93.08% respectively but lower for SFA where they reported SFA ranged from 8.45 - 8.94% and 6.92 -9.22% respectively.

4.2.1 Saturated fatty acids composition

4.2.1.1 Palmitic acid (C16:0)

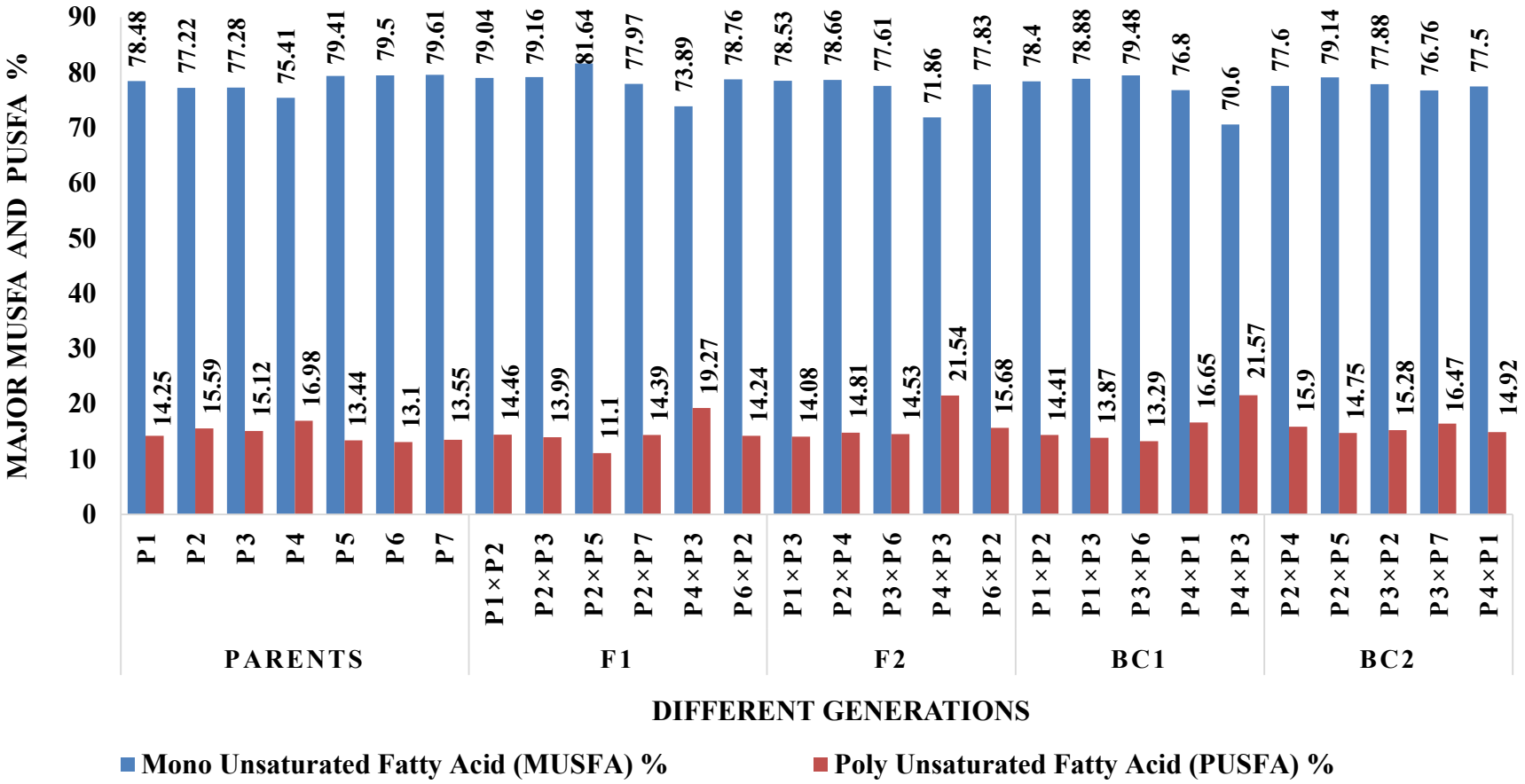
The palmitic acids contents ranged from 1.63 - 2.34%. Among the parents BARI Sar-15 contained the lowest (1.64%) and Tori-7 contained the highest (2.06%) values. In the F_1 generations BARI Sar-15 × Brown Special contained the lowest (1.74%) and Brown Special × BARI Sar-17 contained the highest (2.34%) values. Among F_2 generations it was the lowest (1.83%) in Yellow Special × BARI Sar-15 and the highest (2.15%) in Tori-7 × Yellow Special. In the BC_1 and BC_2 generations the lowest (1.63%) and (1.90%) in Yellow Special × BARI Sar-15 and in Tori-7 × BARI Sar-14 respectively and the highest (2.11%) and (2.21%) in Tori-7 × BARI Sar-14 and in Brown Special × Tori-7 respectively were recorded (Table 25). Therefore, the parents, F_1s, F_2s, BC_1s and BC_2s with the low level of palmitic acids could be used for the improvement of this trait. This results remained



P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. F_1 = First Filial Generation, F_2 = Second Filial Generation, BC_1= Back Cross 1 and BC_2= Back Cross 2.

Major SFA (Minimum = 3.92, Maximum = 5.96, Mean = 4.9, CV% = 0.51 and LSD = 0.04)
Major USFA (Minimum = 92.14, Maximum = 93.89, Mean = 92.93, CV% = 0.02 and LSD = 0.03)
Others (Minimum = 1.08, Maximum = 3.64, Mean = 2.21, CV% = 0.88 and LSD = 0.03)

Figure 4. Saturated and unsaturated fatty acids contents of selected *Brassica rapa* genotypes in different generations.



P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6.
F_1 = First Filial Generation, F_2 = Second Filial Generation, BC_1= Back Cross 1 and BC_2= Back Cross 2.
Major MUSFA (Minimum = 70.60, Maximum = 81.64, Mean = 77.68, CV% = 0.03 and LSD = 0.03)
Major PUSFA (Minimum = 11.10, Maximum = 21.57, Mean = 15.25, CV% = 0.71 and LSD = 0.18)

Figure 5. Major mono and poly unsaturated fatty acids content of selected *Brassica rapa* genotypes in different generations

Table 25. Saturated fatty acid compositions of selected *Brassica rapa* genotypes in different generations

Treatments		Saturated fatty acids (%)			
		Palmitic acid (C16:0)	Stearic acid (C18:0)	Arachidic acid (C20:0)	Lignoceric acid (C24:0)
Parents	P_1	1.82 klm	1.20 d	0.87 gh	0.20 pq
	P_2	2.00 fghi	1.12 ef	0.86 h	0.18 q
	P_3	1.76 mn	1.10 fg	0.86 h	0.24 o
	P_4	2.06 defg	1.27 c	0.96 c	0.21 p
	P_5	1.80 lmn	1.26 c	0.96 c	1.44 f
	P_6	1.64 op	1.44 a	1.24 a	1.64 c
	P_7	1.65 op	1.09 fg	0.91 ef	1.63 c
F_1	$P_1 \times P_2$	2.04 efgh	1.05 hi	0.85 hi	1.48 e
	$P_2 \times P_3$	1.80 lmn	0.92 k	0.75 m	1.77 b
	$P_2 \times P_5$	2.34 a	1.28 c	0.75 m	0.31 m
	$P_2 \times P_7$	2.04 efgh	1.07 gh	0.80 kl	0.27 n
	$P_4 \times P_3$	1.97 ghi	1.26 c	0.91 ef	0.25 no
	$P_6 \times P_2$	1.74 mno	1.02 i	0.85 hi	1.60 d
F_2	$P_1 \times P_3$	2.10 cdef	1.38 b	0.92 de	0.36 l
	$P_2 \times P_4$	1.94 hi	0.97 j	0.75 m	0.26 no
	$P_3 \times P_6$	1.83 jklm	1.40 b	1.05 b	0.44 k
	$P_4 \times P_3$	2.15 bcd	1.10 fg	0.73 m	1.38 g
	$P_6 \times P_2$	1.90 ijkl	1.09 fg	0.82 jk	1.45 f
BC1	$P_1 \times P_2$	1.93 ij	1.14 e	0.83 ij	0.31 m
	$P_1 \times P_3$	1.70 nop	1.28 c	1.04 b	0.37 l
	$P_3 \times P_6$	1.63 p	1.19 d	0.94 cd	1.77 b
	$P_4 \times P_1$	2.11 bcde	1.21 d	0.95 c	1.16 i
	$P_4 \times P_3$	1.79 mn	1.05 hi	0.74 m	2.34 a
BC2	$P_2 \times P_4$	2.21 b	1.14 e	0.78 l	1.02 j
	$P_2 \times P_5$	1.91 ijk	0.87 l	0.69 n	1.25 h
	$P_3 \times P_2$	2.07 cdefg	1.22 d	0.89 fg	1.18 i
	$P_3 \times P_7$	2.17 bc	1.26 c	0.81 jk	0.25 no
	$P_4 \times P_1$	1.90 ijkl	1.09 fg	0.86 h	0.30 m
Minimum		1.63	0.87	0.69	0.18
Maximum		2.34	1.44	1.24	2.34
Mean		1.93	1.16	0.87	0.90
CV%		3.25	1.67	1.78	1.73
LSD		0.10	0.03	0.03	0.03

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. F_1 = First Filial Generation, F_2 = Second Filial Generation, BC_1= Back Cross 1 and BC_2= Back Cross 2.

within the findings of Karmokar (2018) and Islam *et al.* (2020) who reported that palmitic acid contents ranged from 1.68 - 2.68% and 1.77 - 3.44% respectively in different rapeseed and mustard variety.

4.2.1.2 Stearic acid (C18:0)

The stearic acids contents ranged from 0.87-1.44%. Among the parents BARI Sar-6 contained the lowest (1.09%) and BARI Sar-15 contained the highest (1.44%) values. In the F_1 generations Brown Special × Yellow Special contained the lowest (0.92%) and Brown Special × BARI Sar-17 contained the highest (1.28%) amount. Among F_2 generations the lowest (0.97%) in Brown Special × Tori-7 and the highest (1.40%) in Yellow Special × BARI Sar-15 were recorded. In the BC_1 and BC_2 generations the lowest (1.05%) and (0.87%) in Tori-7 × Yellow Special and in Brown Special × BARI Sar-17 and the highest (1.28%) and (1.26%) in BARI Sar-14 × Yellow Special and in Yellow Special × BARI Sar-6 respectively were estimated (Table 24). So, the parents, F_1s, F_2s, BC_1s and BC_2s with the low level of stearic acids could be used for the improvement of this trait. The results exceeded the findings of Karmokar (2018) who reported 0.49-0.74% but remained within the findings of Islam *et al.* (2020) who reported 0.00 - 1.77% stearic acid in different mustard variety while Ko *et al.* (2017) noticed 20.4% stearic acid in his experiment.

4.2.1.3 Arachidic acid (C20:0)

Arachidic acids contents ranged from 0.69-1.24%. Among the parents Brown Special and Yellow Special both contained the lowest amount (0.86%). In the F_1 generations both Brown Special × Yellow Special and Brown Special × BARI Sar-17 contained the lowest (0.75%) while the lowest (0.73%) in Tori-7 × Yellow Special among F_2 generations was estimated. In the BC_1 and BC_2 generations the lowest (0.74%) and (0.69%) in Tori-7 × Yellow Special and in Brown Special × BARI Sar-17 respectively were recorded (Table 24). The result was much lower than the findings of Karmokar (2018) who reported that the arachidic acids content ranged from 3.61-6.60% but within the findings of Islam *et al.* (2020) who reported 0.74- 4.74% arachidic acids in different rapeseed and mustard variety.

4.2.1.4 Lignoceric acid (C24:0)

Lignoceric acids contents ranged from 0.18-2.34%. Brown Special contained the lowest amount (0.18%) among the parents. In F_1 generations Tori-7 × Yellow Special contained the lowest (0.25%) while in F_2 generations the lowest (0.26%) in Brown Special × Tori-7 was recorded. In the BC_1 and BC_2 generation the lowest (0.31%) and (0.25%) in BARI Sar-14 ×

Brown Special and in Yellow Special × BARI Sar-6 respectively were estimated (Table 24). The results exceeded the findings of Karmokar (2018) who reported, it was 0.19-0.35% in different *Brassica rapa* genotypes.

4.2.2 Unsaturated fatty acids composition

4.2.2.1 Monounsaturated fatty acids

4.2.2.1.1 Palmitoleic acid (C16:1)

The palmitoleic acid was found in very negligible amount and ranged from 0.15-0.24%. Among the parents, F_1, F_2, BC_1 and BC_2 generations, parents (Yellow Special and BARI Sar-17), F_1 (BARI Sar-14 × Brown Special), F_2 (Tori-7 × Yellow Special), BC_1 (BARI Sar-14 × Brown Special and Tori-7 × BARI Sar-14) and BC_2 (Brown Special × Tori-7) contained the highest amount 0.21, 0.20, 0.23, 0.21 and 0.24% respectively while parents (BARI Sar-14 and Tori-7), F_1 (Tori-7 × Yellow Special), F_2 (BARI Sar-14 × Yellow Special), BC_1 (BARI Sar-14 × Yellow Special) and BC_2 (Yellow Special × BARI Sar-6 and Tori-7 × BARI Sar-14) contained the lowest amount 0.17, 0.15, 0.15, 0.17 and 0.20% respectively (Table 26). The result was more or less similar with the findings of Amir *et al.* (2012) and Islam *et al.* (2020) who reported less than 1.00% palmitoleic acid in different rapeseed and mustard variety.

4.2.2.1.2 Oleic acid (C18:1, c9)

In this study oleic acid contents ranged from 11.12-16.15%. Among the parents BARI Sar-14 contained the highest (13.58%) followed by Brown Special (12.83%) while the lowest (11.34%) in BARI Sar-15 was reported. In the F_1 generations Brown Special × BARI Sar-17 contained the highest (16.15%) followed by Brown Special × Yellow Special (12.78%) and the lowest (11.68%) in Tori-7 × Yellow Special was estimated. In F_2 generations the highest (13.20%) in Tori-7 × Yellow Special followed by (12.14%) in BARI Sar-14 × Yellow Special and the lowest (11.92%) in Yellow Special × BARI Sar-15 were recorded. In the BC_1 and BC_2 generations the highest (13.21%) and (12.79%) in BARI Sar-14 × Brown Special and in Yellow Special × Brown Special respectively were estimated (Table 26). Therefore, the parents, F_1s, F_2s, BC_1 and BC_2 with the high level of oleic acids could be used for the improvement of this trait. The results matched with the findings of Karmokar (2018) and Islam *et al.* (2020) who reported 11.27-15.16% and 9.03-18.56% oleic acid in different *Brassica rapa* varieties. Fadl *et al.* (2011), Chauhan and Kumar (2011) and Mubashir (2012) also observed 19.08-20.24%, 13.6-32.2% and 12% oleic acid respectively in the rapeseed-

Table 26. Unsaturated fatty acid compositions of selected *Brassica rapa* genotypes in different generations

Generations	Genotypes	Unsaturated fatty acids (%)						
		Monounsaturated fatty acids (%)				Polynsaturated fatty acids (%)		
		Palmitoleic acid (C16:1)	Oleic acid (C18:1,c9)	Octadecenoic acid (C18:1,t9)	Eicosenoic acid (C20:1)	Linoleic acid (C18:2)	Linolenic acid (C18:3)	Arachidonic acid (C20:4)
Parents	**P_1**	0.17 ef	13.58 b	13.05 q	0.34 efg	7.14 o	6.10 q	1.01 a
	P_2	0.18 de	12.83 d	14.49 g	0.40 ab	7.58 k	7.26 h	0.75 hi
	P_3	0.21 bc	12.29 k	13.18 o	0.34 efg	8.16 d	5.96 s	1.00 a
	P_4	0.17 ef	12.44 i	17.42 a	0.41 a	7.35 n	8.97 d	0.66 k
	P_5	0.21 bc	12.54 h	13.80 k	0.33 fgh	5.80 w	6.98 l	0.66 k
	P_6	0.20 cd	11.34 v	14.03 j	0.30 ij	6.52 t	5.92 t	0.66 k
	P_7	0.19 cde	11.47 u	14.27 h	0.29 j	6.78 r	6.16 p	0.61 l
F_1	**$P_1 \times P_2$**	0.20 cd	12.42 ij	13.64 l	0.36 cde	6.70 s	6.97 l	0.79 fg
	$P_2 \times P_3$	0.19 cde	12.78 e	11.31 w	0.32 ghi	7.84 h	5.21 w	0.94 bc
	$P_2 \times P_5$	0.18 de	16.15 a	15.80 d	0.40 ab	5.28 x	5.11 y	0.71 j
	$P_2 \times P_7$	0.18 de	11.73 q	12.04 u	0.31 hij	7.64 j	5.99 r	0.76 gh
	$P_4 \times P_3$	0.15 f	11.68 r	16.34 c	0.35 def	9.68 c	9.08 c	0.51 m
	$P_6 \times P_2$	0.19 cde	12.45 i	11.63 v	0.30 ij	8.13 e	5.15 x	0.96 b
F_2	**$P_1 \times P_3$**	0.15 f	12.14 l	13.52 m	0.26 k	7.58 k	5.68 u	0.82 ef
	$P_2 \times P_4$	0.19 cde	12.12 l	12.79 r	0.37 cd	7.35 n	6.64 n	0.82 ef
	$P_3 \times P_6$	0.17 ef	11.92 o	14.05 ij	0.31 hij	7.59 k	6.29 o	0.65 k
	$P_4 \times P_3$	0.23 ab	13.20 c	12.69 s	0.32 ghi	11.25 a	9.37 b	0.92 c
	$P_6 \times P_2$	0.18 de	12.06 m	15.00 f	0.36 cde	7.43 m	7.66 f	0.59 l

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. F_1 = First Filial Generation, F_2 = Second Filial Generation.

Table 26 (Cont'd).

Generations	Genotypes	Unsaturated fatty acids (%)						
		Monounsaturated fatty acids (%)				Polynsaturated fatty acids (%)		
		Palmitoleic acid (C16:1)	Oleic acid (C18:1,c9)	Octadecenoic acid (C18:1,t9)	Eicosenoic acid (C20:1)	Linoleic acid (C18:2)	Linolenic acid (C18:3)	Arachidonic acid (C20:4)
BC_1	$P_1 \times P_2$	0.21 bc	13.21 c	13.38 n	0.41 a	6.35 v	7.20 j	0.86 d
	$P_1 \times P_3$	0.17 ef	11.56 t	14.08 i	0.29 j	6.38 u	6.83 m	0.66 k
	$P_3 \times P_6$	0.18 de	11.12 w	13.11 p	0.25 k	7.01 p	5.63 v	0.65 k
	$P_4 \times P_1$	0.21 bc	11.97 n	15.18 e	0.42 a	7.06 p	9.01 c	0.58 l
	$P_4 \times P_3$	0.19 cde	11.84 p	12.77 r	0.31 hij	11.18 b	9.62 a	0.77 gh
BC_2	$P_2 \times P_4$	0.24 a	12.72 f	14.28 h	0.36 cde	7.95 g	7.23 i	0.72 ij
	$P_2 \times P_5$	0.21 bc	12.63 g	12.50 t	0.35 def	8.02 f	5.90 u	0.83 de
	$P_3 \times P_2$	0.21 bc	12.79 e	13.34 n	0.38 bc	7.51 l	7.05 k	0.72 ij
	$P_3 \times P_7$	0.20 cd	12.40 j	17.14 b	0.35 def	7.81 i	8.06 e	0.60 l
	$P_4 \times P_1$	0.20 cd	11.61 s	13.64 l	0.37 cd	6.84 q	7.31 g	0.77 gh
	Minimum	0.15	11.12	11.31	0.25	5.80	5.11	0.51
	Maximum	0.24	16.15	17.42	0.42	11.25	9.62	1.01
	Mean	0.19	12.39	13.87	0.34	7.57	6.95	0.75
	CV%	8.72	0.17	0.20	4.43	0.27	0.25	3.10
	LSD	0.03	0.03	0.05	0.02	0.03	0.03	0.04

P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. F_1 = First Filial Generation, F_2 = Second Filial Generation, BC_1= Back Cross 1 and BC_2= Back Cross 2.

mustard oil in their experiments.

4.2.2.1.3 Octadecenoic acid (C18:1, t9)

Octadecenoic acid contents ranged from 11.31-17.42%. Among the parents Tori-7 contained the highest (17.42%) followed by Brown Special (14.49%). In the F_1 generations Tori-7 × Yellow Special contained the highest (16.34%) followed by Brown Special × BARI Sar-17 (15.80%) while in F_2 generations the highest (15.00%) in BARI Sar-15 × Brown Special followed by (14.05%) in Yellow Special × BARI Sar-15 were recorded. Among the BC_1 and BC_2 generation the highest (15.18%) and (17.14%) in Tori-7 × BARI Sar-14 and in Yellow Special × BARI Sar-6 respectively were estimated (Table 26).

4.2.2.1.4 Eicosenoic acid (C20:1)

It ranged from 0.25 - 0.42%. Among the parents Tori-7 contained the highest (0.41%) followed by Brown Special (0.40%). In the F_1 generations Brown Special × BARI Sar-17 contained the highest (0.40%) followed by (0.36%) by BARI Sar-14 × Brown Special while in F_2 generations the highest (0.37%) in Brown Special × Tori-7 followed by (0.36%) in BARI Sar-15 × Brown Special were estimated. Among the BC_1 and BC_2 generations the highest (0.42%) and (0.38%) in Tori-7 × BARI Sar-14 and in Yellow Special × Brown Special respectively were recorded (Table 26). Islam *et al.* (2020) also reported less than 1.00% eicosenoic acids in different rapeseed and mustard variety.

4.2.2.1.5 Erucic acid (C22:1)

The erucic acids contents ranged from 44.97-54.82%. Among the parents Tori-7 had the lowest amount (44.97%) while BARI Sar-15 contained the highest amount (53.63%) followed by (53.39%) in BARI Sar-6. In the F_1 generations the lowest (45.37%) in Tori-7 × Yellow Special and the highest (54.56%) in Brown Special × Yellow Special followed by (54.19%) in BARI Sar-15 × Brown Special were estimated. In F_2 generations the lowest (45.42%) in Tori-7 × Yellow Special and the highest (53.19%) in Brown Special × Tori-7 followed by (52.46%) in BARI Sar-14 × Yellow Special were recorded. In the BC_1 and BC_2 generation the lowest (45.49%) in Tori-7 × Yellow Special (BC_1) and (46.67%) in Yellow Special × BARI Sar-6 (BC_2) respectively while the highest (54.82%) in Yellow Special × BARI Sar-15 (BC_1) and (53.45%) in Brown Special × BARI Sar-17 (BC_2) respectively were estimated (Figure 6). Therefore, the parents, F_1s, F_2s, BC_1s and BC_2s with the low level of erucic acids could be used for further improvement of this trait. The results were more or less similar to Khan *et al.* (2008), Mubashir (2012), Ko *et al.* (2017),

Karmokar (2018) and Islam *et al.* (2020) who observed 48-59%, 42%, 45.3%, 54.08-60.75% and 41.11 to 50.67% erucic acids respectively in different rapeseed-mustard oil.

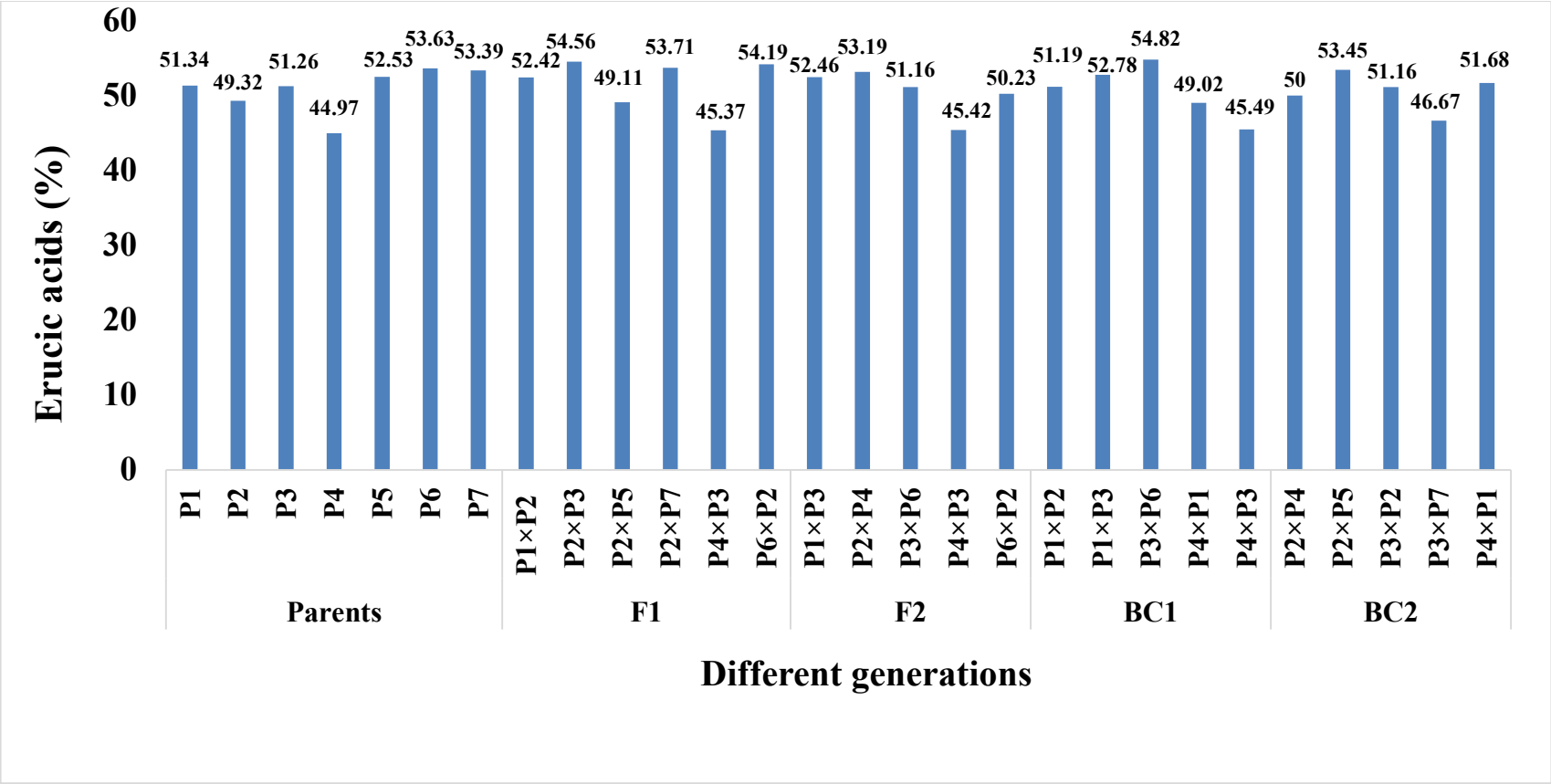
4.2.2.2 Polyunsaturated fatty acids

4.2.2.2.1 Linoleic acid (C18:2)

Linoleic acids contents ranged from 5.80-11.25%. Among the parents Yellow Special contained the highest (8.16%) followed by Brown Special (7.58%) while the lowest (5.80%) in BARI Sar-17 was recorded. In the F_1 generations Tori-7 × Yellow Special contained the highest (9.68%) followed by BARI Sar-15 × Brown Special (8.13%) and the lowest (5.28%) in Brown Special × BARI Sar-17 was recorded. In F_2 generations the highest (11.25%) in Tori-7 × Yellow Special followed by (7.59%) in Yellow Special × BARI Sar-15 and the lowest (7.35%) in Brown Special × Tori-7 were recorded. In the BC_1 and BC_2 generations the highest (11.18%) in Tori-7 × Yellow Special (BC_1) and (8.02%) in Brown Special × BARI Sar- 17 (BC_2) respectively were estimated (Table 26). So, the parents, F_1s, F_2s, BC_1s and BC_2s with the high level of linoleic acids could be used for further improvement of this trait. The result was lower than the findings of Karmokar (2018) and Islam *et al.* (2020) who reported that it ranged from 12.53-14.27% and 12.70-17.75% in different rapeseed and mustard variety. Fadl *et al.* (2011), Amir *et al.* (2012) and Mubashir (2012) also found 12.37-21.36%, 15.87-19.06% and 15% linoleic acid respectively in rapeseed-mustard oil. This low level of linoleic acids might be due to increased amount of erucic acid in them.

4.2.2.2.2 Linolenic acid (C18:3)

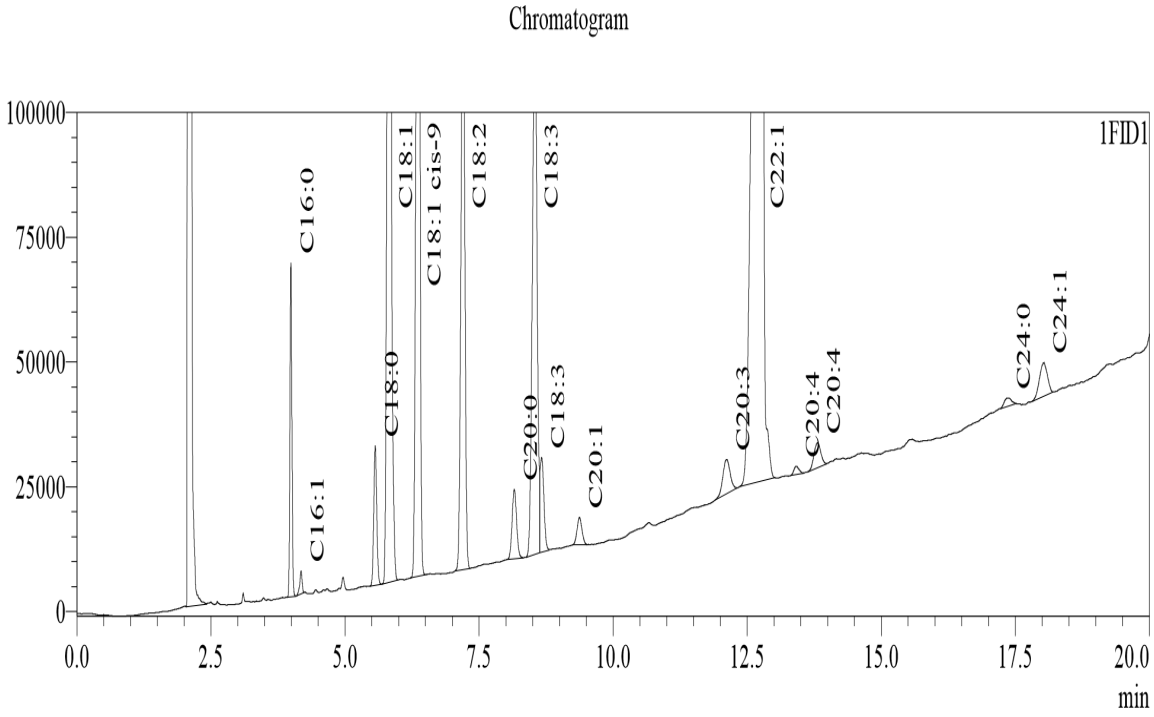
The linolenic acids contents ranged from 5.11 - 9.62 %. Tori-7 had the highest (8.97%) followed by (7.26%) in Brown Special while the lowest (5.92%) in BARI Sar-15 were estimated among the parents. In the F_1 generations Tori-7 × Yellow Special had the highest (9.08%) followed by (6.97%) in BARI Sar- 14 × Brown Special and the lowest (5.11%) in Brown Special × BARI Sar- 17 were recorded. In F_2 generations the highest (9.37%) in Tori-7 × Yellow Special followed by (7.66%) in BARI Sar- 16 × Brown Special and the lowest (5.68%) in BARI Sar-14 × Yellow Special were estimated. In the BC_1 and BC_2 generations the highest (9.62%) in Tori-7 × Yellow Special (BC_1) and (8.06%) in Yellow Special × BARI Sar-6 (BC2) respectively were recorded (Table 26). So, those with the high level of linolenic acid could be selected for further improvement of this trait. The result was more or less similar to Amir *et al.* (2012), Mubashir (2012), Karmokar (2018)



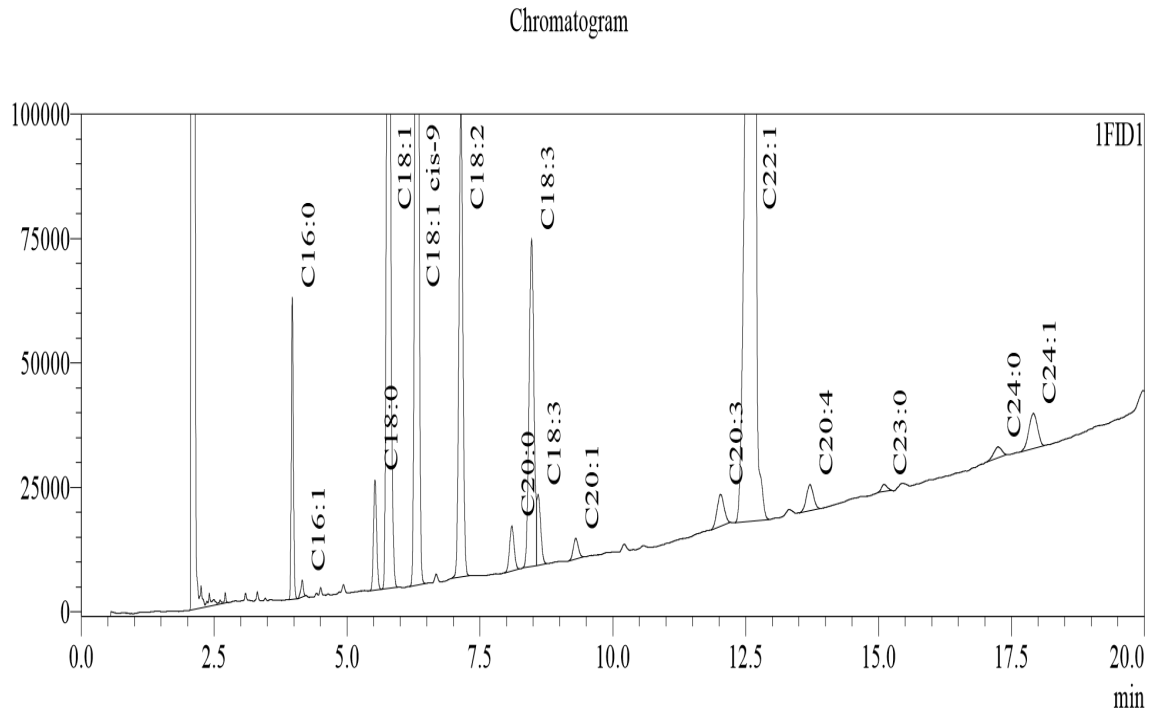
P_1 = BARI Sar-14, P_2 = Brown Special, P_3 = Yellow Special, P_4 =Tori-7, P_5 =BARI Sar-17, P_6 = BARI Sar-15, P_7 = BARI Sar-6. F_1 = First Filial Generation, F_2 = Second Filial Generation, BC1= Back Cross 1 and BC2= Back Cross 2.

Minimum = 44.97, Maximum = 54.82, Mean = 51.02, CV% = 0.03 and LSD = 0.02

Figure 6. Erucic acids contents of selected *Brassica rapa* genotypes in different generations.

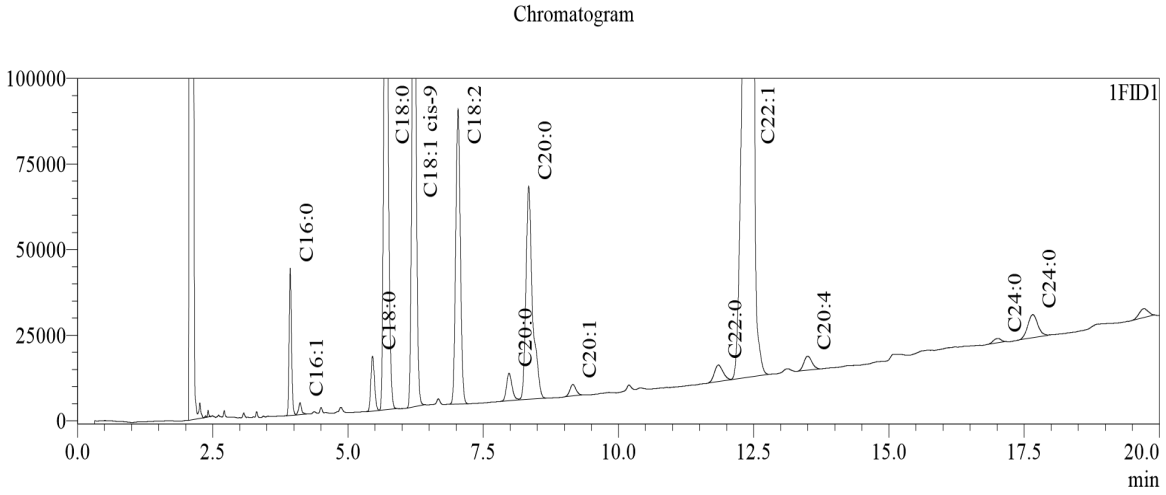


Parent Tori-7

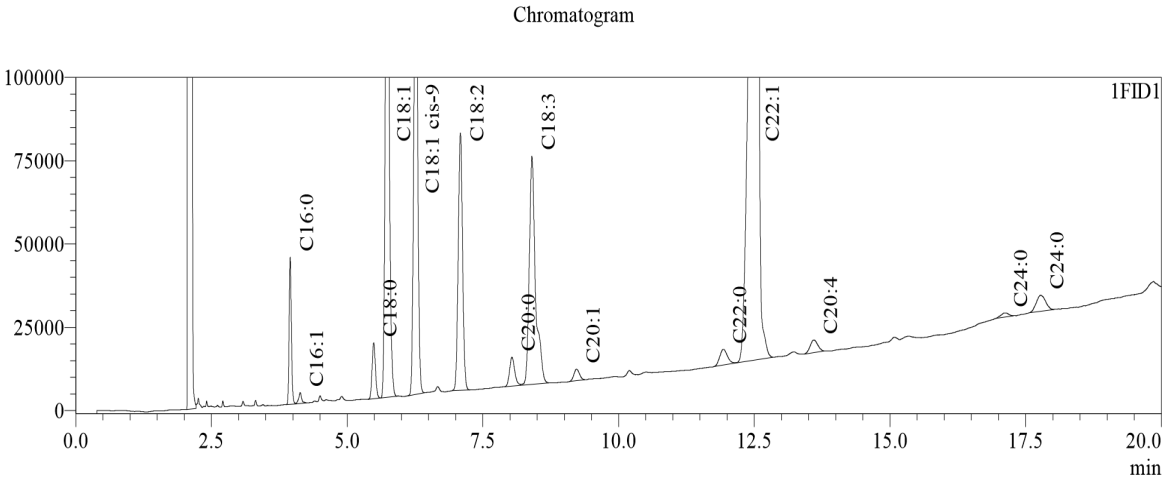


F_1- Tori-7 × Yellow Special

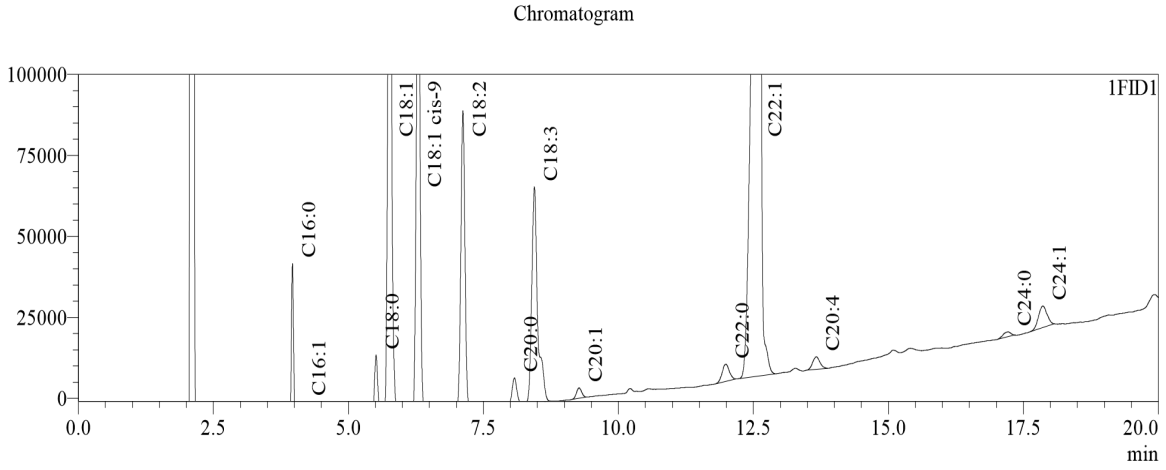
Figure 7. GC chromatogram of FAMEs in low erucic acid containing *Brassica rapa* genotypes



F_2- Tori-7 × Yellow Special



BC_1- Tori-7 × Yellow Special



BC_2- Yellow Special × BARI Sar-6

Figure 8. GC chromatogram of FAMEs in low erucic acid containing *Brassica rapa* genotypes

and Islam *et al.* (2020) who reported 7.55-9.76%, 6%, 6.69-8.65% and 6.27-11.83% linolenic acids in different rapeseed-mustard oil respectively.

4.2.2.2.3 Arachidonic acid (C20:4)

Arachidonic acids contents ranged from 0.51-1.01%. BARI Sar-14 had the highest values (1.01%) followed by (1.00%) in Yellow Special among the parents. In the F_1 and F_2 generations the highest (0.96%) and (0.92%) in BARI Sar-16 × Brown Special and in Tori-7 × Yellow Special respectively were estimated. Among the BC_1 and BC_2 generations the highest (0.86%) and (0.83%) in BARI Sar-14 × Brown Special and in Brown Special × BARI Sar-17 respectively were recorded (Table 26). Islam *et al.* (2020) also reported less than 1.00% arachidonic acids in different rapeseed and mustard varieties.

Findings

Among the parents Yellow Special contained the highest (45.05%) oils. In F_1s Brown Special × Yellow Special contained the highest (39.04%) oil while among F_2s it was the highest (37.71%) in BARI Sar-14 × Yellow Special and in both BC_1 and BC_2 generations Tori-7 × BARI Sar-14 contained the highest (38.98%) and (38.57%) oils respectively.

Among the parent BARI Sar-6 contained the highest (93.16%) unsaturated fatty acids (USFA) and Yellow Special contained the lowest (3.96%) saturated fatty acids (SFA). In F_1 generations BARI Sar-14 × Brown Special contained the highest (93.50%) USFA while the lowest (4.18%) SFA was in Brown Special × BARI Sar-6. In F_2 generations the highest (93.51%) USFA was recorded in BARI Sar-15 × Brown Special while the lowest (3.92%) SFA was in Brown Special × Tori-7. In the BC_1 and in BC_2 generations the highest (93.45%) and (93.89%) USFA were estimated in Tori-7 × BARI Sar-14 (BC_1) and in Brown Special × BARI Sar-17 (BC_2) respectively and the lowest (4.21%) SFA in BARI Sar-14 × Brown Special (BC_1) and (4.15%) in Tori-7 × BARI Sar-14 (BC_2) respectively were estimated. So, these parents, F_1s, F_2s, BC_1s and BC_2s with the high level of USFA and the low level of SFA could be used for further development of this trait.

The highest PUSFA containing parent was Tori-7 (16.98%), F_1 was Tori-7 × Yellow Special (19.27%), F_2 was Tori-7 × Yellow Special (21.54%), BC_1 was Tori-7 × Yellow Special (21.57%) and BC_2 was Yellow Special × BARI Sar-6 (16.47%). Therefore, they could be used for further improvement of these trait.

Though those containing the high level of PUSFA is desirable but those with the high MUSFA along with the higher level of erucic acid is not desirable as it has toxic effect on the heart at the high enough doses. In this study the parent- Tori-7, F_1- Tori-7 × Yellow Special, F_2- Tori-7 × Yellow Special, BC_1- Tori-7 × Yellow Special and BC_2- Yellow Special × BARI Sar-6 contained the lowest (44.97%), (45.37%), (45.42%), (45.49%) and (46.67%) erucic acid respectively. So, they could be used for developing low erucic acid containing variety.

CHAPTER V

SUMMARY AND CONCLUSION

Morphological characterization stated that without some exception, most of the F_1s showed intermediate type characteristics between their parents in terms of leaf, flower and pod characteristics. Tori-7 matured early but had the low yield plant^{-1} (81.66 days and 2.25 g plant^{-1}) while Brown Special matured within a short duration and had moderate yield plant^{-1} (80.66 days and 5.88g plant^{-1}). BARI Sar-15 had moderate yield potential but it required more time to mature (90.33 days and 6.43 g plant^{-1}) than Tori-7 and Brown Special. Another variety of *Brassica rapa* is BARI Sar-6 which required long duration to become matured but had very high yield potential (110.00 days and 8.41 g plant^{-1}). The F_1, Tori-7 × Brown Special was found to be short durable (80.00 days) and yield was 13.24g plant^{-1} in comparison to Tori-7 (81.66 days and 4.25 g plant^{-1}) and Brown Special (80.66 days and 5.88 g plant^{-1}) while Brown Special × BARI Sar-14 matured in 82.00 days and yield was 11.59 g plant^{-1}, Yellow Special × Brown Special matured in 83.00 days and yield was 15.79 g plant^{-1}, BARI Sar-14 × Tori-7 matured in 83.00 days and yield was 13.27 g plant^{-1} and Brown Special × BARI Sar-15 matured in 85.00 days and yield was 26.02 g plant^{-1}. These crosses had short duration than BARI Sar-15 (90.33 days) but more than Tori-7 (81.66 days). While BARI Sar-15 × Brown Special matured in 92.88 days and yield was 22.34 g plant^{-1} and Tori-7 × Yellow Special matured in 96.00 days and yield was 27.67 g plant^{-1} but both showed long duration than Tori-7 and BARI Sar-15 but all the cross combinations had very high yield potential than Tori-7 (4.25 g plant^{-1}) and BARI Sar-15 (6.43 g plant^{-1}). So, these populations possessed excellent potential for use in future trial.

In case of heterosis and combining ability analysis, out of forty two F_1s, the highly significant and the highest negative heterosis for days to 50% flowering and 80% maturity was provided by the reciprocal F_1- BARI Sar-6 × Brown Special (-35.00 %) and (-23.33 %) over the better parents and F_1- BARI Sar-6 × BARI Sar-17 (-22.75 %) and (-13.22 %) over the mid parent respectively thus these could be used for producing genotype with earliness. However, for number of primary branches plant^{-1} reciprocal F_1- BARI Sar-15 × Brown Special and the F_1- Brown Special × Tori-7 showed the highest significant positive heterosis 97.76% and 76.47% over the mid parent and the better parent respectively while the highest

significant and positive heterosis for number of secondary branches plant^{-1} was produced by the reciprocal F_1- BARI Sar-17 × Yellow Special over the both parents. The reciprocal F_1- BARI Sar-15 × Brown Special produced the maximum heterosis for number of siliqua plant^{-1}. The F_1-Tori-7 × BARI Sar-17 gave the highest significant and positive heterosis over the both parents for thousand seed weight while the F_1-Yellow Special × Tori-7 represented the highly significant and positive heterosis over the both parents for seed yield plant^{-1}. The estimates of GCA effects for different characters suggested that the parent Tori-7 was the best general combiner for producing more number of primary branches, secondary branches and siliqua plant^{-1} while Brown Special was the best general combiner for earliness, thousand seed weight and seed yield plant^{-1}. The parent BARI Sar-17 was the best general combiner for plant height and for producing more seeds siliqua^{-1}. For siliqua length BARI Sar-6 was a good general combiner. However the SCA estimates of various traits revealed that the F_1- BARI Sar-6 × Brown Special was the best for plant height (i.e. dwarfness) and earliness while F_1- BARI Sar-14 × BARI Sar-6 was the best for number of primary branches plant^{-1} and F_1- BARI Sar-15 × Brown Special was best for more number of secondary branches plant^{-1}, siliqua plant^{-1} and seed yield plant^{-1} as it represented the highest SCA effects for those traits. The F_1- BARI Sar-14 × BARI Sar-17 showed the highest positive and the highly significant SCA effects for number of seeds siliqua^{-1}. F_1- Tori-7 × BARI Sar-17 was the best for thousand seed weight.

Gene action study revealed that most of the F_1s performed better than their both parents in most of the traits across the crosses. Superiority of F_1s indicated the presence of dominant gene effects while the F_1's with average performance over their two parents indicated partial dominance. However, most of the yield components revealed that the F_2 means were lower than their corresponding F_1 means signifying the presence of inbreeding depression. In general, BC_1s performed better than BC_2s in most of the crosses for the characters such as days to 50% flowering and 80% maturity, number of siliqua plant^{-1} and siliqua length while BC_2s performed better than BC_1s in most of the crosses for the characters viz., number of primary and secondary branches plant^{-1}, 1000 seed weight and seed yield plant^{-1}. Out of twenty one crosses, the highly significant and the highest negative heterosis for days to 50% flowering (-15.90 %) and for 80% maturity (-8.90 %) were recorded by the cross $P_1 \times P_7$ over the mid parents and (-33.33 %) and (-20.61 %) over the better parents respectively. For thousand seed weight the cross $P_4 \times P_3$ gave the highest significant and the positive heterosis

(41.59 %) over the mid parent and in the cross $P_6 \times P_2$ (57.42 %) over the better parent. The highest significant positive heterosis (374.37 %) and (298.97 %) over the mid and better parents respectively were recorded in the cross $P_4 \times P_3$ for seed yield plant^{-1}. Therefore, selection could be effective for these crosses. The highly significant and the highest negative ID (Inbreeding depression) for days to 50% flowering was represented by the cross $P_2 \times P_5$ (-27.91 %) and for 80% maturity by the cross $P_2 \times P_3$ (-15.85 %). The highest negative and significant ID for thousand seed weight was observed in the cross $P_4 \times P_6$ (-22.50 %) and for seed yield plant^{-1} in the cross $P_3 \times P_6$ (-3.01 %) while it was the highly significant and positive for the cross $P_6 \times P_2$ (25.27 %) and the cross $P_2 \times P_5$ (60.57 %) respectively. The positive ID indicated mean values of F_2 progenies were lower than their F_1 generations and vice versa. The highest heritability (Bs) for days to 50% flowering and 80% maturity were exhibited by the cross $P_1 \times P_3$ and $P_3 \times P_5$ respectively while for 1000 seed weight and seed yield plant^{-1} it was highest in $P_2 \times P_4$. For heritability (Ns) it was highest in the cross $P_2 \times P_3$ and $P_3 \times P_5$ for days to 50% flowering and 80% maturity respectively while for 1000 seed weight and seed yield plant^{-1} it was the highest in $P_6 \times P_2$ and $P_1 \times P_2$ respectively. The highest genetic advance for days to 50% flowering and 80% maturity was found in the cross $P_1 \times P_3$ and $P_2 \times P_3$ respectively while for 1000 seed weight and seed yield plant^{-1} it was the highest in $P_2 \times P_4$ and $P_4 \times P_5$ respectively. In most of the cases both heritability and genetic advance were found to be very low due to opposite direction of additive and dominance variance. The phenotypic variance was higher than the genotypic variance for most of the traits across the crosses indicated the predominance of the environmental variance over the genotypic variance. The dominance (H) values were higher than the additive (D) values. Degree of dominance (h/d) was higher than one for most of the traits across the crosses, indicated over dominance effects. If magnitude of D was less, then we could move for heterosis breeding but the significant and the negative estimates of H, I and L gene effects in different traits across the crosses suggested that the selection could be delayed to later generation, so that negative alleles are removed. Hence, improvement of these traits could be achieved through the recurrent selection procedure. The duplicate type epistasis in most of the crosses for majority of the traits also indicated in decreased heterosis and also hindered the rate of progress through selection. Therefore, selection might be delayed to advanced generations for the reduction of di-genic epistasis variation, utilization of both additive and non-additive gene effects and exploit transgressive segregants. But where non-additive effects hold

considerable importance in traits expression, recurrent selection for specific combining ability could be used as a suitable breeding procedure.

The oil content and quality were also estimated. The genotypes for estimating oil content and quality were selected on the basis of their duration and yield performance. Genotypes having short duration and high yield potential were selected. Among the parents Yellow Special contained the highest (45.05%) oils. In F_1s Brown Special × Yellow Special contained the highest (39.04%) oil while among F_2s it was the highest (37.71%) in BARI Sar-14 × Yellow Special and in both BC_1 and BC_2 generations Tori-7 × BARI Sar-14 contained the highest (38.98%) and (38.57%) oils respectively. Among the parent BARI Sar-6 contained the highest (93.16%) unsaturated fatty acids (USFA) and Yellow Special contained the lowest (3.96%) saturated fatty acids (SFA). In F_1 generations BARI Sar-14 × Brown Special contained the highest (93.50%) USFA while the lowest (4.18%) SFA was in Brown Special × BARI Sar-6. In F_2 generations the highest (93.51%) USFA was recorded in BARI Sar-15 × Brown Special while the lowest (3.92%) SFA was in Brown Special × Tori-7. In the BC_1 and in BC_2 generations the highest (93.45%) and (93.89%) USFA were estimated in Tori-7 × BARI Sar-14 (BC_1) and in Brown Special × BARI Sar-17 (BC_2) respectively and the lowest (4.21%) SFA in BARI Sar-14 × Brown Special (BC_1) and (4.15%) in Tori-7 × BARI Sar-14 (BC_2) respectively were estimated. So, these genotypes with the high level of USFA and the low level of SFA could be selected for further development of this trait. The highest PUSFA containing parent was Tori-7 (16.98%), F_1 was Tori-7 × Yellow Special (19.27%), F_2 was Tori-7 × Yellow Special (21.54%), BC_1 was Tori-7 × Yellow Special (21.57%) and BC_2 was Yellow Special × BARI Sar-6 (16.47%). Therefore, they could be selected for further improvement of these trait. Though those containing the high level of PUSFA was desirable but those with the high MUSFA along with the higher level of erucic acid was not desirable as it has toxic effect on the heart at the high enough doses. In this study the parent- Tori-7, F_1- Tori-7 × Yellow Special, F_2- Tori-7 × Yellow Special, BC_1- Tori-7 × Yellow Special and BC_2- Yellow Special × BARI Sar-6 contained the lowest (44.97%), (45.37%), (45.42%), (45.49%) and (46.67%) erucic acid respectively. So, they could be used for developing low erucic acid containing variety.

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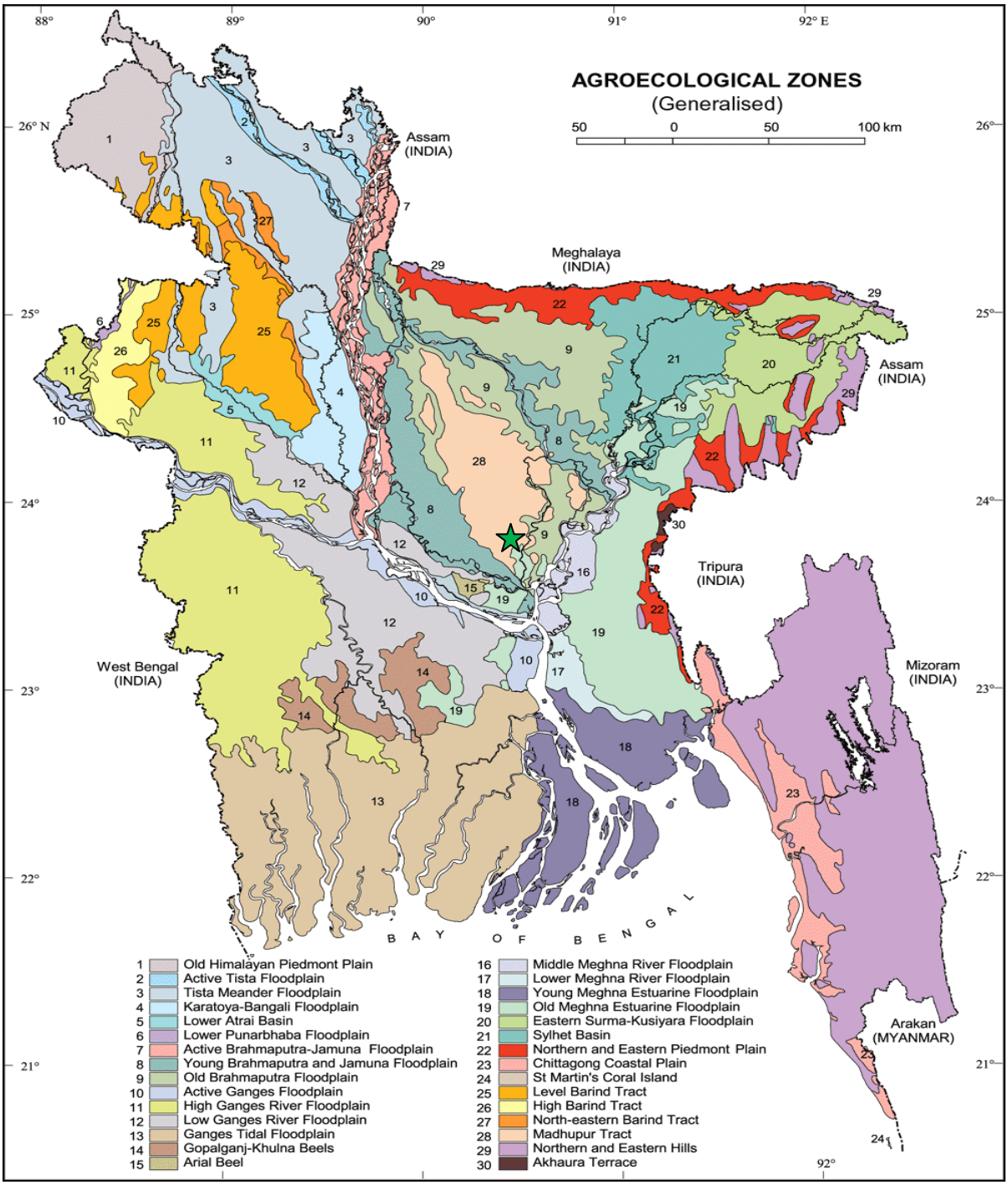
APPENDICES

Appendix I. Map showing the experimental site under the study



★ This sign showing the experimental site under study, at SAU, Dhaka.

Appendix II. Morphological, Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site (1st year)

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. Physical composition of the soil

Soil separates	%	Methods employed
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

C. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (mg $100g^{-1}$ soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

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

Appendix III. Monthly average temperature, relative humidity, total rainfall and sunshine of the experimental site during the period from Nov.,2017 to February, 2018.

Month	Air temperature (°c)		Relative humidity (RH%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2017	28.2	18.0	77	2.27	**5.7**
December, 2017	32.4	16.3	69	0	**7.8**
January, 2018	29.1	13.0	79	0	**3.9**
February, 2018	**28.1**	**11.1**	**72**	**1**	**5.6**

Source: Bangladesh Meteorological Department (BMD)(Climate & Weather Division), Agargoan, Dhaka – 1207.

Appendix IV. Morphological, Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site (2nd and 3rd year)

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Sher-e-Bangla Agricultural University Japani Para, 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. Physical Composition of the Soil

Sl. No	Soil Separates	%	Methods Employed
01	Sands	36.90	Hydrometer Methods (Day, 1915)
02	Silt	26.40	Same
03	Clay	36.66	Same
04	Texture Class	Clay Loam	Same

C. Chemical Composition of the Soil

Sl. No	Soil Characteristics	Analytical data	Methods Employed
01	Organic Carbon (%)	0.82	Walkley and Black, 1947
02	Total Nitrogen (Kg/ha)	1790.0	Bremner and Mulvaney, 1965
03	Total S (ppm)	225.00	Bardsley and Lanester, 1965
04	Total Phosphorus (ppm	840.0	Olsen and Sommers, 1952
05	Available Nitrogen (kg/ha)	54.0	Bremner, 1965
06	Available Phosphorus (kg/ha)	69.00	Olsen and Dean, 1965
07	Exchangeable K (Kg/ha)	89.50	Pratt, 1965
08	Available S (kg/ha)	16.00	Hunter, 1984
09	pH (1:2.5 Soil to Water)	5.55	Jackson, 1955
10	CEC	11.23	Chapman, 1965

Appendix V. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from Nov, 2018 to Feb, 2019.

Month	Air temperature (^{0}c)		Relative humidity (%)	Rainfall (mm)	Sunshine (hr.)
	Minimum	Maximum			
November, 2018	19.2	29.6	53	34.4	11
December,2018	14.1	26.4	50	12.8	11
January, 2019	12.7	25.4	46	7.7	11
February, 2019	15.5	28.1	37	28.9	11

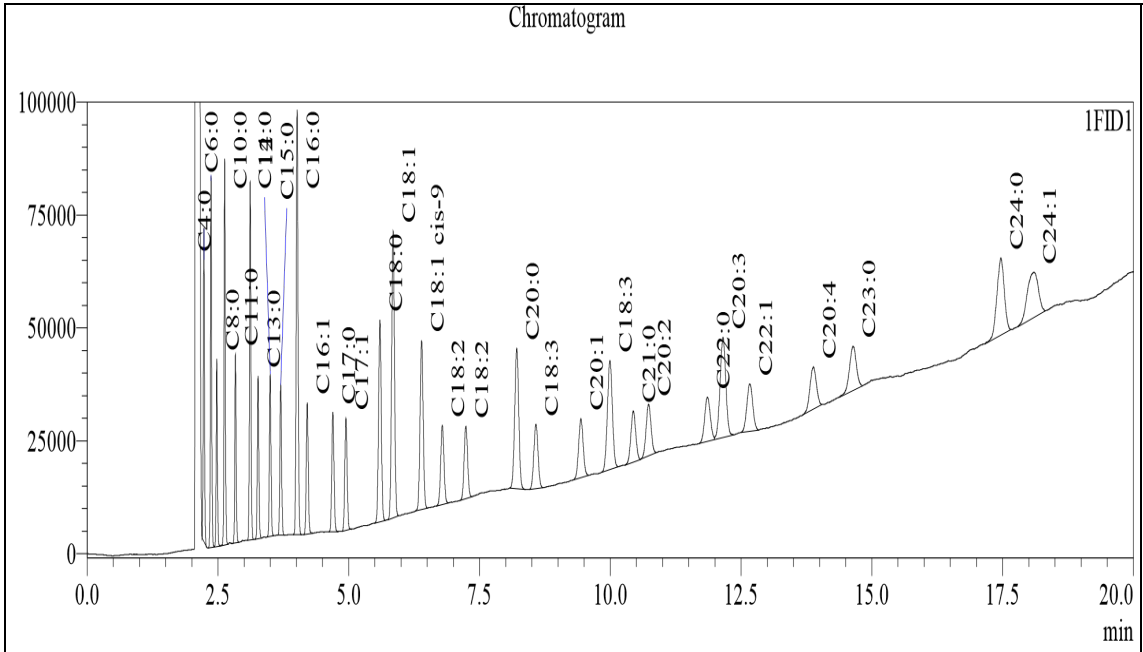
Source: Bangladesh Meteorological Department (BMD)(Climate & Weather Division), Agargoan, Dhaka-1207.

Appendix VI. Analysis of variance (MS value) for seed yield plant^{-1} and its component characters in 7×7 full diallel crosses of *Brassica rapa* genotypes

Source of variation	df	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of siliqua plant^{-1}	Siliqua length	Number of seeds siliqua^{-1}	Thousand seed weight	Days to 50% flowering	Days to 80% maturity	Seed yield plant^{-1}
Replication	2	43.14	2.58	0.69	406	0.62	2.30	0.00	62.85	60.22	5.21
Genotype	48	393.69**	14.47**	116.97**	112986**	0.80**	118.02**	2.47**	86.30**	104.14**	73.60**
Error	96	6.73	1.11	0.92	58	0.05	1.70	0.04	0.43	1.14	1.35

*** and ** significant at 5% and 1% level of probability, respectively**

Appendix VII. GC chromatogram of FAMEs and peak table for the Standard

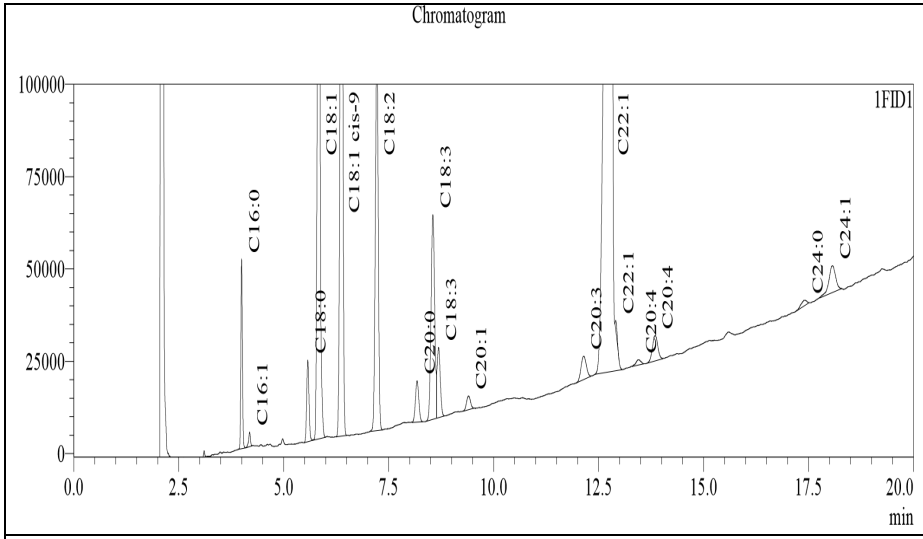


Standard

Peak#	Name	Ret. Time	Area%	Unit
1	C4:0	2.232	3.158	%
2	C6:0	2.369	3.715	%
3	C8:0	2.479	1.879	%
4	C10:0	2.629	3.985	%
5	C11:0	2.835	2.061	%
6	C12:0	3.117	4.248	%
7	C13:0	3.267	2.041	%
8	C14:0	3.499	2.170	%
9	C15:0	3.700	2.140	%
10	C16:0	4.014	6.661	%
11	C16:1	4.207	2.164	%
12	C17:0	4.697	2.239	%
13	C17:1	4.947	2.192	%
14	C18:0	5.598	4.584	%
15	C18:1	5.849	6.838	%
16	C18:1 cis-9	6.394	4.422	%
17	C18:2	6.790	2.193	%
18	C18:2	7.240	2.126	%
19	C20:0	8.213	4.775	%
20	C18:3	8.579	2.276	%
21	C20:1	9.440	2.252	%
22	C18:3	9.994	4.522	%
23	C21:0	10.440	2.079	%
24	C20:2	10.733	2.161	%
25	C22:0	11.857	2.099	%
26	C20:3	12.156	4.851	%
27	C22:1	12.669	2.371	%
28	C20:4	13.886	2.291	%
29	C23:0	14.642	2.554	%
30	C24:0	17.467	4.750	%
31	C24:1	18.097	4.202	%
Total			100.000	

Peak Table

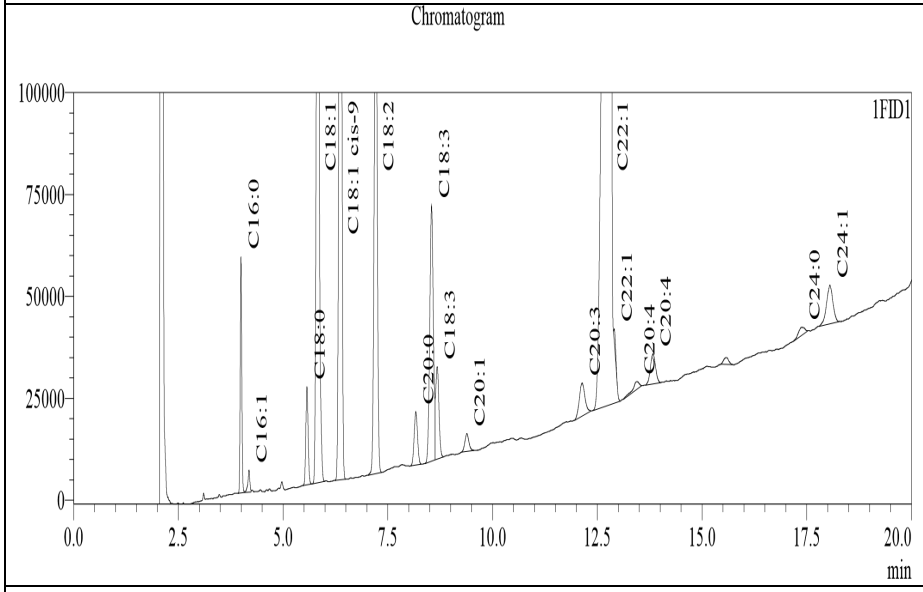
Appendix VIII. GC chromatogram of FAMEs and peak table in *Brassica rapa* genotypes (Parents)



P_1 = BARI Sarisha-14

Peak#	Name	Ret. Time	Area%	Unit
1	C16:0	3.999	1.815	%
2	C16:1	4.190	0.165	%
3	C18:0	5.575	1.189	%
4	C18:1	5.836	13.052	%
5	C18:1 cis-9	6.381	13.580	%
6	C18:2	7.221	7.137	%
7	C20:0	8.178	0.873	%
8	C18:3	8.555	4.714	%
9	C18:3	8.691	1.390	%
10	C20:1	9.403	0.337	%
11	C20:3	12.145	0.777	%
12	C22:1	12.790	51.197	%
13	C22:1	12.908	0.142	%
14	C20:4	13.452	0.157	%
15	C20:4	13.844	0.853	%
16	C24:0	17.418	0.200	%
17	C24:1	18.076	1.126	%
18		20.151	0.822	
19		21.849	0.476	
Total			100.000	

Peak Table

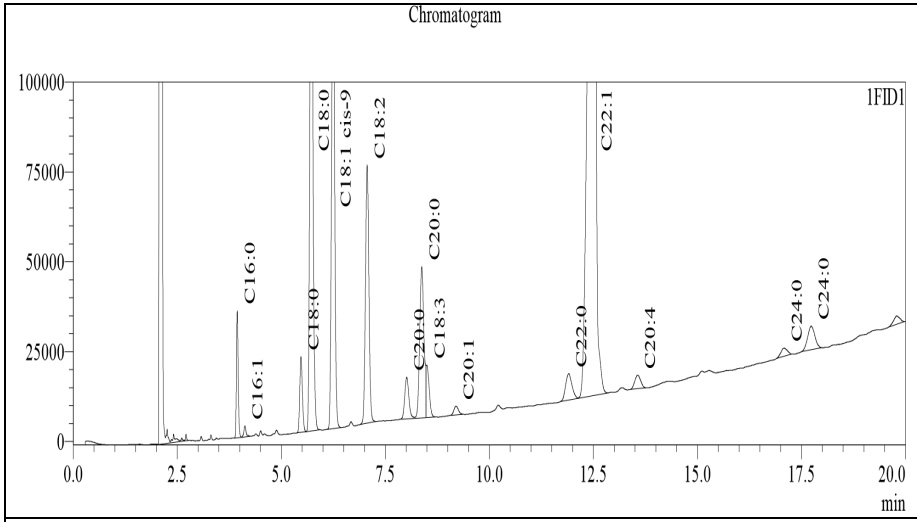


P_3 = Yellow Special

Peak#	Name	Ret. Time	Area%	Unit
1		2.084	97.095	
2	C16:0	3.996	0.051	%
3	C16:1	4.186	0.006	%
4	C18:0	5.571	0.032	%
5	C18:1	5.832	0.383	%
6	C18:1 cis-9	6.374	0.357	%
7	C18:2	7.214	0.237	%
8	C20:0	8.169	0.025	%
9	C18:3	8.544	0.130	%
10	C18:3	8.679	0.043	%
11	C20:1	9.387	0.010	%
12	C20:3	12.142	0.026	%
13	C22:1	12.802	1.485	%
14	C22:1	12.905	0.004	%
15	C20:4	13.444	0.007	%
16	C20:4	13.830	0.022	%
17		15.588	0.005	
18	C24:0	17.383	0.007	%
19	C24:1	18.051	0.035	%
20		20.142	0.024	
21		21.819	0.016	
Total			100.000	

Peak Table

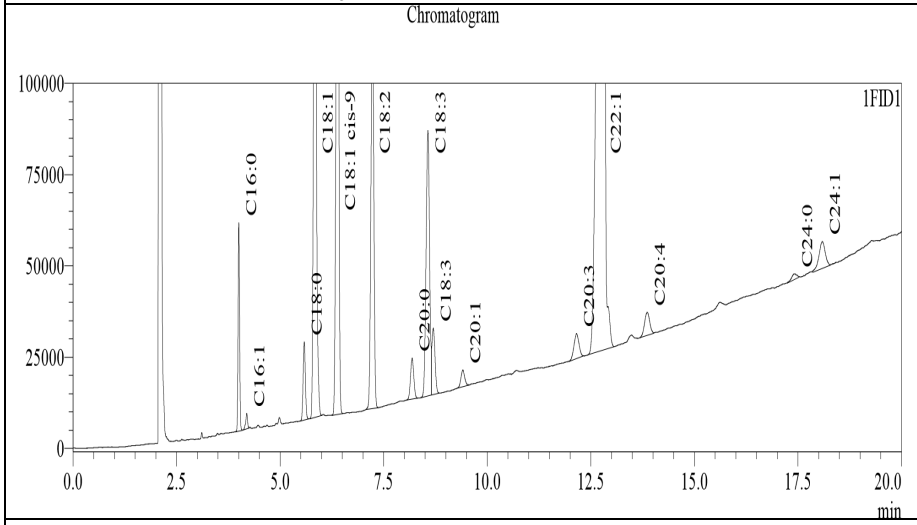
Appendix VIII (Cont'd).



P_6 = BARI Sarisha-15

Peak#	Name	Ret. Time	Area%	Unit
1		2.085	97.990	
2	C16:0	3.942	0.033	%
3	C16:1	4.126	0.004	%
4	C18:0	5.474	0.029	%
5	C18:0	5.722	0.282	%
6	C18:1 cis-9	6.247	0.228	%
7	C18:2	7.064	0.131	%
8	C20:0	8.015	0.025	%
9	C20:0	8.376	0.096	%
10	C18:3	8.503	0.023	%
11	C20:1	9.199	0.006	%
12	C22:0	11.911	0.024	%
13	C22:1	12.518	1.078	%
14	C20:4	13.563	0.012	%
15	C24:0	17.085	0.008	%
16	C24:0	17.734	0.025	%
17		19.789	0.008	
Total			100.000	

Peak Table

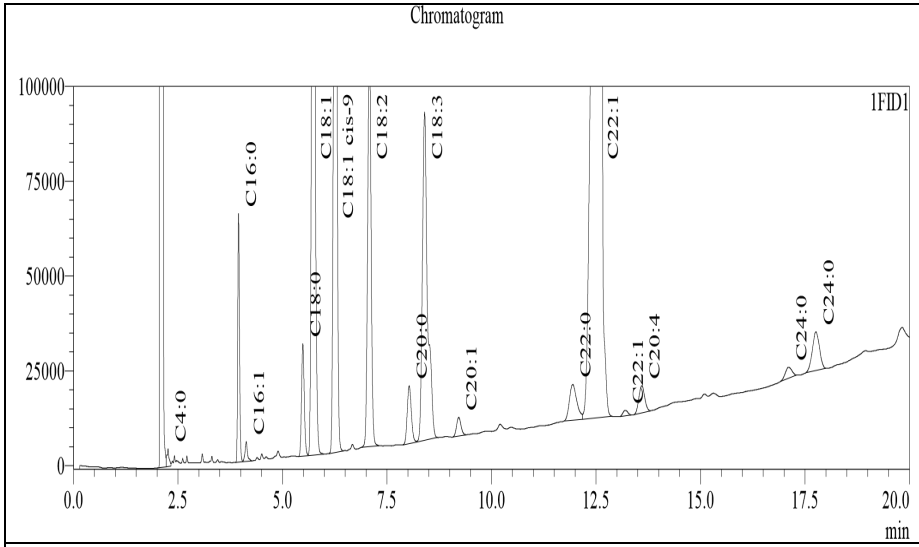


P_2 = Brown Special

Peak#	Name	Ret. Time	Area%	Unit
1	C16:0	4.004	1.994	%
2	C16:1	4.195	0.182	%
3	C18:0	5.583	1.119	%
4	C18:1	5.846	14.486	%
5	C18:1 cis-9	6.388	12.825	%
6	C18:2	7.230	7.584	%
7	C20:0	8.187	0.858	%
8	C18:3	8.570	5.970	%
9	C18:3	8.698	1.288	%
10	C20:1	9.412	0.399	%
11	C20:3	12.155	0.799	%
12	C22:1	12.807	49.320	%
13	C20:4	13.865	0.753	%
14	C24:0	17.423	0.180	%
15	C24:1	18.090	1.086	%
16		20.173	0.801	
17		21.885	0.356	
Total			100.000	

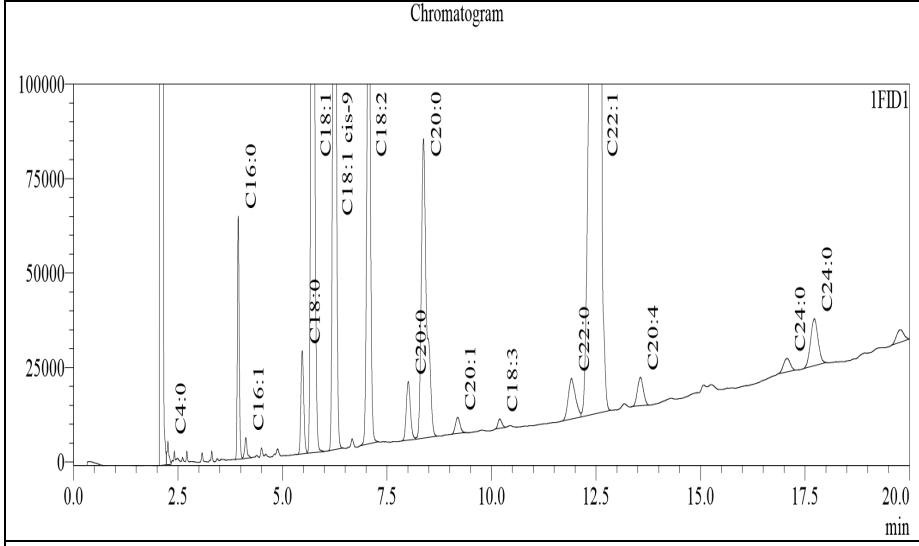
Peak Table

Appendix VIII (Cont'd).



Peak#	Name	Ret. Time	Area%	Unit
1		2.086	96.674	
2	C4:0	2.262	0.005	%
3	C16:0	3.950	0.060	%
4	C16:1	4.133	0.007	%
5	C18:0	5.487	0.042	%
6	C18:1	5.742	0.459	%
7	C18:1 cis-9	6.269	0.417	%
8	C18:2	7.080	0.193	%
9	C20:0	8.032	0.032	%
10	C18:3	8.402	0.232	%
11	C20:1	9.217	0.011	%
12	C22:0	11.948	0.036	%
13	C22:1	12.604	1.743	%
14	C22:1	13.200	0.004	%
15	C20:4	13.601	0.022	%
16	C24:0	17.116	0.010	%
17	C24:0	17.763	0.038	%
18		19.832	0.015	
Total			100.000	

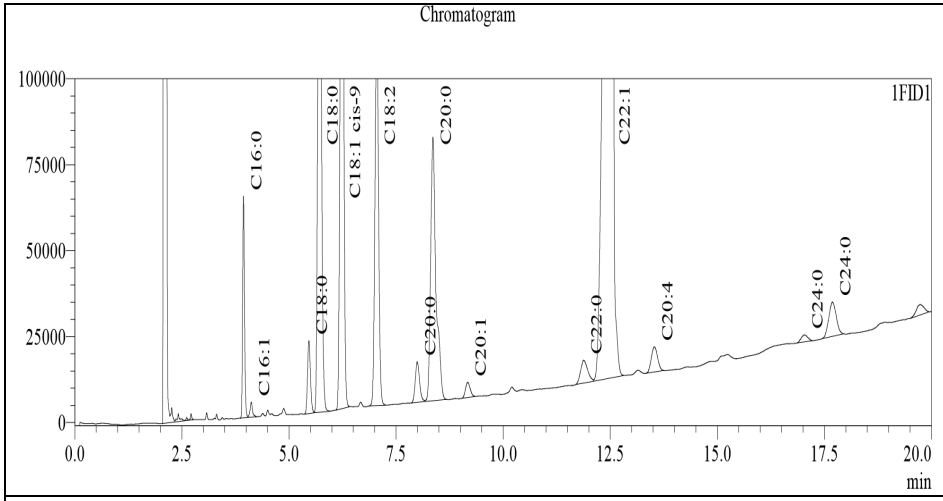
P_5 = BARI Sarisha-17 | **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.086	96.252	
2	C4:0	2.261	0.006	%
3	C16:0	3.942	0.062	%
4	C16:1	4.125	0.007	%
5	C18:0	5.473	0.041	%
6	C18:1	5.730	0.535	%
7	C18:1 cis-9	6.251	0.430	%
8	C18:2	7.064	0.254	%
9	C20:0	8.010	0.034	%
10	C20:0	8.374	0.226	%
11	C20:1	9.193	0.011	%
12	C18:3	10.198	0.005	%
13	C22:0	11.914	0.041	%
14	C22:1	12.592	2.001	%
15	C20:4	13.560	0.023	%
16	C24:0	17.078	0.012	%
17	C24:0	17.728	0.049	%
18		19.779	0.013	
Total			100.000	

P_7 = BARI Sarisha-6 | **Peak Table**

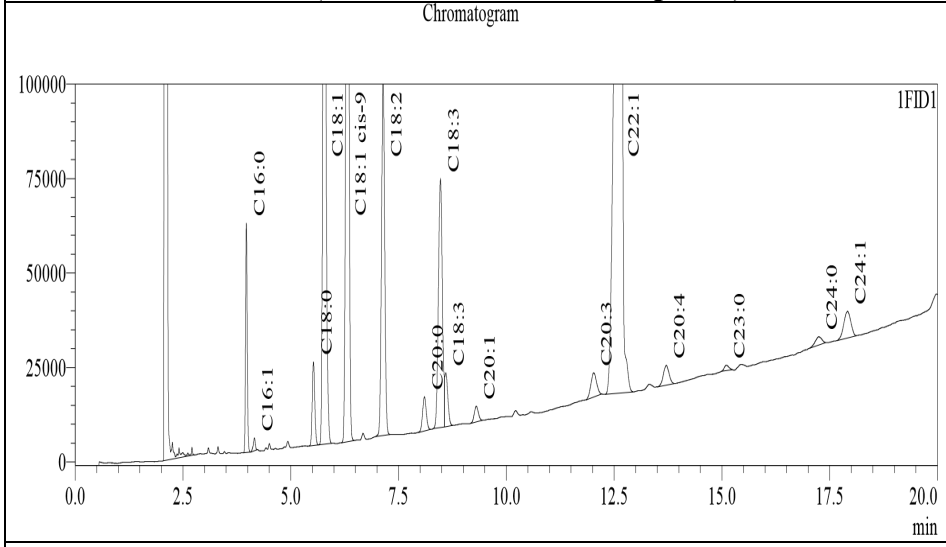
Appendix IX. GC chromatogram of FAMEs and peak table in *Brassica rapa* genotypes (Selected F_1s)



$P_1 \times P_2$ (BARI Sar-14 × Brown Special)

Peak#	Name	Ret. Time	Area%	Unit
1		2.087	96.957	
2	C16:0	3.939	0.062	%
3	C16:1	4.121	0.006	%
4	C18:0	5.465	0.032	%
5	C18:0	5.718	0.415	%
6	C18:1 cis-9	6.240	0.378	%
7	C18:2	7.051	0.204	%
8	C20:0	7.995	0.026	%
9	C20:0	8.361	0.212	%
10	C20:1	9.173	0.011	%
11	C22:0	11.876	0.024	%
12	C22:1	12.535	1.595	%
13	C20:4	13.532	0.024	%
14	C24:0	17.035	0.007	%
15	C24:0	17.687	0.038	%
16		19.734	0.012	
Total			100.000	

Peak Table

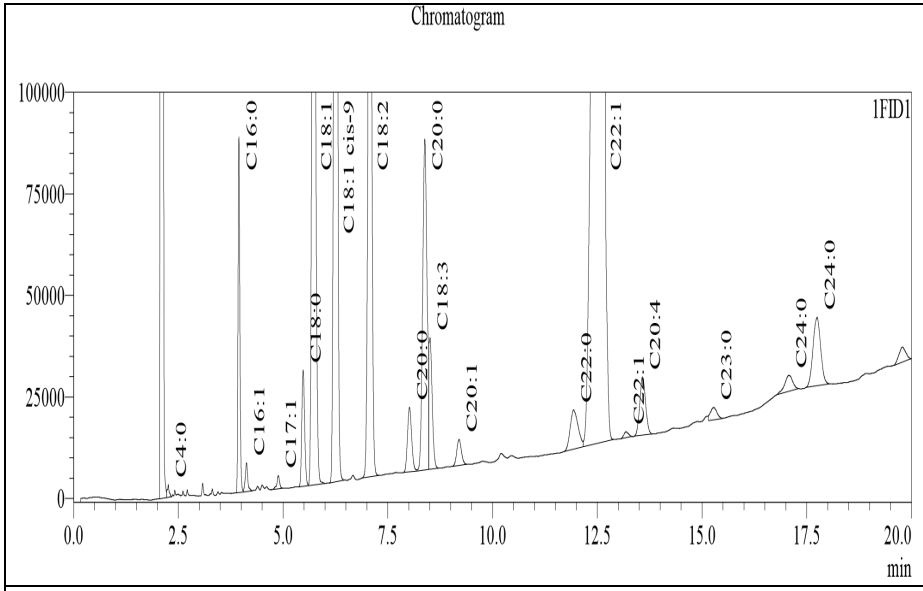


$P_2 \times P_5$ (Brown Special × BARI Sar-17)

Peak#	Name	Ret. Time	Area%	Unit
1		2.084	97.734	
2	C16:0	3.971	0.053	%
3	C16:1	4.158	0.004	%
4	C18:0	5.527	0.029	%
5	C18:1	5.784	0.358	%
6	C18:1 cis-9	6.320	0.366	%
7	C18:2	7.144	0.159	%
8	C20:0	8.101	0.017	%
9	C18:3	8.473	0.138	%
10	C18:3	8.595	0.023	%
11	C20:1	9.305	0.009	%
12	C20:3	12.022	0.019	%
13	C22:1	12.648	1.028	%
14	C20:4	13.707	0.016	%
15	C23:0	15.105	0.004	%
16	C24:0	17.246	0.007	%
17	C24:1	17.911	0.026	%
18		19.979	0.010	
Total			100.000	

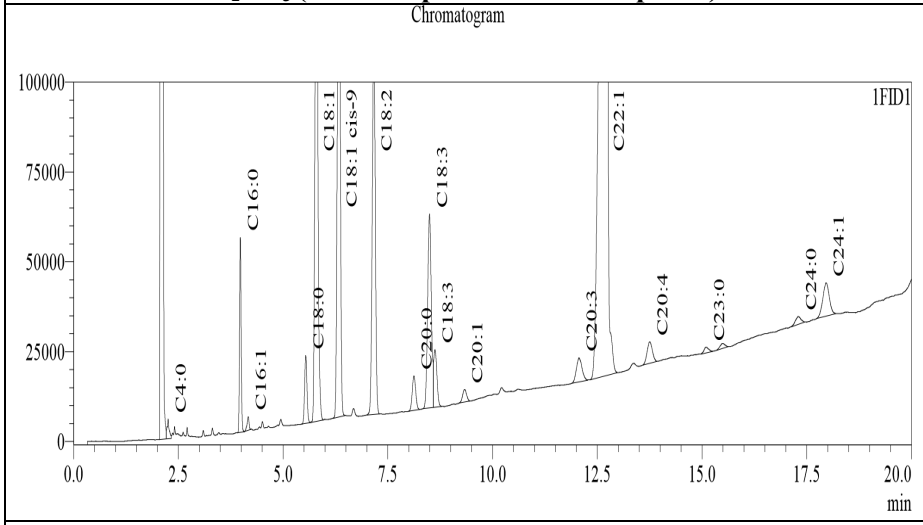
Peak Table

Appendix IX (Cont'd).



Peak#	Name	Ret. Time	Area%	Unit
1		2.086	95.330	
2	C4:0	2.262	0.003	%
3	C16:0	3.946	0.084	%
4	C16:1	4.128	0.009	%
5	C17:1	4.887	0.004	%
6	C18:0	5.479	0.043	%
7	C18:1	5.735	0.528	%
8	C18:1 cis-9	6.266	0.597	%
9	C18:2	7.079	0.366	%
10	C20:0	8.017	0.035	%
11	C20:0	8.383	0.189	%
12	C18:3	8.508	0.054	%
13	C20:1	9.204	0.015	%
14	C22:0	11.935	0.040	%
15	C22:1	12.645	2.548	%
16	C22:1	13.188	0.003	%
17	C20:4	13.578	0.044	%
18	C23:0	15.280	0.010	%
19	C24:0	17.069	0.016	%
20	C24:0	17.750	0.067	%
21		19.783	0.013	
Total			100.000	

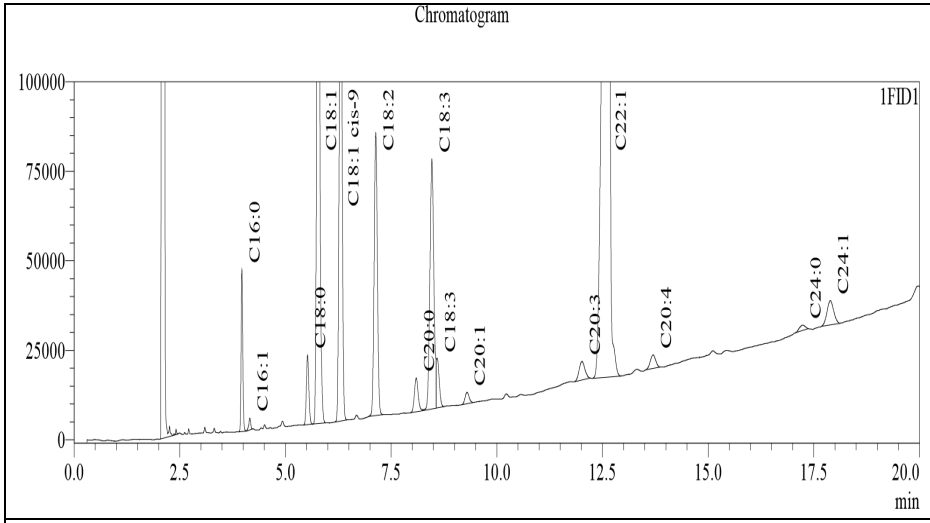
P_2× P_3 (Brown Special × Yellow Special) **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.085	97.749	
2	C4:0	2.258	0.006	%
3	C16:0	3.980	0.046	%
4	C16:1	4.169	0.004	%
5	C18:0	5.542	0.024	%
6	C18:1	5.799	0.271	%
7	C18:1 cis-9	6.333	0.264	%
8	C18:2	7.167	0.172	%
9	C20:0	8.124	0.018	%
10	C18:3	8.496	0.107	%
11	C18:3	8.625	0.028	%
12	C20:1	9.336	0.007	%
13	C20:3	12.063	0.020	%
14	C22:1	12.713	1.209	%
15	C20:4	13.755	0.017	%
16	C23:0	15.106	0.004	%
17		15.492	0.004	
18	C24:0	17.300	0.006	%
19	C24:1	17.960	0.032	%
20		20.045	0.007	
21		21.715	0.007	
Total			100.000	

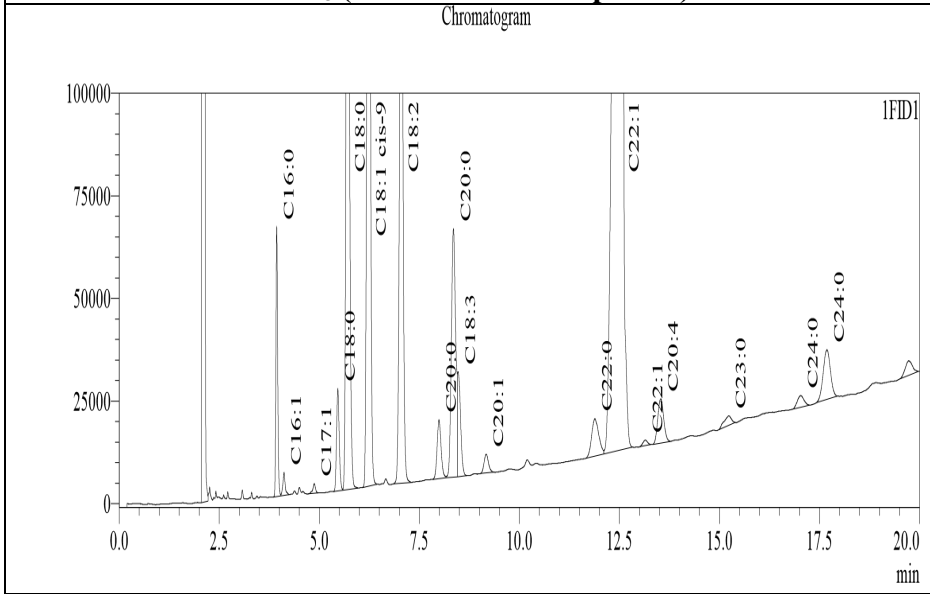
P_2× P_7 (Brown Special × BARI Sar-6) **Peak Table**

Appendix IX (Cont'd).



Peak#	Name	Ret. Time	Area%	Unit
1		2.086	98.023	
2	C16:0	3.971	0.039	%
3	C16:1	4.158	0.003	%
4	C18:0	5.523	0.025	%
5	C18:1	5.780	0.323	%
6	C18:1 cis-9	6.309	0.231	%
7	C18:2	7.138	0.132	%
8	C20:0	8.095	0.018	%
9	C18:3	8.464	0.144	%
10	C18:3	8.596	0.021	%
11	C20:1	9.297	0.007	%
12	C20:3	12.020	0.016	%
13	C22:1	12.630	0.971	%
14	C20:4	13.702	0.010	%
15	C24:0	17.239	0.005	%
16	C24:1	17.894	0.024	%
17		19.968	0.010	
Total			100.000	

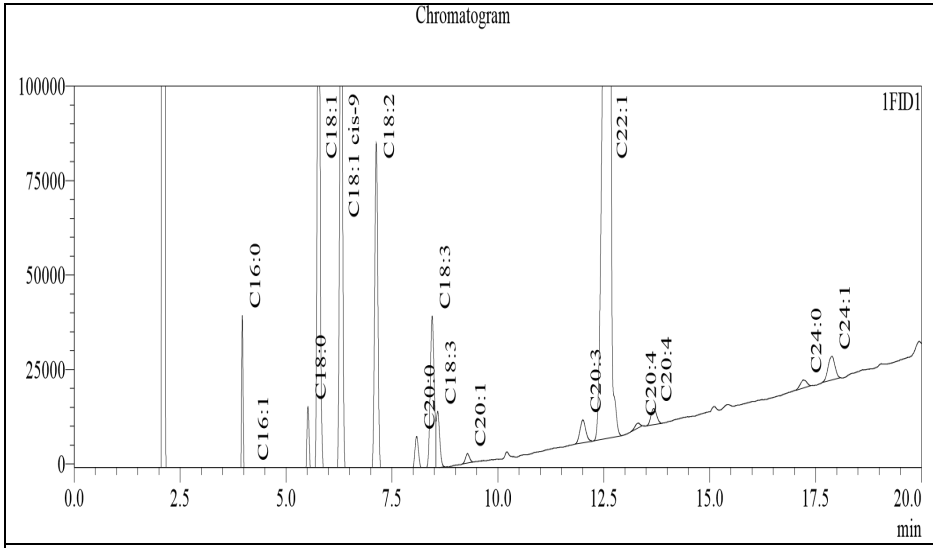
P_4× P_3 (Tori-7 × Yellow Special) | **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.087	96.370	
2	C16:0	3.938	0.063	%
3	C16:1	4.120	0.007	%
4	C17:1	4.875	0.003	%
5	C18:0	5.464	0.037	%
6	C18:0	5.715	0.422	%
7	C18:1 cis-9	6.240	0.452	%
8	C18:2	7.052	0.295	%
9	C20:0	7.994	0.031	%
10	C20:0	8.354	0.144	%
11	C18:3	8.471	0.043	%
12	C20:1	9.172	0.011	%
13	C22:0	11.889	0.036	%
14	C22:1	12.560	1.967	%
15	C22:1	13.150	0.003	%
16	C20:4	13.538	0.035	%
17	C23:0	15.232	0.009	%
18	C24:0	17.028	0.010	%
19	C24:0	17.685	0.048	%
20		19.730	0.014	
Total			100.000	

P_6 × P_2 (BARI Sar-15 × Brown Special) | **Peak Table**

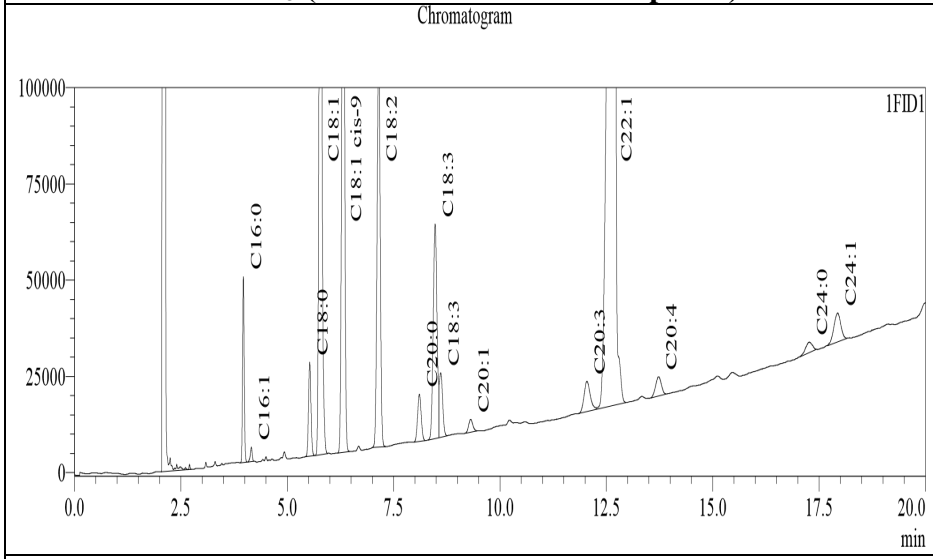
Appendix X. GC chromatogram of FAMEs and peak table in *Brassica rapa* genotypes (Selected F_2s)



P_1 × P_3 (BARI Sar-14 × Yellow Special)

Peak#	Name	Ret. Time	Area%	Unit
1		2.086	98.048	
2	C16:0	3.968	0.041	%
3	C16:1	4.155	0.003	%
4	C18:0	5.518	0.027	%
5	C18:1	5.772	0.264	%
6	C18:1 cis-9	6.303	0.237	%
7	C18:2	7.130	0.148	%
8	C20:0	8.085	0.018	%
9	C18:3	8.451	0.085	%
10	C18:3	8.580	0.026	%
11	C20:1	9.285	0.005	%
12	C20:3	12.010	0.018	%
13	C22:1	12.624	1.024	%
14	C20:4	13.314	0.003	%
15	C20:4	13.679	0.013	%
16	C24:0	17.213	0.007	%
17	C24:1	17.886	0.023	%
18		19.946	0.010	
Total			100.000	

Peak Table

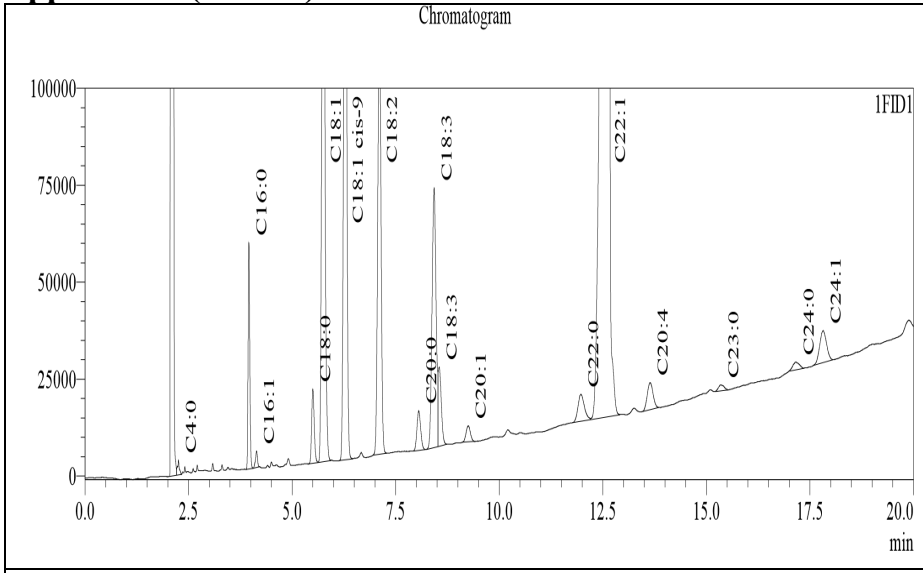


P_3× P_6 (Yellow Special × BARI Sar-15}

Peak#	Name	Ret. Time	Area%	Unit
1		2.081	97.709	
2	C16:0	3.970	0.042	%
3	C16:1	4.157	0.004	%
4	C18:0	5.530	0.032	%
5	C18:1	5.786	0.322	%
6	C18:1 cis-9	6.318	0.273	%
7	C18:2	7.150	0.174	%
8	C20:0	8.107	0.024	%
9	C18:3	8.477	0.115	%
10	C18:3	8.608	0.029	%
11	C20:1	9.314	0.007	%
12	C20:3	12.043	0.026	%
13	C22:1	12.672	1.172	%
14	C20:4	13.726	0.015	%
15	C24:0	17.269	0.010	%
16	C24:1	17.940	0.028	%
17		20.018	0.010	
18		21.674	0.007	
Total			100.000	

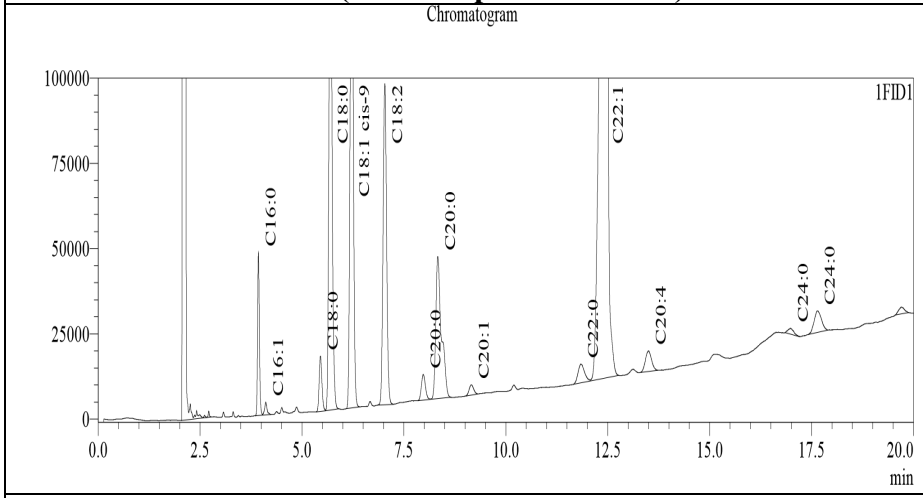
Peak Table

Appendix X (Cont'd).



Peak#	Name	Ret. Time	Area%	Unit
1		2.084	97.319	
2	C4:0	2.258	0.004	%
3	C16:0	3.958	0.052	%
4	C16:1	4.142	0.005	%
5	C18:0	5.501	0.026	%
6	C18:1	5.756	0.343	%
7	C18:1 cis-9	6.285	0.325	%
8	C18:2	7.108	0.197	%
9	C20:0	8.057	0.020	%
10	C18:3	8.429	0.144	%
11	C18:3	8.552	0.034	%
12	C20:1	9.249	0.010	%
13	C22:0	11.972	0.023	%
14	C22:1	12.617	1.426	%
15	C20:4	13.641	0.022	%
16	C23:0	15.352	0.004	%
17	C24:0	17.166	0.007	%
18	C24:1	17.822	0.030	%
19		19.889	0.011	
Total			100.000	

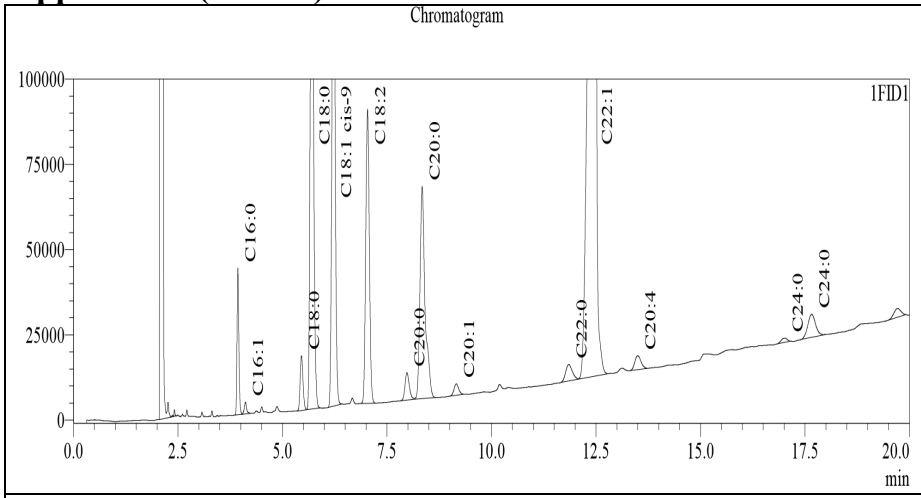
P_2× P_4 (Brown Special × Tori-7) **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.087	97.818	
2	C16:0	3.932	0.047	%
3	C16:1	4.114	0.005	%
4	C18:0	5.454	0.024	%
5	C18:0	5.700	0.277	%
6	C18:1 cis-9	6.222	0.288	%
7	C18:2	7.034	0.180	%
8	C20:0	7.976	0.016	%
9	C20:0	8.332	0.128	%
10	C20:1	9.160	0.007	%
11	C22:0	11.836	0.019	%
12	C22:1	12.452	1.133	%
13	C20:4	13.501	0.020	%
14	C24:0	16.985	0.005	%
15	C24:0	17.646	0.025	%
16		19.704	0.006	
Total			100.000	

P_4× P_3 (Tori-7 × Yellow Special) **Peak Table**

Appendix X (Cont'd).

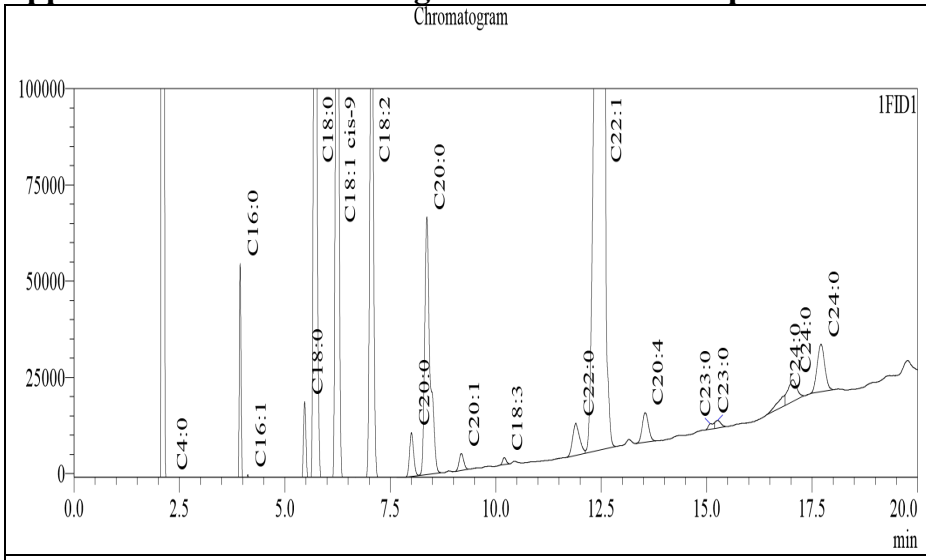


$P_6 \times P_2$ (BARI Sar-15 × Brown Special)

Peak#	Name	Ret. Time	Area%	Unit
1		2.087	97.794	
2	C16:0	3.933	0.042	%
3	C16:1	4.115	0.004	%
4	C18:0	5.455	0.024	%
5	C18:0	5.705	0.331	%
6	C18:1 cis-9	6.223	0.266	%
7	C18:2	7.036	0.164	%
8	C20:0	7.978	0.018	%
9	C20:0	8.342	0.169	%
10	C20:1	9.161	0.008	%
11	C22:0	11.851	0.017	%
12	C22:1	12.461	1.108	%
13	C20:4	13.498	0.013	%
14	C24:0	17.024	0.004	%
15	C24:0	17.662	0.028	%
16		19.727	0.010	
Total			100.000	

Peak Table

Appendix XI. GC chromatogram of FAMEs and peak table in *Brassica rapa* genotypes (Selected BC_1s)

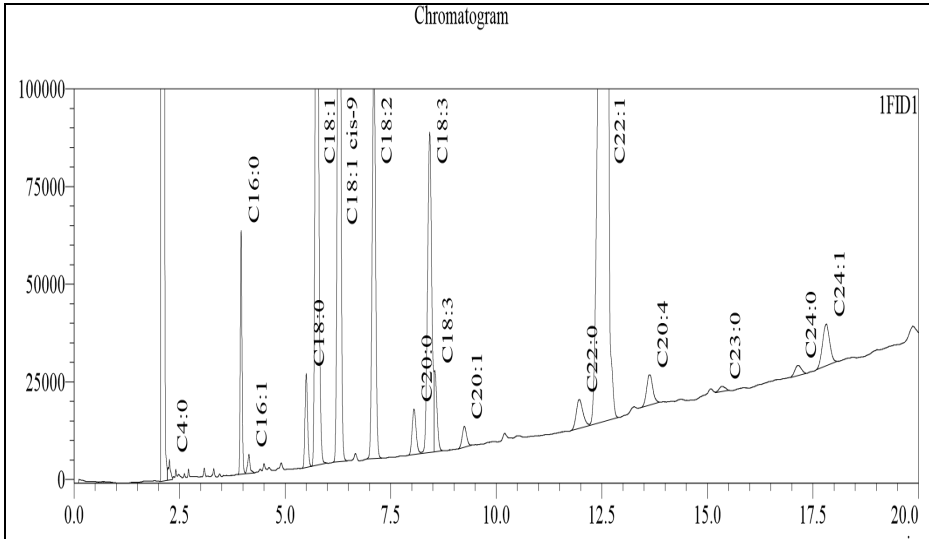


$P_4 \times P_3$ (Tori-7 × Yellow Special)

Peak#	Name	Ret. Time	Area%	Unit
1		2.087	96.757	
2	C4:0	2.261	0.005	%
3	C16:0	3.941	0.058	%
4	C16:1	4.123	0.006	%
5	C18:0	5.470	0.034	%
6	C18:0	5.722	0.414	%
7	C18:1 cis-9	6.245	0.384	%
8	C18:2	7.061	0.264	%
9	C20:0	8.002	0.024	%
10	C20:0	8.369	0.189	%
11	C20:1	9.185	0.010	%
12	C18:3	10.205	0.003	%
13	C22:0	11.901	0.030	%
14	C22:1	12.556	1.686	%
15	C20:4	13.538	0.025	%
16	C23:0	15.083	0.004	%
17	C23:0	15.259	0.006	%
18	C24:0	16.801	0.011	%
19	C24:0	17.048	0.027	%
20	C24:0	17.714	0.049	%
21		19.764	0.013	
Total			100.000	

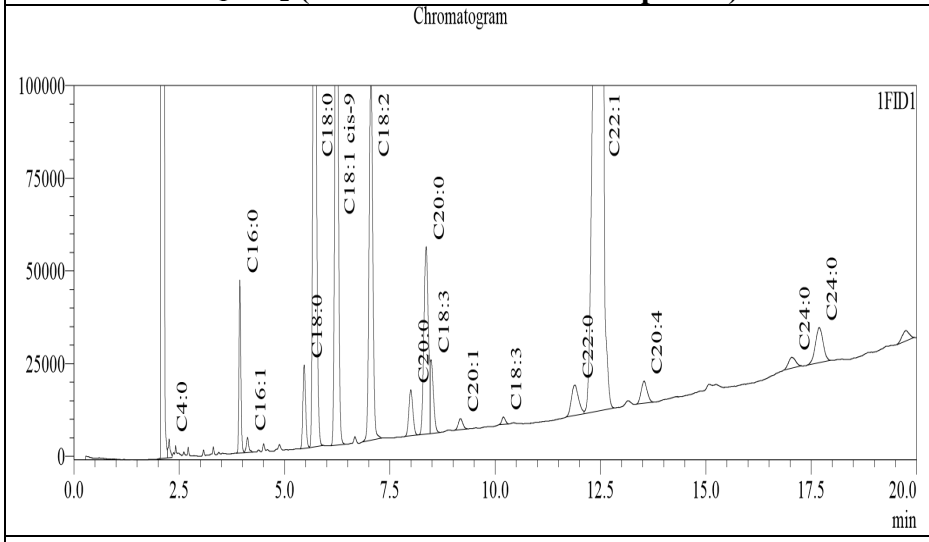
Peak Table

Appendix XI (Cont'd).



Peak#	Name	Ret. Time	Area%	Unit
1		2.085	97.101	
2	C4:0	2.260	0.006	%
3	C16:0	3.957	0.056	%
4	C16:1	4.141	0.006	%
5	C18:0	5.501	0.033	%
6	C18:1	5.757	0.388	%
7	C18:1 cis-9	6.285	0.383	%
8	C18:2	7.103	0.184	%
9	C20:0	8.052	0.024	%
10	C18:3	8.425	0.179	%
11	C18:3	8.545	0.030	%
12	C20:1	9.243	0.012	%
13	C22:0	11.972	0.026	%
14	C22:1	12.620	1.484	%
15	C20:4	13.638	0.025	%
16	C23:0	15.354	0.004	%
17	C24:0	17.152	0.009	%
18	C24:1	17.823	0.039	%
19		19.862	0.011	
Total			100.000	

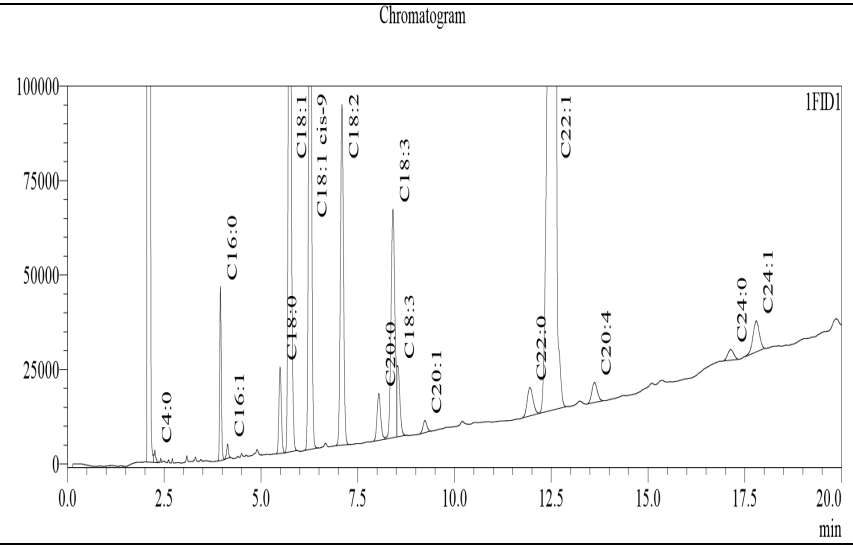
$P_1 \times P_2$ (BARI Sar-14 × Brown Special) **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.087	97.231	
2	C4:0	2.262	0.005	%
3	C16:0	3.939	0.045	%
4	C16:1	4.122	0.005	%
5	C18:0	5.467	0.033	%
6	C18:0	5.717	0.363	%
7	C18:1 cis-9	6.238	0.308	%
8	C18:2	7.051	0.194	%
9	C20:0	7.998	0.026	%
10	C20:0	8.363	0.119	%
11	C18:3	8.477	0.033	%
12	C20:1	9.175	0.007	%
13	C18:3	10.194	0.004	%
14	C22:0	11.898	0.031	%
15	C22:1	12.529	1.518	%
16	C20:4	13.535	0.018	%
17	C24:0	17.041	0.011	%
18	C24:0	17.690	0.038	%
19		19.756	0.010	
Total			100.000	

$P_3 \times P_6$ (Yellow Special × BARI Sar-15) **Peak Table**

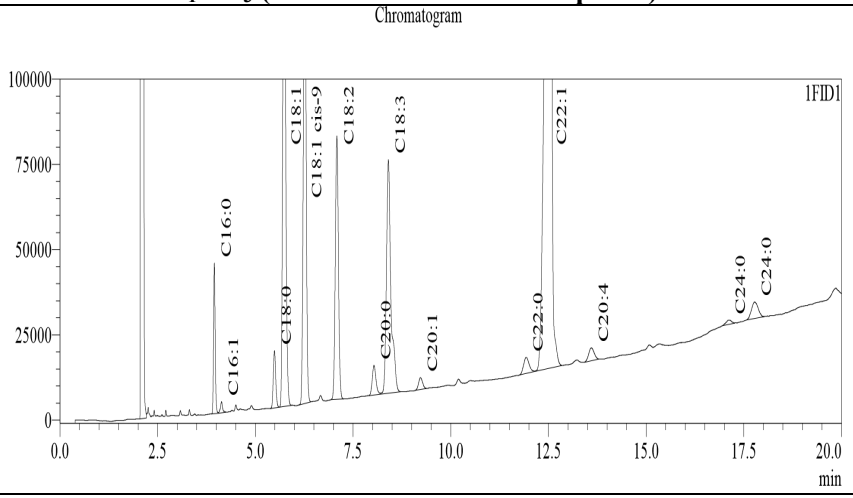
Appendix XI (Cont'd).



$P_1 \times P_3$ (BARI Sar-14 × Yellow Special)

Peak Table

Peak#	Name	Ret. Time	Area%	Unit
1		2.085	97.586	
2	C4:0	2.260	0.003	%
3	C16:0	3.954	0.041	%
4	C16:1	4.138	0.004	%
5	C18:0	5.495	0.031	%
6	C18:1	5.747	0.340	%
7	C18:1 cis-9	6.273	0.279	%
8	C18:2	7.095	0.154	%
9	C20:0	8.045	0.025	%
10	C18:3	8.409	0.135	%
11	C18:3	8.531	0.030	%
12	C20:1	9.236	0.007	%
13	C22:0	11.945	0.025	%
14	C22:1	12.580	1.274	%
15	C20:4	13.616	0.016	%
16	C24:0	17.124	0.009	%
17	C24:1	17.799	0.029	%
18		19.865	0.009	
Total			100.000	

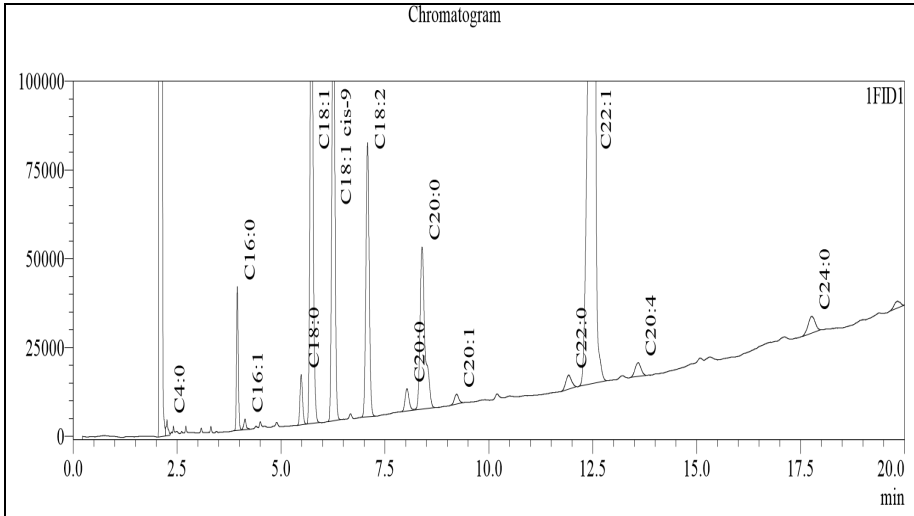


$P_4 \times P_1$ (Tori-7 × BARI Sar-14)

Peak Table

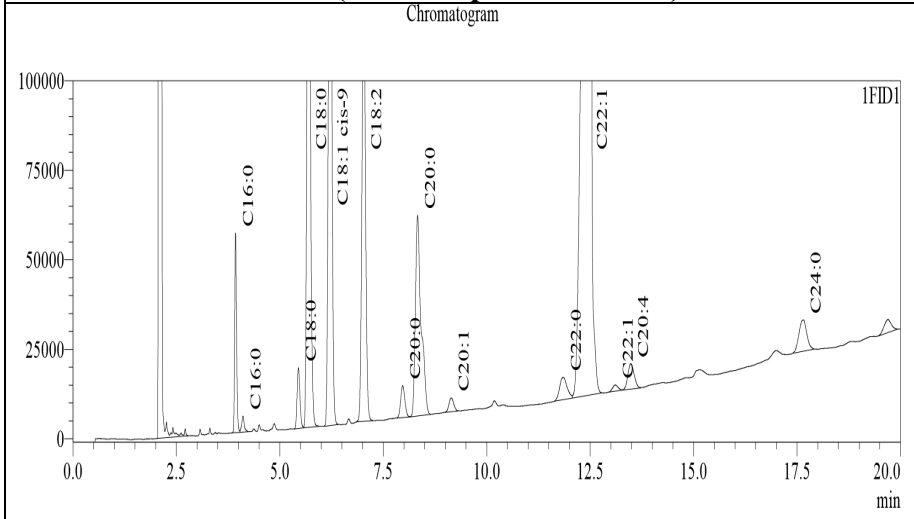
Peak#	Name	Ret. Time	Area%	Unit
1		2.085	98.103	
2	C16:0	3.952	0.040	%
3	C16:1	4.136	0.004	%
4	C18:0	5.490	0.023	%
5	C18:1	5.741	0.288	%
6	C18:1 cis-9	6.265	0.227	%
7	C18:2	7.088	0.134	%
8	C20:0	8.036	0.018	%
9	C18:3	8.405	0.171	%
10	C20:1	9.228	0.008	%
11	C22:0	11.932	0.014	%
12	C22:1	12.535	0.930	%
13	C20:4	13.604	0.011	%
14	C24:0	17.107	0.004	%
15	C24:0	17.776	0.018	%
16		19.857	0.008	
Total			100.000	

Appendix XII. GC chromatogram of FAMEs and peak table in *Brassica rapa* genotypes (Selected BC_2s)



Peak#	Name	Ret. Time	Area%	Unit
1		2.085	98.326	
2	C4:0	2.259	0.005	%
3	C16:0	3.950	0.037	%
4	C16:1	4.134	0.004	%
5	C18:0	5.487	0.019	%
6	C18:1	5.735	0.239	%
7	C18:1 cis-9	6.262	0.213	%
8	C18:2	7.083	0.133	%
9	C20:0	8.033	0.013	%
10	C20:0	8.395	0.121	%
11	C20:1	9.223	0.006	%
12	C22:0	11.923	0.012	%
13	C22:1	12.517	0.837	%
14	C20:4	13.591	0.012	%
15	C24:0	17.776	0.017	%
16		19.834	0.006	
Total			100.000	

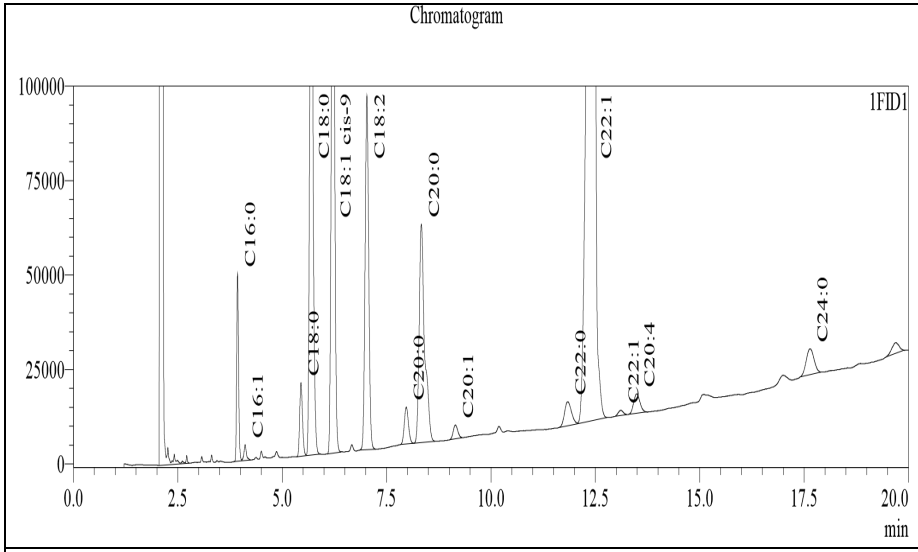
P_2× P_4 (Brown Special × Tori-7) — **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.087	97.119	
2	C16:0	3.930	0.055	%
3	C16:0	4.111	0.006	%
4	C18:0	5.451	0.025	%
5	C18:0	5.698	0.360	%
6	C18:1 cis-9	6.220	0.364	%
7	C18:2	7.029	0.231	%
8	C20:0	7.969	0.020	%
9	C20:0	8.330	0.170	%
10	C20:1	9.142	0.010	%
11	C22:0	11.851	0.024	%
12	C22:1	12.483	1.535	%
13	C22:1	13.108	0.005	%
14	C20:4	13.480	0.024	%
15	C24:0	17.649	0.036	%
16		19.700	0.014	
Total			100.000	

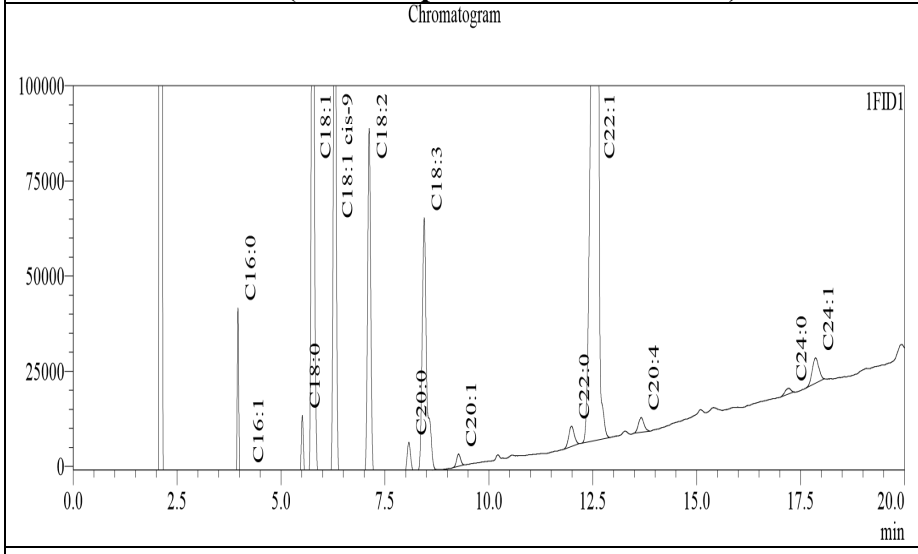
P_3 × P_2 (Yellow Special × Brown Special) — **Peak Table**

Appendix XII (Cont'd).



Peak#	Name	Ret. Time	Area%	Unit
1		2.087	97.631	
2	C16:0	3.931	0.049	%
3	C16:1	4.113	0.005	%
4	C18:0	5.451	0.029	%
5	C18:0	5.699	0.316	%
6	C18:1 cis-9	6.220	0.303	%
7	C18:2	7.030	0.178	%
8	C20:0	7.971	0.021	%
9	C20:0	8.333	0.167	%
10	C20:1	9.149	0.009	%
11	C22:0	11.841	0.023	%
12	C22:1	12.459	1.209	%
13	C22:1	13.114	0.003	%
14	C20:4	13.492	0.017	%
15	C24:0	17.640	0.028	%
16		19.697	0.011	
Total			100.000	

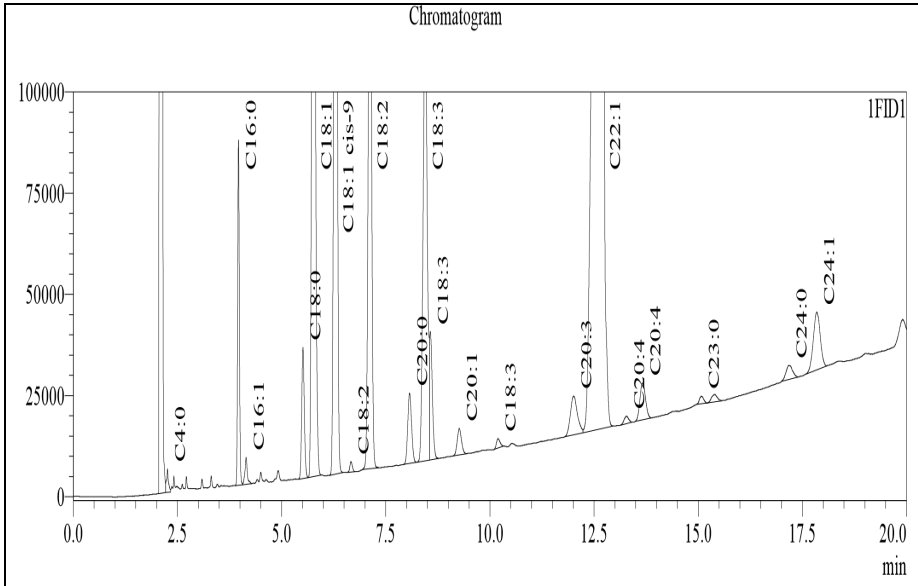
P_2× P_5 (Brown Special × BARI Sar-17) **Peak Table**



Peak#	Name	Ret. Time	Area%	Unit
1		2.086	98.016	
2	C16:0	3.965	0.043	%
3	C16:1	4.151	0.004	%
4	C18:0	5.514	0.025	%
5	C18:1	5.769	0.340	%
6	C18:1 cis-9	6.295	0.246	%
7	C18:2	7.122	0.155	%
8	C20:0	8.076	0.016	%
9	C18:3	8.446	0.160	%
10	C20:1	9.273	0.007	%
11	C22:0	11.991	0.015	%
12	C22:1	12.598	0.926	%
13	C20:4	13.665	0.012	%
14	C24:0	17.218	0.005	%
15	C24:1	17.862	0.024	%
16		19.932	0.009	
Total			100.000	

P_3× P_7 (Yellow Special × BARI Sar-6) **Peak Table**

Appendix XII (Cont'd).



P_4× P_1 (Tori-7 × BARI Sar-14)

Peak#	Name	Ret. Time	Area%	Unit
1		2.086	95.952	
2	C4:0	2.262	0.006	%
3	C16:0	3.965	0.077	%
4	C16:1	4.150	0.008	%
5	C18:0	5.513	0.044	%
6	C18:1	5.775	0.552	%
7	C18:1 cis-9	6.303	0.470	%
8	C18:2	6.668	0.003	%
9	C18:2	7.124	0.274	%
10	C20:0	8.073	0.035	%
11	C18:3	8.450	0.247	%
12	C18:3	8.571	0.045	%
13	C20:1	9.266	0.015	%
14	C18:3	10.195	0.004	%
15	C20:3	12.012	0.035	%
16	C22:1	12.704	2.092	%
17	C20:4	13.282	0.004	%
18	C20:4	13.669	0.027	%
19	C23:0	15.075	0.004	%
20		15.403	0.005	
21	C24:0	17.179	0.012	%
22	C24:1	17.845	0.052	%
23		19.910	0.019	
24		20.866	0.004	
25		21.563	0.013	
Total			100.000	

Peak Table

INTRODUCTION

REVIEW OF LITERATURE

MATERIALS AND METHODS

RESULTS AND DISCUSSION

Summery and Conclusion

REFERENCES

APPENDICES