FATTY ACID COMPOSITIONS ANALYSIS OF F_1 POPULATIONS DERIVED FROM 7×7 HALF DIALLEL CROSS IN MUSTARD (*Brassica juncea* L.)

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BY

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CERTIFICATE

This is to certify that thesis entitled, **“FATTY ACID COMPOSITIONS ANALYSIS OF F_1 POPULATIONS DERIVED FROM 7×7 HALF DIALLEL CROSS IN MUSTARD (*Brassica juncea* L.)”** *submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE*** *in* ***GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by* ***Niloy Gain****, Registration No.:* ***19-10330*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2021
Place: Dhaka, Bangladesh

(Dr. Jamilur Rahman)
Professor
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DEDICATED

TO

MY BELOVED

PARENTS

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ABSTRACT

The study was conducted to evaluate the 21 F_1 hybrids of Indian mustard (*Brassica juncea* L.*)* for yield and eleven yield attributes and fatty acid compositions. The seven parents including one canola grade genotype were mated in rabi season 2019-20 to develop 21 F_1 hybrids. These F_1 lines and their parents were used to estimate the genetic variability, combining ability, heterosis and fatty acid compositions at Sher-e-Bangla Agricultural University during rabi season 2020-21 in a randomized complete block design with three replications. High heritability in broad sense was observed for all the traits except days to siliqua maturity, siliqua length (cm) and seeds per siliqua; suggested that major proportions of total variance was due to high genotypic effects. Higher σ^2gca than σ^2sca was found in days to first flowering, 50% flowering, plant height and harvest index indicating additive genetic effects were predominant for these traits. Furthermore, days to siliqua maturity (51.02%) of the F_1 lines displayed high narrow sense heritability; and plant height (46.28%), days to first flowering (42.52%) and seeds per siliqua (33.56%) showed moderate narrow sense heritability. The parental lines P1, P3 and P4 were found as the best general combiner for earliness and dwarfness. For yield contributing traits, the parents, P2 and P7 showed the best combiner genotypes. Among the cross combinations, the hybrids G3, G7, G11 and G13 indicated the best specific combiners for yield and yield attributes. While the crosses, G4, G6, G17 and G21 found for early maturity and short stature trait. The hybrid G3 followed by G5 and G17 manifested the highest heterosis for early maturity over both the better parent and check variety BARI sharisha-11. In case of plant height, the hybrids G4, G14 and G21 whereas hybrid G7 followed by G1, G11 and G13 manifested the highest desirable heterobeltiosis and standard heterosis for yield and yield related traits. In the fatty acid compositions analysis, the parent P6 had the lowest erucic acid (0.81%); while the cross combination G19-S4 (22.14%) and G5-S1 (22.19%) contained low erucic acid. In hybrids, total saturated fatty acid (TSFA) ranged from 10.81% (G5-S1) to 16.53% (G20-S1), whereas mono unsaturated fatty acid (MUFA) was ranged from 40.60% (G20-S2) to 59.18% (G5-S1). The ratio of oleic acid (ω-9) to linoleic (ω-6) acid was found the highest in P6 (1.70) followed by G5-S1 (1.19). Moreover, P6 (4.21) showed the highest ratio of linoleic (ω-6) to linolenic (ω-3) acid followed by G19-S4 (3.58). Considering the altogether, the hybrids viz., G4, G5, G7, G11, G17, G19 and G21 were selected and these lines could be utilized further to develop early matured and high yielding having low erucic acid, but higher ω-9, ω-6 and ω-3 fatty acids containing improved variety.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF PLATES

LIST OF APPENDICES

SOME COMMONLY USED ABBREVIATIONS

FULL WORD	**ABBREVIATION**
At the rate	@
Agro ecological zone	AEZ
Agriculture	*Agric*
Agronomy	*Agron.*
Analysis of variance	ANOVA
And others	*et al.*
Applied	*Appl.*
Achieves	*Arch.*
Australia	Aus.
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Bangladesh Institute of Nuclear Agriculture	BINA
By the way of	*Via*
Biology	*Biol.*
Botany	*Bot.*
Breeding	*Breed.*
Cellular	Cell.
Cultivars	cv.
Current	*Curr*.
Centimeters	cm
Chemistry	Chem.
Degree Celsius	°C
Degree of freedom	d.f
Days to first flowering	DFF
Days to 50% flowering	D50%F
Days after sowing	DAS

Days to maturity	DM
Ecology	*Eco.*
Electronic	*Electron.*
Etcetera	*etc.*
Environment	*Environ.*
Environmental variance	σ^2_e
Food and Agricultural Organization	FAO
Frontiers	*Front.*
Genetics	*Genet.*
Genotypic variance	σ^2_g
Gram	g
Genotype	G
Genetic advance	GA
Genotypic coefficient of variation	GCV
Heritability in broad sense	H^2_b
Heritability in narrow sense	H^2_n
Horticulture	*Horti.*
International	*Int.*
Industrial	*Ind.*
Journal	*J.*
Kilogram	Kg
Meter	m
Mean sum of square	MS
Muriate of potash	MOP
Ministry of agriculture	MOA
Number	No.
Namely	*Viz.*
Phenotypic coefficient of variation	PCV
Percent	%

Phenotypic variance	$\sigma^2{}_p$
Percentage of coefficient of variation	CV%
Properties	*Prop.*
Residual effect	R
Research	*Res.*
Randomized Complete Block Design	RCBD
Science	*Sci.*
Serial	Sl.
Standard error	SE
Siliqua length	SL
Seeds per siliqua	SPS
Seed yield per plant	SYP
Square meter	m^2
Sher-e-Bangla Agricultural University	SAU
Studies	*Stud.*
Total saturated fatty acid	TSFA
Microbiology	*Microbiol.*
Mono unsaturated fatty acid	MUFA
Poly unsaturated fatty acid	PUFA
Technology	*Tech.*
Triple super phosphate	TSP
University	*Uni.*
Variety	var.

CHAPTER I

INTRODUCTION

Indian mustard (*Brassica juncea* L.), which is also known as rye sharisha, is one of the prominent oilseed crops in Bangladesh and India. This mustard is very popular in the subcontinent due to its supreme percentage of edible oil as well as higher nutritious and medicinal values. *Brassica juncea,* belonging to the *Brassicaceae* family, is a natural amphidiploid (AABB genome, 2n=36) hybrid derived from *Brassica rapa* (AA genome, 2n=20) and *Brassica nigra* (BB genome, 2n=16). It is originated in Asiatic region and its prime center of diversity found in China from where it is migrated to India and other subcontinental countries. Oil content in *Brassica juncea* generally varies from 30 to 48 % (Saikia *et al*. 2018) and protein content varies in 28 to 36 % (Das *et al*., 2009). Oil of *B. juncea* is beneficial as the cheapest and healthiest source of balanced diet; it is not only served as source of high energy food, but also supply fat soluble vitamins. Moreover, as a by-product mustard oil cake is an important feed for livestock production and its dry straw products are used as a fuel (Gadei *et al*., 2012).

Mustard oil is the third largest edible oil produced in the world after soybean oil and palm oil (Devi, 2018). According to FAOSTAT, (2020) total mustard oil production is 75,711,806 MT. During 2018-19 total cultivated land under mustard cultivation is 0.308 million ha with 351597 MT production of oilseeds (BBS, 2019). In Bangladesh consumption of edible oil is increasing day by day. In 2019 calendar year, the rate of annual edible oil consumption is 2.85 million MT, exceeded the rate in 2018 by 11% (Sultana *et al*., 2021). To meet the annual demand Bangladesh imported about 2.8 million MT of edible oil during 2019-2020 (USDA, 2019). Due to lack of sufficient domestic production, perhaps 90% of the yearly requirement of oils and fats are assembled through importation (Quaiyum *et al*., 2015).

In Bangladesh three *Brassica* species has been cultivated as oilseed crop, among them *Brassica juncea* is one of the species of oil seed crops. *Brassica juncea* generally required longer period for being matured hence, it fits well in cropping patterns, viz., mustard-jute-T. aman, mustard-maize- T. aman or mustard-mung bean/black gram- T. aman etc. However, lack of high yielding variety with improved and quality oil content, well adapted varieties in natural calamities and higher price than soyabean as well as shortage of mustard cultivable land developed a farmers' a negative attitude towards rye mustard cultivation in Bangladesh.

Since ancient times *Brassica juncea* is well known for its economic importance as well as its medicinal values (Szollosi, 2011). Various parts of the plants are used as medicines and spices. In a balanced diet it provides 541 calorie energy with 829.8 µg vitamin K, 865.0 µg vitamin A, 35.4 mg vitamin C, 2.49 mg vitamin E, 0.137 mg vitamin B6, 0.8 mg selenium, 165 mg calcium, 1.22 mg iron and 0.3 µg betaine all of which play a vital role in controlling arthritis, urinary stones, colds and flu, acne etc. It contains several classes of phytochemicals which are possessed anti-bacterial, anti-malarial, anti-hyperglycemic, anti-aging, anti-proliferative, anti-ulcer, anti-hyperlipidemic, anti-genotoxic, neuroprotective, antidiabetic and antioxidant properties (Kumar *et al.*, 2011).

Mustard oil is the most beneficial oil for all cooking, containing significant amount of omega-3 and omega-6 fatty acids. Oleic acid, linoleic, linolenic, palmitic, stearic are most prominently found in mustard oil (Gunstone *et al*, 1994 and Hui, 1996). The saturated fatty acids (SFAs) include palmitic acid whereas the unsaturated fatty acids are either monounsaturated (MUPAs) viz. erucic acid and oleic acid or polyunsaturated fatty acids (PUFAs) such as omega-3- alpha- linolenic acid and omega-6 linoleic acid are nutritionally important. Nutritional quality of the edible oils depends on the presence and absence of these fatty acids (Sultana *et al.*, 2021). Erucic acid having more than 2% in the edible oil makes it anti-nutritional, whereas higher amount of erucic acid in mustard oil makes it industrially important (Sharafi *et al.*, 2015). Low saturated fats (<6%), high oleic acid (>50%), moderate amounts of linoleic (<40%) and low linolenic acid (<14%) is the standard form of edible oil in considering health benefit (Potts *et al.,* 1999). FAO/WHO recommended that the fatty acid composition of improved edible oil should have a high ratio of MUFA/SFA, a significant proportion of two essential PUFAs, i.e.C18:2 (ω-6) and C18:3 (ω-3), with a desirable ratio between 5:1 and 10:1. Hence, developing the high yielding variety containing desirable ration of MUFA: SFA; ω-6:ω-3 and low erucic acid containing variety (i.e. canola grade mustard) are the major breeding objectives to improve the *Brassica juncea* mustard varieties at the international standard.

Nowadays, canola which is considered the second major oilseed crop after soybean produced 33.6 million tones oil worldwide (AOF 2007; CODEX 2009)**.** Erucic acid, a 22-carbon monosaturated fatty acid, comprised of 30-60% of the total fatty acids and high glucosinolates of traditional mustard varieties have been described as potentially toxic for humans and animals (Sawicka *et al*., 2020). While canola grade oil contains <2% erucic and <30ppm glucosinolates and high proportion of other essential fatty acids e.g., 63.7% monosaturated fats, 28.2% polyunsaturated fats, and oil content is 41.5% (GRDC, 2009). Considering the beneficial impacts of canola grade mustard oil, breeding of canola grade mustard varieties of *B. juncea* is a promising research area in Bangladesh.

Again, regarding climatic changing aspect Rye or Indian mustard has several advantages over the other Brassica oilseed species, e.g. *B. rapa* and *B. napus*. Rye or Indian mustard shows greater advantages in low rainfall environments, more tolerant to heat and resistant to fungus disease (Woods *et al*. 1991, Burton *et al*. 1999, 2003) as well as, can be grown on low to moderate saline soils (Gan *et al.*, 2007). Higher percentage of oil plus protein due to thinner yellow seed coat with lower siliqua shattering made *Brassica juncea* the preferred species for production of canola quality oil for low rainfall areas (Norton *et al*., 2004). It can be adopted to high temperature and where, drought stresses exist. Improved cultivar of *Brassica* species possesses some phenological traits like earlier flowering, longer duration of flowering and maturity, and improved drought tolerance during the reproductive growth period. Therefore, it can be grown in the northern region of Bangladesh, where the water stress or drought is a big problem for crop cultivation especially in winter season. Resistance to lodging and lower siliqua shattering are another important phenological traits of Indian mustard (Hossain *et al.* 2012; Salisbury and Wratten, 1999). Reduced plant height decreases the risk of lodging, while shattering resistance facilitates direct harvesting of *B. juncea* variety (Salisbury and Wratten 1999).

For a successful breeding program, analysis of genetic variability and the association of the yield and yield related traits has a great importance (Mary and Gopalan, 2006). Estimation of genetic heritability along with genetic advance and correlation coefficients analysis among the variables provide valuable information about the expected genetic gain in the future generations (Shukla *et al*. 2006). Hybridization creates the genetic variability in the segregating population; thus, the desired lines can be selected from the segregating populations. Hybrids performance is evaluated through diallel analysis (Jinks and Hayman, 1953). The analysis helps to identify the best combiner lines as well as to select the superior recombinant lines. Heterosis is one of the important ways of measurement to access the robustness of F_1 hybrids lines over the better parent and a commercially popular variety.

B. juncea is more climate resilient compared to *B. napus and B. rapa* would be more suitable for cultivation in unfavorable ecosystems of Bangladesh. Till date around 10 varieties of *B. juncea* have been released in Bangladesh. All of the released *B. juncea* varieties has brown-black seeded and high erucic acid (~40-48%) content. None of them are canola grade (<2% erucic acid) and yellow seeded. Hence, the present research work was undertaken with a goal to improve the *B. juncea* varieties having the desired agronomic traits (e.g. short duration and high yielding) and low erucic acid (<2% erucic acid) trait. Considering the above circumstances, the present investigation was conducted to meet up the following objectives:

1. To estimate the genetic variability and character association of yield attributes in *B. juncea*
2. To assess the general combining ability (GCA) and specific combining ability (SCA) of the parental lines *B. juncea* and F_1 hybrids
3. To evaluated the heterosis of F_1 hybrids derived from the 7x7 half diallel mattings
4. To compare the fatty acid profile of the parents and the F_1 hybrid lines

CHAPTER II

REVIEW OF LITERATURE

A large number of researchers given their attention for the improvement of *Brassica juncea* species on the various aspects of its production and utilization in consideration of its adaptability to the upcoming environmental changes. *Brassicaceae* species is one of the most valuable sources of oil production crops around the world as well as in Bangladesh. Several studies on genetic variability, heritability, interrelationship, combining ability and fatty acid composition of *Brassica juncea* have been carried out in many countries of the world. The review of literature concerning the studies represented under the following head:

2.1 Genotypic and phenotypic variability

Yadava *et al*. (2011) studied genetic variability and trait association in *Brassica juncea* L. on eighteen characters in twenty Indian mustards and reported characters like seed yield per plant, biological yield per plant, harvest index, primary branches as well as secondary branches showed highly significant coefficient of variation for GCV and PCV.

In another experiment Alam (2010) used 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* and found higher phenotypic variations in comparison to the genotypic variation. While Singh *et al*. (2010) reported higher genotypic variation than phenotypic variation in seed per plant, primary and secondary branches per plant from the study of 62 F_1 and 24 parental lines of *Brassica juncea*.

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

Tripathi *et al.* (2019) did a case study in twenty diverse genotypes of Indian mustard (*Brassica juncea*) for thirteen characters, revealed high heritability in broad sense for the characters of days to 50% flowering and primary branches per plant. While days to maturity showed moderate heritability with high genetic advance as per cent of mean.

Yadava *et al.* (2011) studied thirty varieties of Indian mustard (*Brassica juncea*) for fourteen quantitative characters. From the estimation of mean, range, phenotypic, genotypic and environmental variance, phenotypic and genotypic coefficient of variations, the used materials showed diversification in their nature.

Patel *et al*. (2019) evaluated sixty diverse genotypes of Indian mustard (*Brassica juncea*) for seed yield to estimate the genetic variability and association of yield components who indicated highly significant differences among the coefficient of variation, however moderate genotypic coefficient was observed for seed yield per plant whereas seed yield per plant and number of branches per plant exhibited moderate phenotypic coefficient of variation.

Muhammad and Waluyo (2019) arranged an experiment on fifty-seven tested genotypes of *brassica* species and 3 varieties as check for 24 quantitative characters and found a wide variability in the character of seeds per siliqua, number of siliquas per plant, and fresh weight. High heritability was found in the character of age of seed harvest, number of siliquae per plant, length of siliquas and number of seeds per siliqua indicating an efficient selection for the crop improvement.

Amsalu (2020) was executed an experiment on forty-nine genotypes of Ethiopian mustard to estimate the genetic and phenotypic coefficient of variations of yield contribution traits that revealed significant differences among genotypes for all the traits. High genotypic and phenotypic coefficients of variations for yield components were observed in seed yield (kg/ha) and oil yield indicating, selection of these traits based on phenotype may be useful for yield improvement.

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

Ullah *et al*. (2015) used six advanced lines ($F_{10:11}$) of *Brassica* species to estimate genetic variability for morphological and biochemical traits. Significant differences at ($p \leq 0.01$) were recorded for plant height, main, siliquas per main raceme, siliqua length, seed yield per plant and protein content at ($p \leq 0.05$) for 100-seed weight, oil content. He observed high heritability for majority of the traits except 100-seed weight.

Fayyaz *et al*. (2014) conducted an experiment with the materials of ten parental lines and the four intraspecific and four interspecific F_2 populations of *Brassica* for the estimation of variability, heritability and genetic advance. In all genotypes highly significant ($p \leq 0.01$) differences were recorded for protein, glucosinolates, oleic acid, oil, erucic acid and linolenic acid content. Among the F_2 populations, oil, glucosinolate, erucic acid, protein, oleic acid and linolenic acid content with had high range of genetic variability, heritability and genetic advance.

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

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

Akoju *et al.* (2020) found high heritability for 1000-seed weight and siliqua length, moderate heritability observed for days to 50% flowering and days to physiological maturity revealed the presence of additive gene action and minimum influence of environment in expression of these characters.

Nagoo *et al.* (2021) was carried out an experiment for the estimation of the genetic variability, heritability, genetic advance and correlation analysis in fifty-seven *B. rapa* lines during rabi 2019-2020 who found all the characters exhibited large amount of variability. Significant differences were observed in the studied genotypes for all characteristics which give an insight into the existence of genetic variation in the available genotypes, indicating a great scope for selection and further improvement of *Brassica rapa* in terms of quality and quantity.

Merah (2015) studied on 190 collection of *Brassica juncea* from different origins to study the genetic variability for different agronomical traits within genotypes. He observed large variability between genotypes for the measured traits. Total glucosinolates varied twofold between extreme genotypes. Values of sinigrin content varied from 0 to more than 134 μmol·g-1.

Yared and Misteru (2010) studied on sixty-four *Brassica* breeding lines for investigating morphological traits to identify the nature of genetic variability. Considerable genetic variability was found among the lines that can be used for further selection and hybridization efforts. The maximum number of secondary branches per plant was observed by the line code for 64 and the highest yield per plot was recorded by the breeding line coded 48. Breeding line 53 exhibited the maximum 1000 seed weight.

Khan *et al.* (2013) evaluated 30 F_7 segregation lines and two parents of *Brassica rapa* to study the variability. The result revealed that except 1000 seed weight, significant variation was observed among the all the genotypes. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest variation was found in length of siliqua followed by thousand seed weight.

Jahan *et al*. (2008) carried out a study to determine 10 locally collected *Brassica rapa* (*Brassica campestris*) for genetic variability tested in RCBD with 3 replications. Highly significant differences were observed in all traits except siliqua width. Hence, great proportion of genetic variability was found in indigenous accessions can be manipulated in future breeding programs to fully utilize their genetic potential.

Bibi *et al.* (2016) conducted an experiment to check accessions for genetic variability in *Brassica juncea*. The experimental consisted of 10 *Brassica juncea* genotypes based on RCBD design. He was studied on 8 quantitative parameters. Highly significant differences were taken in days to 50% flowering, days to maturity, plant height, number of primary branches, siliqua length, number of seeds per siliqua, 1000 seed weight and seed yield which illustrated significant variation.

Salam *et al*. (2017) carried out a program on 30 F_1 from 6×6 diallel crosses to estimate the genetic variability. Sufficient variability in biometrical analysis except for days to maturity and oil content (%) were observed. Magnitude of PCV was higher than the GCV. The high GCV and PCV were found only for two traits viz. number of branches per plant and harvest index (%). Moderate GCV and PCV were found in case of plant height, siliqua length, number of siliquae per plant and yield per plant.

Rauf and Rahim (2018) evaluated 35 genotypes of *Brassica napus* based on RCBD with 3 replications. The genotypes were indicated significant amount of variations for the most pf the characters. Comparatively phenotypic variances were higher than the genotypic variances for most of the characters to be studied.

Gupta *et al*. (2019) carried out an experiment to estimate genetic variability among the 35 genotypes of oilseed *Brassica*, including 20 F_2/F_3 populations and 15 parents. Considerable variability was observed for all the 14 characters. The estimates of GCV and PCV were comparatively higher for plant height, number of primary and secondary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua, 1000 seed weight seed yield per plant and oil yield per plant.

2.2 Heritability and genetic advance

Heritability ($h^2{}_b$) and genetic advance (GA) from selection are prerequisites for starting a breeding program. Study about related works on the *Brassica* species for heritability and genetic advance are reviewed below:

Jahan *et al*. (2015) conducted an experiment in 10F_4 lines with 8 released varieties of *Brassica rapa*. High heritability with low genetic advance in percent of mean was observed for days to maturity. High heritability with moderate genetic advance in percent of mean was found for plant height and days to 50% flowering.

Bibi *et al*. (2016) checked heritability and genetic advance in *Brassica juncea*. in RCBD with 3 replications. The high heritability along with high genetic advance was noted in plant height, siliqua length and seed yield while days to flowering and maturity, number of branches per plant, number of seeds per siliqua and 1000 seed weight exhibited variable trends.

Salam *et al*. (2017) estimated the heritability in 30F$_1$ from a 6×6 diallel crosses. High heritability was observed for erucic acid content followed by plant height, branches per plant, seed yield per plant, siliqua length, days to 50% flowering, and harvest index (%). Genetic advances as percent of mean were high for number of siliquae per plant, followed by seed yield per plant days to maturity and plant height.

Nagoo *et al*. (2021) was carried out an experiment for the estimation of the genetic variability, heritability, genetic advance and correlation analysis in the set of 57 *B. rapa* lines during rabi 2019-2020 revealed the high amount of PCV and GCV along with high values of broad sense of heritability and genetic advance was found, no. of seeds per siliqua, no. of siliqua per plant followed by seed weight.

Ali (2017) evaluated *Brassica juncea* germplasm to estimate divergence, associations among traits and heritability for various bio-chemical traits in RCB design. Maximum heritability was observed for glucosinolate content, protein content and erucic acid content, whereas moderate heritability was recorded for oil content, oleic acid content and linolenic acid. The high heritability was coupled with appreciable selection response.

Karmokar (2018) studied heritability and genetic advance for 10 yield and yield related characters of 13 advanced line of *Brassica rapa*. High heritability coupled with high genetic advance in percent of mean were observed for days to 50% flowering, number of secondary branches per plant, siliqua per plant, number of seeds per siliqua and yield per plant.

Rauf and Rahim (2018) evaluated 35 genotypes of *Brassica napus* based on RCBD with 3 replications. Seed yield per plant exhibited the highest value of heritability followed by number of siliquae per plant while plant height exhibited the lowest value of heritability.

Gupta *et al.* (2019) estimated heritability and genetic advance in 35 genotypes of *Brassica rapa* L. High heritability was recorded for all the characters. Genetic advance was also high for number of siliquae per plant and plant height. Number of siliquae per plant showed high heritability with high genetic advance and genetic advance percent of mean.

Aktar *et al*. (2019) estimated variability ranges in 18 *Brassica* genotypes. All traits showed high heritability. High heritability values with high genetic advance in percent of mean was observed for number of branches per plant, number of siliquas per plant, number of seeds per siliqua and yield per plant.

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

Alam (2010) conducted an experiment by using twenty-six F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the variation among them. Most of the traits showed high heritability with genetic advance. He reported, plant height had high broad sense heritability while days to 80% maturity showed lowest heritability.

Gangapur *et al*. (2009a) was dealing with forty diverse genotypes of Indian mustard (*Brassica juncea*) High heritability in conjunction with high genetic advance were observed for seed yield per plant, number of siliquas per plant, leaf area index and secondary branches per plant suggesting predominant role of additive gene action for expression of these traits.

Ali *et al*. (2013) investigated an experiment to estimate variation and heritability of some morphological and biochemical traits of introduced Ethiopian mustard genotypes. The highest heritability values were recorded for siliqua length (0.83) followed by siliquas on main raceme (0.82). Genetic advance (as percent of mean) was the highest for seed yield plant-1 and siliquas on main raceme.

Khan *et al*. (2019) was carried out an investigation to study the correlation and path analysis of thirteen quantitative traits in 12 Indian mustard (*Brassica juncea*) Biological yield per plant, siliqua on main raceme, grain yield per plant and number of seeds per siliqua exhibited higher heritability and higher genetic advance.

Kimbonguila *et al*. (2019) was evaluated seven genotypes of green mustard (*Brassica juncea*) in order to study the genetic variability, degree and direction of association between yield and its components characters. High heritability with high genetic advance as percent of mean was registered for plant height, vitamin C content and yield per plant (g) indicating, additive gene effects controlled their expression.

Czern *et al*. (2003) was conducted an experiment on Indian mustard (*Brassica juncea*) to estimate genetic variability, correlation and path analysis. The higher estimates of heritability coupled with higher genetic advance was found in yield per plant, siliqua on main branch, and branches per plant indicated that heritability of the trait is mainly due to additive effects and selection is effective for such traits. High heritability accompanied with medium to low genetic advance for plant height, length of main branch, days to flowering is indicative of non-additive gene action and the high heritability is being exhibited due to favorable influence of the environment rather than genotypes.

Sharma and Ram (2021) was undertaken an experiment to find the correlation and path analysis of fourteen quantitative traits in 50 Indian mustard (*Brassica juncea*) germplasm lines. Higher heritability and higher genetic advance observed in the following characters seed yield per plant, thousand seed weight, fruiting zone length, days to initial flowering, first basal branch.

Akoju *et al*. (2020) was conducted an experiment to estimate the genetic variability and path coefficient analysis among the Indian mustard genotypes during rabi, 2019. High heritability was recorded for character 1000-seed weight and siliqua length, moderate heritability observed for days to 50% flowering and days to maturity revealed the presence of additive gene action. High heritability estimates in broad sense coupled with low genetic advance as percent of mean was observed for siliqua length and 1000-seed weight indicated presence of non-additive gene action.

Nagoo *et al.* (2021) was carried out the study with 57 genotypes of brown sarson (*Brassica rapa*) during rabi 2019-2020 for the estimation of the genetic variability, heritability, genetic advance and correlation analysis. The high amount of PCV and GCV along with high values of broad sense of heritability and genetic advance was found in no. of seeds per siliqua, no. of siliqua per plant followed by seed weight.

Muhammad and Waluyo (2019) found high heritability was found in the character of cotyledons, number of leaf consumption, fresh weight, age of seed harvest, number of siliquas per plant, length of siliquas, width of siliquas, and number of seeds per siliqua by conducting an experiment on 57 genotypes of Indian mustard.

Amsalu (2020) executed an experiment in Ethiopian mustard (*Brassica carinata* A. Braun) landraces to evaluate genetic and phenotypic coefficient of variations of yield and its contribution traits. The highest heritability in broad sense was recorded for thousand seed weight (68.80%) followed by days to flowering (65.91%), stand percent (63.14%), days to maturity (60.43%), plant height (59.63%), seed yield kg/ha (42.99%), and primary branches (34.20%). This suggests that large proportion of the total variance was due to the high genotypic and less environmental variance.

Tripathi *et al*. (2019) evaluated twenty diverse genotypes of Indian mustard (*Brassica juncea*) with four checks for thirteen quantitative traits under. High heritability coupled with high genetic advance as percent mean was observed for secondary branches per plant followed by plant height, length of main raceme, siliqua on main raceme, 1000-seed weight, biological yield per plant, seed yield per plant and harvest index.

Shekhawat *et al*. (2014) studied in 60 Indian mustard genotypes including three checks to estimate the variability and heritability for various traits. The heritability ranged from 27.54% (biological yield per plant) to 99.66% (1000-seeds weight). The Genetic advance in percent of mean ranged from 3.04% (3.04) to 24.91% (1000-seeds weight). Test weight (1000-seeds weight) showed high estimates (>20%) of genetic advance in percent of mean.

Patel *et al.* (2019) were evaluated seed yield and its attributes to determine the genetic variability and association of yield and its components by using sixty diverse genotypes of Indian mustard (*Brassica juncea*). A high heritability value was recorded for 1000 seed weight, oil content, days to flowering and seed yield per plant. The highest value of genetic advance (per cent mean) was observed for seed yield per plant.

Khan *et al*. (2008) evaluated six $F_{3:4}$ derived interspecific *Brassica* populations together with three checks for their genetic variability and correlation among quality traits. Heritability estimates were high (>0.70) for glucosinolate, linolenic acid, oleic acid and erucic acid contents, while low heritability (< 0.50) was observed for protein content.

Yadava *et al*. (2011) was undertaken an investigation to study the variability and trait association of eighteen quantitative in twenty Indian mustard (*Brassica juncea*) germplasm lines. Test weight, biological yield per plant, seed yield per plant and silique on primary mother axis exhibited higher heritability with higher genetic advance.

Stanley (2021) studied heritability and genetic advance under generation mean analysis, using three high yielding varieties. High heritability (broad sense) associated with moderate to high genetic advance was recorded for 1000-seed weight, seed yield per plant, harvest index, palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic and erucic acid contents, suggested that these traits can be further improved through selection in segregating generations.

Mishra and Nath (2022) carried an experiment consisting of 57 treatments in a RBD with three replications during Rabi 2021-22. High heritability and high genetic advance were observed for number of siliquae on main raceme followed by 1000 seed weight, while high heritability coupled with moderate genetic advance in per cent of mean was recorded for number of primary branches, number of secondary branches, harvest index and seed yield per.

Mahmood *et al*. (2002) was investigated an experiment on Summer mustard *(Brassica juncea*) to evaluate genetic variability and heritability for its yield and yield related components. High heritability was recorded for 1000 seed weight and yield per plant where genetic advance as percent of mean was greatest for yield per plant, followed by plant height and number of branches per plant.

Singh *et al.* (2011) was conducted a field experiment during rabi 2004-05 in Indian mustard (*Brassica juncea*) who observed high heritability for all the selected traits. Moderate genetic advance was observed for number of primary branches per plant and number of secondary branches per plant whereas low genetic advance was observed for number of siliquae per plant, seed yield per plant, length of main raceme, days to 50% flowering, plant height, oil content, days to maturity, 1000-seed weight and number of seeds per siliqua.

Alamerew and Woyessa (2017) studied genetic variability, heritability, genetic advance, genetic advance as a percent of mean and character association for forty-nine genotypes of Ethiopian mustards. The highest heritability in broad sense was recorded for thousand seed weight (68.80%) followed by days to flowering (65.91%), linolenic acid (62.58%), days to maturity (60.43%), plant height (59.63%), palmitic acid

(58.19%), linoleic acid (57.46%), seed yield per plot (42.99%), and primary branches (34.20%).

2.3 Correlation analysis among variables

As yield is a complex trait, many component influences on yield either their single effects or their combined effects. Hence, selection for yield based on single factor performance test may not be effective, therefore a biometrical analysis named correlation coefficient and path analysis of associated variables can be taken into consideration for more effective selection of yield and yield attributes characters. Their correlation may be either due to genetic linkage or physiological and development relationship. It is often assumed that association between characters is evidence of pleiotrophy rather than linkage, under complex situations; path coefficients analysis is a powerful tool for studying character association (Gangapur *et al*., 2009). Phenotypic correlation reflects the observed relationship whereas genotypic correlation indicated the true relationship among the characters. Several literatures revealed about the statements on correlation related studies.

Khan *et al*. (2019) was undertaken an investigation to study the correlation and path analysis of thirteen quantitative traits in twelve Indian mustard (*Brassica juncea*). Correlation study revealed that biological yield per plant and siliqua on main raceme exerted high positive significant genotypic correlation with grain yield per plant and secondary branches per plant was found negatively correlated with grain yield per plant.

Saiyad *et al.* (2020) was carried out the experiment with sixty diverse genotypes of Indian mustard (*Brassica juncea*) in order to study correlation and path analysis for seventeen quantitative and qualitative traits who found seed yield per plant was significantly and positively correlated with plant height, number of branches per plant, number of siliquae per plant, seeds per siliqua, length of siliqua, 1000-seed weight, oil content, linolenic acid and erucic acid at genotypic level.

Akoju *et al*. (2020) studied on *Brassica juncea* revealed genotypic and phenotypic correlation coefficient of seed yield per plant had significant positive correlation with plant height at genotypic level. However, seed yield per plant recorded negative correlation with days to 50% flowering at both levels but was significant at genotypic level.

Tadesse *et al.* (2014) observed that seed yield exhibited positive and significant association with plant height, number of primary branches per plant, number of secondary branches per plant, siliqua per plant, seeds per siliqua and 1000 seed weight.

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

Ashraf *et al*. (2000) was carried out the research on ten accessions of *Brassica* species for the study of correlation in different yield contributing characters. Positive correlation was observed between primary branches and seed yield both at genotypic and phenotypic levels. Similarly seed yield showed positive correlation with siliqua per plant, number of secondary branches and siliqua length. Whereas seed yield was negatively and non-significantly correlated with seeds per siliqua and 1000-seed weight.

Dubey *et al*. (2019) In correlation analysis, seed yield per plant had significant and positive correlation with secondary branches per plant, siliqua per plant, biological yield per plant, harvest index, days to maturity, 1000 seed weight and oil content at both genotypic and phenotypic levels.

Patel *et al*. (2019) observed significant and positive correlation of seed yield per plant with days to flowering, days to maturity, plant height, length of main branch, number of siliquae per plant, 1000 seed weight at phenotypic levels.

Gangapur *et al*. (2009a) did an experiment on forty-six germplasm accessions of Indian mustard for seed yield and its yield components (eleven characters). The correlation study revealed that seed yield per metre was highly and significantly correlated with seed yield per plant, number of siliquae per plant, number of primary and secondary branches per plant, biological yield per plant, 1000- seed weight, number of seeds per siliqua at both genotypic and phenotypic levels in protected and unprotected conditions.

Kimbonguila *et al*. (2019) was undertaken seven genotypes of green mustard (*Brassica juncea*) to determine the genetic variability, degree and direction of association between yield and its components characters. The correlation studies revealed strong positive association of yield with Leaf area index (LAI), dry matter yield, number of leaves per plant at genotypic level, whereas at phenotypic level only dry matter yield showed a significant positive correlation.

Kumar *et al.* (2016) was undertaken an investigation to study the correlation and path coefficient analysis of twelve quantitative traits in 30 Indian mustard (*Brassica Juncea*) germplasm lines. Correlation study revealed that harvest index and total biological yield per plant exerted high significant positive correlation coefficients with seed yield at both genotypic and phenotypic level. Seed yield is negatively correlated with days to 50 % flowering and days to maturity which promotes early flowering and early maturing genotypes.

Sharma and Ram (2021) was conducted an experiment to find out the correlation and path analysis of fourteen quantitative traits in Indian mustard (*Brassica juncea*) germplasms. Correlation study revealed that plant height, secondary branch, main shoot length, siliqua on main shoot, maturity exerted high positive significant genotypic correlation with seed yield per plant. In phenotypic correlation was observed that siliqua on main shoot, maturity showed highly significant and positive correlation with seed yield per plant.

Meena *et al*. (2020) was carried out a study of correlation and path coefficient analysis in Indian mustard (*Brassica juncea*) conducted during 2010-2011who observed genotypic correlation were higher than their corresponding phenotypic correlation. Seed yield per plant showed positive and highly significant association with days to 75% maturity, number of secondary branches per plant, length of siliqua, 1000-seed weight, biological yield per plant and harvest index. However, days to 50% flowering showed positive and significant correlation with plant height.

IaasT (2019) was conducted the research project with two hundred diverse germplasm lines of Indian mustard. Seed yield per plant was found to be positively and significantly correlated with number of primary branches per plant, number of secondary branches per plant, hence these characters might bring priority in selection in view of improvement in seed yield of mustard.

Tadesse and Alemu (2019) was carried out an experiment in order to evaluate the association of characters and path coefficient analysis on yield contributing traits in Ethiopian mustard. The correlation analysis showed seed yield per plot was highly significant and positively correlated with oil yield, biomass per plot, harvest index, plant height and thousand seed weight both at genotypic and phenotypic level.

Tariq *et al*. (2020) was conducted the field experiments with fifteen accessions of *Brassica napus* to estimate correlation and path analysis for both qualitative and quantitative parameters. The results reflected that correlation coefficient yield was positively and significantly correlated with seeds in a silique and protein contents. Whereas yield was negatively correlated with weight of 1000 seeds, oleic acid contents, linolenic acid and erucic acid contents.

Kumar *et al.* (2021) studied genetic variability, heritability, correlation and genetic advance among F_5 populations of ten genotypes *in Brassica* species. A significant positive correlation with seed yield per plant was found in days to 50% flowering (0.578**), the plant height, (0.787**), siliqua length (PL) (0.406*), seeds per plant (SP) (0.369*), siliqua per plant (0.697**) and hundred seeds weight (HSW) (0.500**), but significantly negative correlation found in primary branches per plant (-0.046*).

Khayat, Lack and Karami (2012) was carried out an experiment with ten Canola varieties to determine the most important traits affecting grain yield in Canola. The evaluation of correlation coefficients illustrated that the total dry matter, harvest index, 1000- grain weight, the number of grains per siliqua, number of siliquas per plant, plant height; days to maturity and flowering period trait have a positive significant correlation with grain yield.

Ali *et al*. (2013) was undertaken a field experiment to estimate variation and heritability of some morphological and biochemical traits of introduced Ethiopian mustard genotypes. Highly significant positive phenotypic correlation for seed yield per plant was observed with plant height and primary branches per plant whereas significant positive phenotypic correlation was observed with seeds per siliqua, while oil content was significantly positive correlated only with erucic acid.

Dawar *et al.* (2018) was carried out the research activities to determine the selection criteria for yield improvement in selected thirty genotypes of Indian mustard. The correlation coefficient of the seed yield per plant (g.) had significant and positive correlation with plant height; number of primary branches, total no. of siliqua per plant and 1000-seed weight at genotypic level.

Siddique *et al*. (2017) conducted a study using six genotypes and reported positively significant correlation in siliquas per plant and plant height with yield per plant, days to flower with seed index, days to flower with single plant, siliquas per plant with seed index, and seed index with single plant yield. Negative and significant relationship was estimated between plant height and seeds per siliqua, branch per plant and ripeness days and siliquas per plant and seeds per siliqua.

Karmokar (2018) carried out an investigation to assess the interrelationship among ten yield contributing characters of thirteen advanced line of *Brassica rapa* who reported genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Yield per plant was highly significant and positive with number of primary branches per plant and number of siliquae per plant at both genotypic and phenotypic level.

2.4 Heterosis

Heterosis is the superiority of F_1 hybrid over both of the parents. Heterosis has been increasingly applied in **crop** production for nearly a century, with the aim of developing more vigorous, higher yielding and better performing cultivars. One of the ways to improve seed yield in oilseed rape is heterosis, which is hybrid vigor that results in a greater biomass, increased seed yield, and faster development. The review of literature concerning the studies are presented below:

Rameeh (2019) evaluated heterobeltiosis effects of 8 genotypes of *Brassica napus* in half diallel crosses. Most crosses showed significant positive high parent heterosis for seed yield with significant heterotic effects for siliqua per plant. He identified L41×LF2 and L31×L41 with highly significant heterobeltiosis of grain yield were superior combinations for breeding this trait.

Wolko *et al.* (2019) estimated heterosis of oilseed rape (*Brassica napus*) 600 double haploid lines and 2 generations of hybrid were evaluated. Plant height, siliqua length and number of seeds per siliqua a large number of hybrids showed significant positive heterosis. Whereas number of branches and silique per plant and 1000 seed weight, hybrids exhibited both positive and negative significant heterosis.

Singh *et al.* (2011) assess the heterosis among the quantitative traits in 6 intra-specific crosses in yellow sarson with 6 parental genotypes along with 12 F_1 and F_2 populations, in RCBD with 3 replications. In all cross combinations, hybrids performed better than their respective parents and significant positive standard and better parent heterosis was observed for the trait seed yield per plant.

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

Mohammed (2011) estimated heterosis in *Brassica carinata* with 7 parental lines along with 21 F_1 crosses. Standard heterosis of the crop parameters ranged from -8.22% for harvest index to 191.57% for number of siliquas per plant, while for seed yield per plant ranged from -16.64% to 66.09%.

Gupta *et al*. (2010) studied 12 *Brassica juncea* × *Brassica campestris* F_1 crosses for some yield contributing traits. Heterosis was calculated over mid parent and better parent. The hybrids RLM-514×M-91, M-261×Sampad, RLM-514×M-91, M-7×Sampad, M-26×Dholi and RLM-514×M-91 were excellent for days to flowering, pollen sterility percentage, plant height, secondary branches per plant, number of siliquae per plant and seed yield on the basis of heterosis value.

Singh *et al*. (2012) estimated mid and better parent heterosis among the various traits of Indian mustard and their F_1 hybrids. Significant positive heterosis over mid parent was registered for plant height, secondary branches per plant, seed yield per plant in all crosses. However, significant positive heterobeltiosis was observed for seed yield per plant and number of siliquae on main raceme in all crosses except cross-I and plant height and number of secondary branches per plant, showed significant heterobeltiosis and it ranged from 1.01% in cross-I to 24.77% in cross-III.

Meena *et al.* (2014) was carried out an experiment with the use of 13 *Brassica juncea* parents along with their 36 F_1 crosses to estimate the better parent heterosis and standard heterosis. Five crosses viz., DRMR 2486 × Ashirwad, DRMR 2243 × NRCHB 101, DRMR 2269 × NRCHB 101, DRMR 2341 × NRCDR 2, and DRMR 2613 × NRCDR 2 possessed high heterosis over better parent and standard check. The high yielding cross combinations from this study can be utilized in future breeding program for development of high yielding genotypes.

Becker *et al.* (2015) studied in 25 accessions of *Brassica juncea* in a half diallel fashion to estimate general combining effects and heterosis. Significant heterosis over better parent for single plant yield was recorded in CIS × Indian and synthetic × CIS crosses followed by Indian × synthetic types. Plot level yield trials of two selected hybrids over two growing seasons revealed 29.4% to 91.8% heterosis over better yield parent.

Singh *et al.* (2012) was undertaken an investigation to study the heterosis in Indian mustard. Ten lines and five testers and their 50 F_1 s were grown in randomized block design with three replications. The crosses GM-3 x RGN-145, RGN-48 x Kranti and Gm-3 x Kranti took lesser days in flowering, as they had highest negative and significant heterosis. The most heterotic cross was RGN-48 x Kranti for days to 50% flowering, days to maturity, plant height, number of primary branches per plant and biological yield per plant.

Singh, (2022) carried out a study to estimate Heterosis for physiological traits in Indian mustard (*Brassica juncea*) with 45 F_1 hybrids along with 10 parents in randomized block design. The analysis revealed that one F_1 hybrid (BPR 543-2 × Rohini) showed heterobeltiosis (51.84%) for seed yield per plant whereas two hybrids (Urvashi × DRMR 1165-40; Urvashi × Rohini) exhibited average heterosis for thousand seed weight. Three crosses (NRCDR 02 × Rohini, NRCHB 101 × DRMR IJ-31, NRCHB 101 × Rohini) exhibited significant heterosis in desired directions.

Kaur *et al.* (2001) studied with *Brassica rapa* comprising toria, brown sarson, yellow sarson and some toria introgression lines besides six land races for various morphophysiological traits. Estimated standard heterosis ranged from -5.4 to 102.0 per cent (average 31%) whereas values for inter- group hybrids were -45.9 to 103.5 per cent (average 17%). Similarly, better parent heterosis ranged from -32.2 to 231.6 per cent (average 92%) for intra-group hybrids, and -44.8 to 82.6 per cent (average 0.1%) for inter-group hybrids

Shehzad *et al*. (2015) estimated heterosis by using three *Brassica napus* testers and five lines were crossed through line × tester design. Cross 13 showed maximum values of siliqua length (14.3%, 11.1%), seed yield/plant (45.3%, 35.9%) and Lnic C (-43.7%, -37.6%) for mid parent heterosis and better parent heterosis as well as Lnic C (-38.3%) for standard heterosis. Cross 3 revealed highest PC (5.5%, 4.4%), Cross 4 for NSP (28.4%, 25.3%), Cross 10 for GLC (-13.5%, -33.2%) and Cross 15 for NSS (22.8%, 10.8%) mid parent heterosis and better parent heterosis.

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

Breeding *et al*. (2015) studied 10 parents diallel comprising 10 strains and their 45 F_1 hybrids of Indian mustard to evaluate heterosis over mid parent (MP) and superior parent (SP) or heterobeltiosis. The highest heterosis for seed yield over mid parent was recorded as high as 47.36% and 40.85% by crosses Kranti x BEC-144 and RH-30xBEC-286 respectively. The heterosis for seed yield over superior parent was recorded highest 57.0% by cross combination Kranti x BEC-144 followed by 50.89% by cross combination Pusa Bold x BEC-144.

Gul *et al.* (2019) studied 8 parental lines with 56 F_1 to estimate general means, heterosis and combining ability effects. Significant ($p \leq 0.01$) differences were observed among the parental genotypes and their F_1 hybrids for all the studied traits. The F_1 hybrids NIFA Gold × Rustam Canola, Rustam Canola × Punjab Sarsoon and Punjab Sarsoon × Abasin-95 exhibited best mean performance and maximum mid- and better-parent heterosis for plant height, 1000-seed weight and seed yield per plant.

2.5 Combining ability analysis

Combining ability or productivity in crosses is the estimation of the value of genotypes on the basis of their offspring performance in some definite mating design. Combining ability analysis tool is useful for selecting favorable parents and provides information concerning the nature of gene effects influencing both quantitative traits as well as qualitative traits. For the characters studied, both significant and non-significant results were noted in the literatures discussed in this chapter:

Singh *et al.* (2012) was undertaken an experiment with a set of 4 diverse parental lines of *Brassica juncea* crossed in half diallel mating design. Combining ability analysis revealed importance of both additive and non- additive genetic variances for the control of various traits and found that Pusa Mahek is a best general combiner for most of the traits, followed by TM-2. Out of the 16 characters studied, seven characters exhibited significant GCA and SCA effects.

Kaur *et al*. (2019) evaluated Indian mustard through diallel analysis to estimate general and specific combining ability of parents and crosses, respectively during winter season 2017-18. He suggested that the high magnitude of general combining ability and specific combining ability effects indicated the presence of both additive and non-additive gene interactions for the inheritance of different studied traits.

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

Atikunnahe *et al*. (2017) used 21 plant materials in the experiment whereas six were used as parents and 15 were as F_2 segregating generations to estimate combining ability. Analysis of combining ability showed highly significant GCA (general combining ability) and SCA (specific combining ability) effects for the studied traits. The higher magnitude of GCA variance was observed than that of SCA variance for all the studied characters except days to 50% flowering and number of secondary branches per plant.

Gul *et al*. (2019) carried out an experiment in eight *Brassica napus* genotypes and crossed them in 8 × 8 complete diallel fashion generated 56 F_1 hybrids. Parental genotypes Abasin-95 and Punjab Sarsoon were found as best general combiners and performed better in combination with other genotypes for the majority of the traits. The variances due to σ^2SCA were higher than σ^2GCA and σ^2RCA. The ratios of σ^2GCA/ σ^2SCA were noted, indicating all the traits were controlled non- additively.

Shrimali *et al*. (2016) conducted half diallel analysis, comprised of ten parents and their hybrids was carried out general and specific combining ability (GCA and SCA) in Indian mustard. Ratio of GCA and SCA variances was below unity for all the characters except days to flowering, plant height and harvest index, which suggested superior role of non-additive genetic variance in the inheritance of these traits. The parents GM 3, GDM 4, RH-0555 and RSK-29 were good combiners for seed yield and its component characters.

Maurya *et al*. (2014) evaluated a set of 8×8 diallel crosses (excluding reciprocals) of Indian mustard along with their parents to identify heterotic crosses and estimate general and specific combining ability of parents and crosses, respectively. Parents viz., GM-3, ZEM-1, Varuna and PM-67 were good general combiner for yield per plant, while HYOLA 401 and HNS 0004 were good general combiner for earliness and dwarfness and oil and protein content respectively. Based on SCA effects, the high-ranking crosses for yield and its component traits were HYOLA 401 × GM-1, PM 67 × ZEM-1 and GM-2 × GM-3.

Saeidi *et al*. (2018) used eight genotypes of rapeseed (*Brassica napus*) to determine the genetic parameters based on Hayman’s method that revealed significant general (a) and specific (b) combining ability mean squares for all traits except for 1000-seed weight, which indicated the importance of additive and non-additive genetic effects. For 1000-seed weight, only the general combining ability mean square was statistically significant. High narrow-sense heritability estimates were observed for 1000-seed weight which indicated the importance of additive genetic effects for these traits.

Kumar *et al*. (2021) studied combining ability analysis of 10×10 diallel set of crosses in Indian mustard for ten quantitative traits which revealed preponderance of non-additive gene effects for plant height, number of primary branches per plant and seed yield per plant, whereas additive gene effects was found to be predominant for the inheritance of rest of the characters. Most of the crosses involving high × low general combining parents, exhibited high SCA effects for various traits.

Inayat *et al*. (2019) conducted this study to evaluate the performance of eight Mustard genotypes and their 56 combinations in F_2 population. Combining ability studies revealed that all the traits showed significant general combining ability (GCA) effects. The genotype NUMYT-103 and NUMYT-123 proved to be the best general combiner among all the cultivars. F_2 specific cross combination, NUMYT-103 × NUMYT-117 showed highest desirable positive SCA effects for seed yield plant^{-1}.

Akabari *et al.* (2017) investigated combining ability and nature of gene interaction that contribute to seed yield attributing traits in Indian mustard using 60 hybrids. The results revealed that GCA and SCA ratio (σ2GCA/σ2SCA) was less than unity for all the traits except for days to 50 % flowering indicating non-additive components played relatively greater role in the inheritance of all the traits except days to 50 % flowering for which greater role of additive components was found. The estimate of GCA effects indicated that the parents GM-2, NRCM-120, PAB-9511 and IC-261670 were identified as good general combiners.

Singh *et al.* (2015) studied Line × tester analysis involving 14 lines and five testers that revealed both additive and non-additive gene actions were important in controlling yield-contributing traits. Variety Pusa Mustard 25 was identified as best general combiner among the parents. Significant and positive SCA effects were observed for seed yield in 17 hybrids.

Singh *et al.* (2022) estimated combining ability of fifteen quantitative traits was in 7 lines, 3 testers and 21 F_1 to know the inheritance pattern of yield attributes of *Brassica campestris*. Amongst the parents, PT-303 was a good general combiner for seed yield contributing characters. The hybrid Bhawani x G-14 showed high positive significant SCA effects for seed yield, siliqua length and length of main raceme. The hybrid SDS-22 x Uttara also showed high positive significant SCA effects for seed yield, siliqua length and also reported SCA variance was higher than GCA variance, indicating the preponderance of non-additive gene action.

Gagandeep *et al.* (2020) identified the best parents and F_1 hybrids on the basis of general, specific combining ability and high heterotic performance for yield characters of Indian mustard. Parent Geeta was found to be the best combiner for seed yield with significant and positive GCA effects. Out of fifteen, four cross combination shows positive significant SCA effects for seed yield/plant (g) trait.

Meena (2017) conducted Line × tester analysis to estimate combining ability and heterosis of 18 hybrids developed by crossing 9 lines with 2 testers of Indian mustard Estimates of GCA effects indicated that RH 749, RH 406, Rohini, NRCHB 101 and

NPJ 112 were good general combiner. Significant SCA effects for seed yield, 1000-seed weight, number of seeds/ siliqua and other attributing traits in desirable direction were recorded in a series of hybrids.

Rameeh (2011) carried out a Line × tester analysis of two testers of spring type and six lines of winter type oil seed rape varieties to estimate combining ability of yield components. High narrow sense heritability estimated for 1000-seed weight indicating the prime importance of additive genetic effects for this trait. Significant positive general combining ability (GCA) effects of seed yield and siliquas per plant were observed for parents. Most of the crosses with significant positive specific combining ability (SCA) effects for siliquas per plant had significant positive SCA effects of seed yield.

2.6 Gene interaction studies

The adequacy of different genetic models and nature and magnitude of gene effects responsible for the expression of seed yield and important yield contributing characters were studied in mustard. Statement reviewed from different literature are noted below:

Shweta (2013) studied an experiment comprising 100 treatments (10 parents with 45 F_1s and 45 F_2s) carried out in a randomized block design with three replications. Analysis of the data on seed yield and its ten component characters suggested that dominant alleles were more frequent for most of the traits. Additive and non-additive gene actions were found important in the inheritance of most of the characters.

Philanim *et al.* (2019) conducted an investigation with 6 generations of two crosses viz; MRNJ 88-1 X JMWR 9081-1, MRNJ 131 X JMWR 9081-2. Data recorded showed the predominance of both Main effects (additive-dominance) and interaction effects for most of the yield and component traits except in number of primary branches per plant and number of secondary branches per plant where the role of main gene effects was distinct.

Arifullah (2013) investigated on *Brassica juncea* genotypes is an attempt to obtain genetic information on some yield attributes. Estimates for genetic components of variation revealed that additive effects were more important for seeds per siliqua and 1000-seed weight indicating possibility of selection for these traits in early segregating generations. Dominance effects were more prominent for plant height, number of primary branches per plant, number of siliquae per plant, siliqua length and seed yield per plot, thus suggesting that selection could be effective in latter generations.

Jana *et al.* (2018) examined the genetic basis of variation in 10 X 10 diallel, diverse lines of *Brassica juncea*. Analysis of variance showed highly significant differences for these traits. The estimated components of variation revealed that dominance genes were more pronounced than additive genes. Estimates of narrow sense heritability for number of seeds per siliqua, 1000 seed weight, seed yield per plant and oil content were of medium range pointing out better inheritance pattern which may be helpful during selection in future generations.

Mumtaz *et al.* (2015) studied in *Brassica rapa* to estimate genetic expression (i.e. gene action) by using Hayman and Jinks model on quality-related using four lines and their hybrids in a diallel fashion. All traits other than oil percentage and linolenic acid were found to be controlled by dominant gene action. The best parents were TP-124-1 and UAF-11, which had the maximum dominant and maximum recessive genes, respectively and they can be used as parents in future hybrid breeding programs.

Senapati *et al.* (2009) carried out an experiment with eight varieties of Indian mustard (*Brassica juncea*). Both dominant and recessive alleles indicated to play important role in expression of different characters. Partial dominance type of gene action was observed in plant height, 100 seed weight, number of seeds per siliqua and weight of 25 siliquas. The nature of gene action suggested early generation selection may be followed for some of the characters that can be used in the future mustard breeding program.

Ranjana *et al.* (2021) undertaken a study to know the nature of gene action governing the characters. 6 generations mean analysis in the cross PCL55LLA5 revealed that dominance genetic variance was documented for the important yield traits like, number of siliquae per plant, 1000 seed weight and yield per plant.

Fouad *et al.* (2020) estimated gene effects through generation mean analysis in 2 faba bean crosses. The significant positive additive gene effects for days to 50% flowering and plant height in cross 1 and biological yield and 100 seed weight in cross 2 indicated effective selection for the traits. Values of dominance effects were greater than the additive effects for all the traits.

Yao *et al.* (2011) investigated an incomplete diallel cross study comprising of seven bread wheat (*Triticum aestivum*) cultivars with parents and F_1 progeny to determine heterosis, combining ability, gene action. Estimates of the genetic components of variation as well as ratio of GCA/SCA showed that all the characters were predominantly controlled by additive gene action. Plant height and its components were governed by partial dominance with additive type of gene action.

Labdi *et al.* (2015) studied in ascochyta blight resistance in half-diallel cross involving eight genotypes involving 28 F_1 and their F_2. The results were analyzed with the Hayman and Griffing methods. This result reflects a strong preponderance of additive effects and additive × additive with respect to dominance effects in this material for the two generations, which shows the predominance of additive versus dominance gene actions.

2.8 Fatty acid composition

Fatty acids from dietary lipids can impart both beneficial and harmful health effects. The compositional balance between saturated and unsaturated fatty acids plays a decisive role in maintaining the physiological harmony, proper growth and development in the human system. In order to improve the seed oil quality of mustard, profiling of fatty acids is essential. Review research papers are discussed below:

Walczak (2014) evaluated fatty acids of mustards by gas chromatography method and found that SFA participation were on average 5.86%, PUFA participation were on average 26.07% and erucic acid participation was on average 12,95% while the percentage of monounsaturated fatty acids (MUFAs) in analyzed mustards amounts to 68%. Estimated results revealed that erucic acid (C22:1) content ranges from 4.4-27, linoleic acid (C18:2) was 9.3 to 15.5 to, where α-Linolenic acid (C18:3) varied from 11.2 to 16.00.

Rai *et al.* (2018) was conducted an experiment during 2014-2015 to study the oil and fatty acids content in 26 genotypes of *Brassica* species. In *Brassica juncea,* the saturated fatty acid (Palmitic acid) content is in the range of 3.08–3.85 and oleic acid content is in the range of 0.80–48.70, linoleic acid content varied from 11.00- 45.30% and linolenic acid content varied from 11.10- 26.72%. The minimum Erucic acid content was recorded in *Brassica juncea* genotypes PM-24 (0.80%) whereas maximum Erucic acid content was recorded in Pusa Bold (49.40%) in *Brassica juncea*.

Sawicka *et al.* (2020) analyzed fatty acids derived from Two cultivars of white mustard (*Sinapis alba*) were evaluated: ‘Borowska’, and ‘Bamberka. The oil from ‘Borowska’ contained less saturated fatty acids (4.86%) in comparison to ‘Bamberka’ (10.36%). The content of erucic acid was 22.2% in the ‘Borowska’ oil, while the oil from ‘Bamberka’ contained only 3.8% of this component. Suggested that the oil derived from the cultivar ‘Bamberka’ can be used for food purposes due to the low content of erucic acid in the fatty acid composition and the beneficial fatty acid composition.

Ostrikov *et al*. (2020) studied the composition of mustard oil by using gas-liquid chromatography. A composition of acids - palmitic (4%), stearic (3%), polyunsaturated acids - linoleic (32%), linolenic (8%) and eicosenic (2%), monounsaturated acid - oleic (47%) were found from the estimation.

Sharafi *et al.* (2015) studied in seeds of 20 accessions of six Brassica species including cultivated and five wild relatives, analyzed for oil and fatty acid composition. The main fatty acids of oleic, linoleic, linolenic, erucic, palmitic, and stearic acids accounted for 89–94% of the total fatty acids in all species. The highest content of linolenic (20%) and linoleic (19%) acid was observed for *B. juncea.*

Nasr *et al.* (2006) studied 5 important fatty acids viz. oleic, linoleic, linolenic, stearic and palmitic acid in rapeseed released and line cultivars. 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.

Fadl *et al*. (2011) reported high erucic acid (37.89 and 23.90) % in yellow and brown mustards oils respectively. Both yellow and brown mustard seeds oils contained a little amount 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 mustards oils.

Amir *et al*. (2012) studied fatty acids in the seed oils of spring and winter rapeseed and reported oleic acid (63.62 to 67.38) %, linoleic acid (15.87 to 19.06) %, linolenic acid (7.55 to 9.76) %, palmitic acid (3.55 to 4.51) % and stearic acid (1.54 to 2.3) %.

Moreover, arachidic, erucic, gadoleic and palmitoleic acid were also found in lowest percentages counted less than 1%.

Tiwari *et al.* (2021) was carried out an experiment during 2017-2018 to estimate fatty acids in fifteen *Brassica napus* genotypes. The saturated fatty acid (SFA) includes the Palmitic acid (PA) in *Brassica napus* seeds varied in between the range of 2.68–4.43% and oleic acid (OA) content lied between 8.88-56.18% respectively where, polysaturated fatty acids, the content of linoleic acid (LA) lies in the range between 12.97- 17.98% respectively and linolenic acid (LNA) content varied from 13.41-23.42% respectively. Erucic acid, another essential trait, significant differences were noted amongst the *Brassica* species genotypes i.e. 12.96-48.80%.

CHAPTER III

MATERIALS AND METHODS

This chapter deals with the information that were related to the materials and methods subjected to conduct this experiment. The experiment was conducted in two successive Rabi seasons. At the first year, genetic variability and traits association of the parents was studied and crossing in half diallel fashion among the selected parents was done whereas during second year 21 F_1 hybrids derived from half diallel mating was evaluated. The details of material and methods and the experimental procedure implemented during the course of research work are described below:

3.1 Experimental site

The research experiment was carried out to evaluate the 21 F_1s at the research farm of Sher-e-Bangla Agricultural University, Dhaka-1207 during the period from mid November 2020 to March 2021. Earlier the diallel crossing pattern among seven (7) parental lines had performed during mid November 2019 to March 2020 of winter season. It was situated at 23°46’16”N latitude and 90°22’46”E longitude at an altitude of 8.8 meter from the sea level. The experimental field belongs to the Agro-ecological zone of “the Modhupur Tract”, AEZ-28. Photograph illustrates the experiment field (Appendix I).

3.2 Soil characteristics

The prevailed soil of the experimental field belonged to general soil type, shallow red brown terrace soils under Tejgaon Series. The soil was clay loam in texture. The land was medium high and the pH varies from 5.6 to 5.8. The experimental field was flat, facilitated easy irrigation and drainage. Physicochemical properties of the soil are presented in Appendix II.

3.3 Climate

The experimental site was under the sub-tropical climate zone. Climatic feature of the area was covered by hot or dry summer season, rainy season and dry winter season. During the rabi season scanty precipitation was observed from October to March with moderate temperature and a shorter day length coverage. According to the Bangladesh Metrological Department, Agargaon, Dhaka-1207, the recorded mean of air, temperature, humidity and rainfall data at the time of experiment conducting period were shown in Appendix III.

3.4 Design and layout

The experiment was carried out in a Randomized Complete Block Design (RCBD) with three replications. 225 m^2 (25×9 $m^{2)}$) area was allocated for conducting this experiment. Breadth of each replication was 2.5 m^2 with 25 m^2 in length. For drainage and irrigation facilities 0.5 m^2 channel was kept between two rows. The distance between line to line was 50 cm and plant to plant distance was 10 cm for evaluating the morphological characters as well as performing the hybridization program.

3.5 Planting materials

The present investigation was consisted of two years experiment. In the 1st year six (6) released varieties of *Brassica juncea* and one canola grade germplasm of *Brassica juncea* were used in the 7x7 half diallel experiment presented in Table 1 and Plate 1. While in the 2nd year the 21 F_1 cross-combinations derived from the 7x7 half diallel mating were used as plant materials shown in Table 2 and Plate 2.

3.6 Land preparation

The land preparation activities were taken into action before 15 days of seed sowing on 2 November, 2019. Under optimum field condition, the final land was prepared by several ploughing and cross ploughing followed by laddering and harrowing with the tractor and power tiller to get good tilt. All the undesirable materials like weeds, stables, dry leaves were eliminated from the field during last stage of land preparation. Before the preparation of land according the layout the field should get under the zoe condition, land was kept under open sunlight for few days. During the 2nd year, land was prepared on 10 November, 2020. Operations conducted during land management were shown in the Plate 3.

Table 1. List of the selected seven *Brassica juncea* L. germplasm used as parent materials

Designation	**Genotype**	**Sources**
P1	BINA-7	BINA, Mymensingh
P2	RYE-5	BARI, Gazipur
P3	DAULAT	BARI, Gazipur
P4	BARI Sharisha-10	BARI, Gazipur
P5	BARI Sharisha-16	BARI, Gazipur
P6	BJ00 (Canola grade and yellow seeded)	Dept. of Genetics and Plant Breeding, SAU, Dhaka
P7	BARI Sharisha-11	BARI, Gazipur, Dhaka

Note

BARI-Bangladesh Agricultural Research Institute,

BINA-Bangladesh Institute of Nuclear Agriculture.

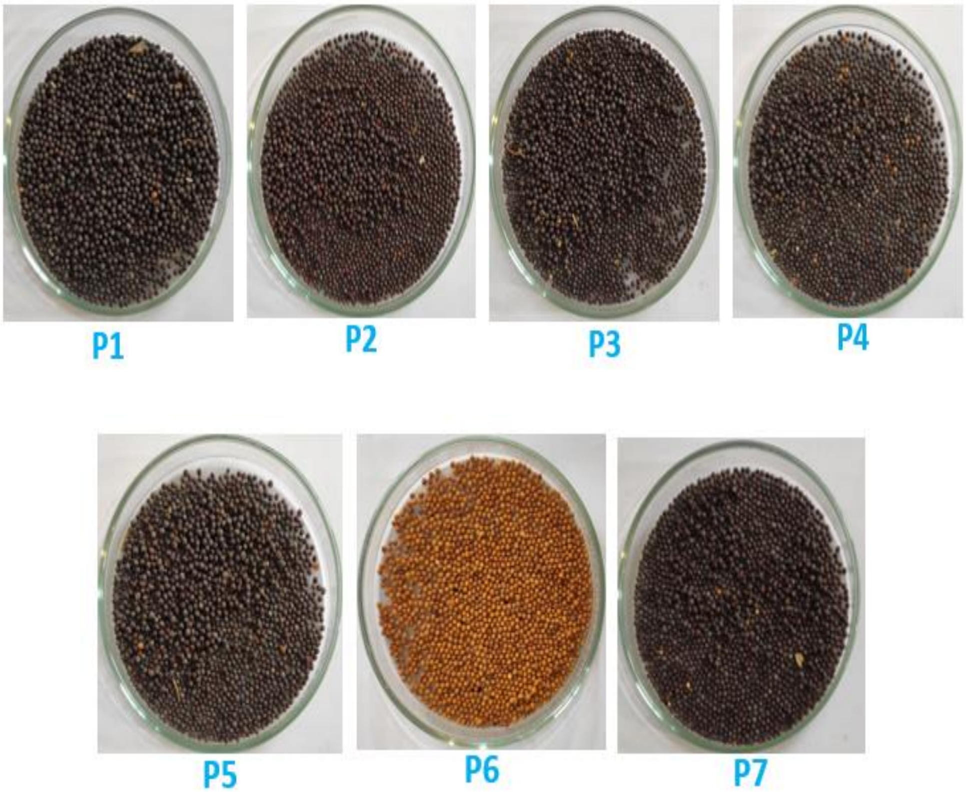


Plate 1: Seeds of seven *Brassica juncea* parents used in the half diallel 7x7 crossing program.

Table 2. List of 21 F_1 populations obtained from seven varieties of selected *Brassica juncea* varieties

F_1 Hybrids	
Designation	**Populations**
G1=P1 × P2	BINA7 × Rye5
G2=P1 × P3	BINA7 × Daulat
G3=P1 × P4	BINA7 × BS10
G4=P1 × P5	BINA7 × BS16
G5=P1 × P6	BINA7 × BJ00
G6=P1 × P7	BINA7 × BS11
G7=P2 × P3	Rye5 × Daulat
G8=P2 × P4	Rye5 × BS10
G9=P2 × P5	Rye5 × BS16
G10=P2 × P6	Rye5 × BJ00
G11=P2 × P7	Rye5 × BS11
G12=P3 × P4	Daulat × BS10
G13=P3 × P5	Daulat × BS16
G14=P3 × P6	Daulat × BJ00
G15=P3 × P7	Daulat × BS11
G16=P4 × P5	BS10 × BS16
G17=P4 × P6	BS10 × BJ00
G18=P4 × P7	BS10 × BS11
G19=P5 × P6	BS16 × BJ00
G20=P5 × P7	BS16 × BS11
G21=P6 × P7	BJ00 × BS16

Note:

BS- BARI Sharisha BJ 00-*Brassica juncea* Canola Grade

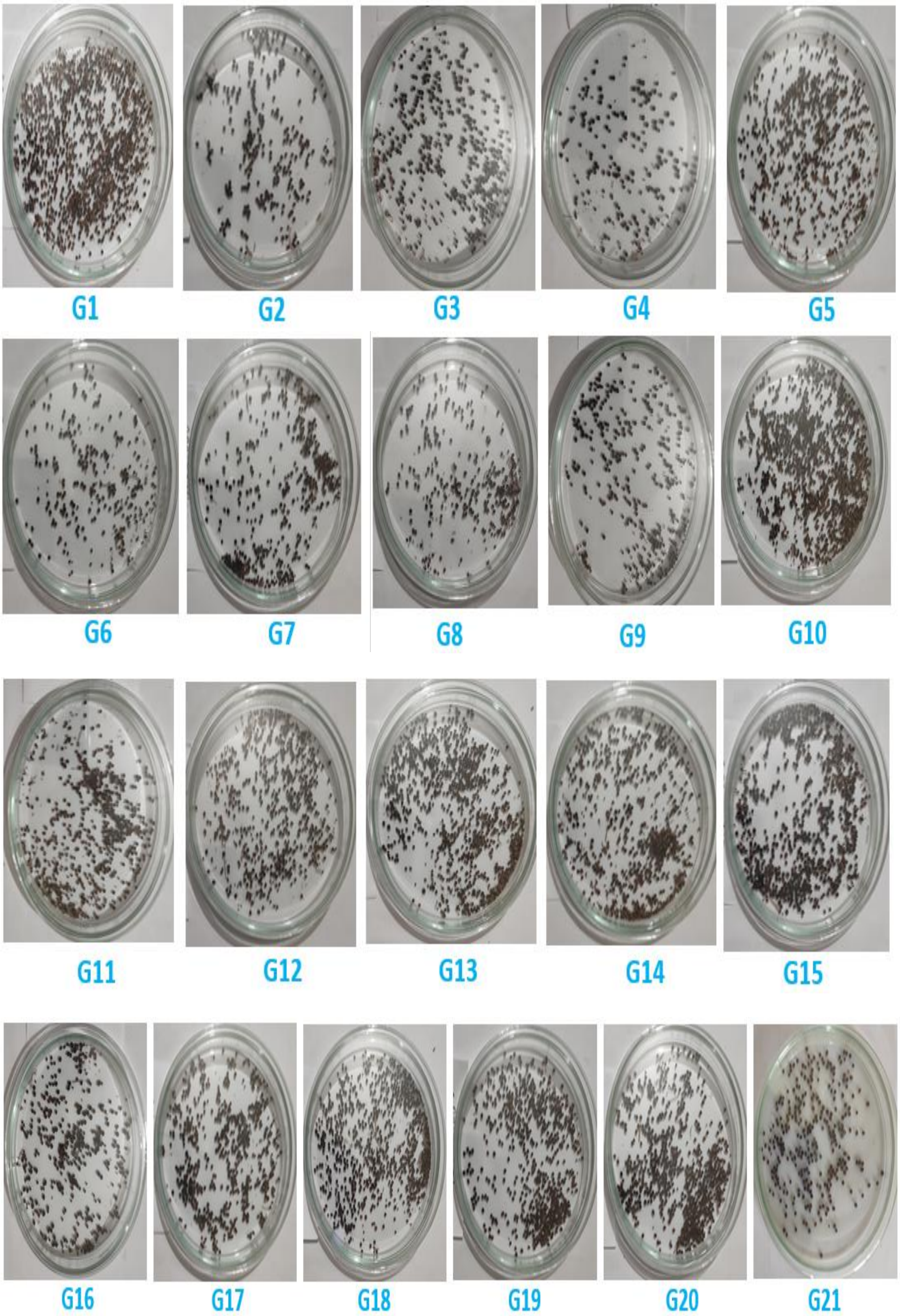


Plate 2: Seeds obtained from 21 F_1 hybrids derived from 7×7 half diallel cross of *Brassica juncea* parents.

3.7 Fertilizer application

All the essential fertilizers including both organic and inorganic viz. cow dung, urea, TSP, MOP, gypsum, zinc oxide and boric acid were applied in the field according to the dose required for 225 m^2 area of land. All fertilizers were nicely incorporated into the soil and a light irrigation was given after fertilizer application. The recommended dose of fertilizer was mentioned in the Table 2 for cultivating the mustard varieties in field.

Table 3: List of fertilizers with dose and application procedure

Sl. No.	**Fertilizer name**	**Fertilizer dose (225 m^2)**	**Application procedure**
1.	Cow dung	225kg	Basal dose
2.	Urea	5.00 kg	50% urea was used as basal dose and rest was applied before first flower initiation (approx. 30 DAS).
3.	TSP	3.52 kg	Basal dose
4.	MoP	1.76 kg	Basal dose
5.	Gypsum	2.97 kg	Basal dose
6.	Zinc Oxide	100 gm	Basal dose
7.	Boric acid	220 gm	Basal dose

Plate 3: Photograph showing final land preparation.

Plate 4: Pictorial view of seed sowing to the line to line direction.

Plate 5: Weeding and thinning was carried out to eliminate undesired plants from the plot.

3.8 Seed sowing

Seeds were sown in the experimental plot on 02 November, 2019 according to the line to line system whereas during the evaluation F_1 hybrids the seeds were sown on 17 November, 2020 that was demonstrated in the Plate 4. Due to dry condition, a light irrigation was provided to get optimum moisture for germination before seed sowing. Seeds were placed 1.5 cm depth in the soil. After sowing, the seeds were covered with soil carefully therefore no clods were on the seed.

3.9 Intercultural operations

Light irrigation was given after the emergence of seedlings. A good drainage system was also maintained to remove the excess water from the experimental plot during the growth period. Irrigation at 15 days interval was followed to provide optimum condition for plant growth. The 1st weeding was done after 15 DAS along with thinning practices was also carried out. 2nd thinning program was performed just after 7 days later to confirm plant to plant distance at 10 cm. Before the application of the rest of urea fertilizer 2nd weeding was done, hence plant would have got their nutrient properly. The total plot was tagged before evaluating the morphological traits. To control aphid and Alternaria leaf spot infection Malathion-57 EC @ 2ml/liter was applied once in the field. The pesticide was applied in the afternoon. Pictorial view of intercultural practices was presented in Plate 5.

3.10 Half diallel mating procedure

Seven selected varieties of *Brassica juncea* were crossed among themselves followed by half diallel mating design. Pictorial demonstration of different crossing step is shown in Plate 6.

3.10.1 Plant selection

During the flowering stage 20 plants were selected for doing crossing program for each cross combination. Plants are selected on the basis of stem thickness, stem color, leaf hairiness, leaf apex shape and size (Plate 6a).

Plate 6a: Honorable supervisor Dr. Jamilur Rahman sir given instruction on plant selection and crossing procedure

Plate 6b: Emasculation of buds on the selected plant

Plate 6c: Pollens were dusted on the emasculated buds

Plate 6d: Pollinated buds were covered with bags

Plate 6e: Part of the research plot of completing crossing program

Plate 6f: Siliqua setting after crossing

Plate 6: Half daillel (7x7) crossing program among seven selected genotypes of *Brassica juncea*.

3.10.2 Emasculation

Floral buds that were ready to open were selected for emasculation. Removal of petal, sepal and pollen was done at morning usually 6:30 am to 9:00 am. Special care was taken to remain the stigma unaffected. It is shown in Plate 6b.

3.10.3 Hand pollination

Crossing was made by hand pollination to get the desired cross combinations. Pollen was collected from the selected plant when it started shadding. Desired pollens were dusted on each of the stigma of the emasculated bud, it is demonstrated in Plate 6c.

3.10.4 Bagging

After hand pollination bagging was done to proctect the crossings from unwanted pollination (Plate 6d). The bag was removed after a week ensuring optimum growth of siliqua.

3.10.5 Tagging:

Each of the cross combinations were tagged carefully to collect the appropriate seeds (Plate 6e). Siliqua setting is represented in Plate 6f.

3.10.6 Seed collection:

From the above crossing program a total number of 21 cross cmbination’s seeds were obtained to grow F_1 hybrids. Obtained seeds are presented in Plate 2.

3.11 Crop harvesting

Plants that showed 80% symptoms of maturity like straw color of siliqua, leaves, stems and desirable seed color were harvested. At maturity 15 plants were selected for morphological analysis from each of the lines. The sample plants were harvested by uprooting carefully and tagging was kept for analyzing morphological and biochemical traits.

3.12 Threshing and storage

Plants were harvested on individual line basis and seeds of F_1 populations were stored for their oil content and fatty acids analysis. Besides this, seeds were stored for generating the next segregating generations.

3.13 Data collection

Twelve yield and yield related traits were taken into consideration for studying different genetic parameters analysis. Data was recorded by the random selection of fifteen plants for each genotype. Characters selected for morphological analysis are as follows:

3.13.1 Days to first flowering

Days to first flowering were recorded from sowing date to the date of 5% flowering of every entry.

3.13.2 Days to 50% flowering

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

3.13.3 Days to siliqua maturity

The data were recorded from the date of sowing to silique maturity of 80% plants od each entry.

3.13.4 Plant height (cm)

Plant height was measured from the base of the plant to the tip of the longest inflorescence. Data were taken after harvesting.

3.13.5 Number of primary branches per plant

The total number of branches arisen from main stem was accounted to measure this trait.

3.13.6 Number of secondary branches per plant

The total number of branches arisen from the primary branches was counted to measure the data.

3.13.7 Number of siliquae per plant

The total number of siliquae produced each plant was considered as the number of siliquae per plant.

3.13.8 Siliqua length (cm)

This measurement was taken into centimeter(cm), from the base to the tip of the siliqua.

3.13.9 Number of seeds per siliqua

Seeds that were well filled counted from siliqua was considered as the number of seeds per siliqua.

3.13.10 Thousand seed weight (g)

Weight in grams of randomly counted thousand seeds of each entry was recorded.

3.13.11 Yield per plant (g)

All the seeds produced by a plant was weighed in grams and considered as yield per plant.

3.13.12 Harvest index (%)

Harvest index (%) was measured by dividing seed yield per plant to the total dry matter per plant (shoot dry matter and seed yield) and expressed in percentage.

3.14 Statistical analysis

Mean values of nine randomly selected plants were used for recording the data. The observed data were computed for each of the twelve traits for each genotype in each replication and were sebjected to statistical analysis. Least significant difference (LSD) test was performed for all characters to estimate the differences between the means of the genotype. Mean, range, co-efficient of variation was estimated using Statistix 10 software. Diallel analysis was performed by using AGD-R (version 5.0) whille, genetic variability of parental lines, correlation co-efficient between selected variables, combining ability test and genetic components were performed by using R 4.2.1 software, heterosis was calculated though microsoft excel and correlation coefficients was computed with the help of SPSS (version 26) software.

3.14.1 Analysis of variance

The analysis of variance (ANOVA) for different characters was used to determine whether there is any difference between two or three means. Formula given by Cochran and Cox (1957) the goal of ANOVA is to check for variability within the groups as well as among the groups. The level of significance was tested at 5% and 1% level using "t" test.

Analysis of variance (ANOVA)

Source of variation	Degree of freedom (df)	Mean sum of squares(MSS)	Expected MSS
Replication	(r-1)	Mr	$g\sigma_r^2+\sigma^2_e$
Genotypes	(g-1)	Mg	$r\sigma^2_g+\sigma^2_e$
Error	(g-1)(r-1)	Me	σ^2_e
Total	(rg-1)		

Where,
r= number of replications
g= number of treatments (genotypes)
σ_r^2= variance due to replications
σ^2_g= variance due to treatments (genotypes)
σ^2_e= variance due to errors

To test significance of the difference between any two-adjusted genotypic mean, the standard error of mean was computed using the formula,

S.E = √2Ee/r(1+rqu/q+1)

Where,
S.E = Standard error of mean
E= Mean sum squares for error (Intra block)
r= Number of replications
q= Number of genotypes in each sub-block
u= Weightage factor computed

3.14.2 Genotypic and phenotypic variance

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

Genotypic variance ($\sigma^2{}_g$) = GMS-EMS/r

Phenotypic variance ($\sigma^2{}_p$) = $\sigma^2{}_g+\sigma^2{}_e$

Where,
GMS = Genotypic mean sum of squares
EMS = Error mean sum of squares
r = Number of replications
$\sigma^2{}_g$ = Genotypic variance
$\sigma^2{}_r$= Error variance

3.14.3 Genotypic and phenotypic co-efficient of variation

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

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

Where,
$\sigma^2{}_g$ = Genotypic variance
$\overline{x}$ = Population mean

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

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

Where,
$\sigma^2{}_p$ = Phenotypic variance
$\overline{x}$ = Population mean

GCV and PCV were classified into three following categories as suggested by Sivasubramannian and Madhamenon (1973).

Categories of GCV and PCV

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

3.14.4 Heritability

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

Heritability in broad sense, $H^2 = \sigma^2_g/\sigma^2_p \times 100$

Where,
H^2 = Heritability in broad sense
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance
Similarly, narrow sense heritability was calculated from the following formula,

Heritability in narrow sense, $h^2 = \sigma^2_{g(additive)} /\sigma^2_p \times 100$

Where,
h^2 = Heritability in narrow sense
σ^2_p = Phenotypic variance
$\sigma^2_{g(additive)}$ **=** Variance due to additive genetic action
Estimation heritability in cultivated plants could be placed in the following categories as suggested by the Robinson *et al.* (1966).

Categories of Heritability in broad sense

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

3.14.5 Genetic advance

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

Genetic advance, $GA = K. H^2. \sigma_p$

Or, genetic advance, $GA = K. \sigma^2_g/\sigma^2_p. \sigma_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity
σ_p = Phenotypic standard deviation
H^2 = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Categories of Genetic advance

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

3.14.6 Genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by (Comstock and Robinson1952).

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

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

Categories of Genetic Advance as percentage of mean

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

3.14.7 Genotypic and phenotypic correlation co-efficient

The calculation of Genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic correlation, $r_{gxy} = GCOV_{XY}/\sqrt{}GV_x.GV_Y = \sigma_{gxy}/\sqrt{}(\sigma^2_{gx}.\ \sigma^2_{gy})$

Where,

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

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

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

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

Where,

σ_{pxy} = Phenotypic co-variance between the traits x and y
σ^{2}_{px} = Phenotypic variance of the trait x
σ^{2}_{py} = Phenotypic variance of the trait y

3.14.8 Combining ability in relation to diallel analysis:

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

The mathematical model for the analysis was:

$Y_{ij} = m + g_{i} + g_{j} + S_{ij} + 1/bc \sum \sum kl$ €ijkl

Where,

i,j = 1,2,3,…………….., p
k = 1,2,3,………………, b
l = 1,2,3,………………., c
P = Number of parents
B = Number of blocks or replications
C = Number of observations in each plot
Y_{i} =The mean of i×jth genotype over k and l
m = The population mean
g_{j} =The general combining ability (GCA) effects to ith parent
g_{j} = The GCA of jth parent
S_{ij} =The SCA effects such that $S_{ij} = S_{ji}$
$1/bc \sum \sum kl$ €ijkl = The mean error effects
The restriction imposed are: $\sum g_{i} = 0$ and $\sum S_{ij} + S_{ii} = 0$

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

ANOVA

Sources	d.f.	Sum of squares	Mean sum of squares	Expected MSS
GCA	p-1	Sg	Mg	σ^2_e +(P+2).1/(P-1) $\sum g_i^2$
SCA	P(p-1)/2	S_s	M_s	σ^2_e+2/p(p-1) $\sum_i\sum_j S_{ij}^2$
Error	(b-1) (e-1)	Se	M_e	σ^2_e

Where,

GCA= General combining ability

SCA= Specific combining ability

p = Number of parents

b = Number of blocks or replications

e = Number of entry (family)

Y_i = Array total of the i^{th} parent

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

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

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

S_e = Sum of square due to error

$S_g = 1/(P+2)\ [\sum_I (Y_i + Y_{ii})^2 - 4/p.y^2]$

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

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

$g_i = 1/(P+2)\ [\sum_I (Y_i + Y_{ii})^2 - 2/p.y]$

$S_{ij} = Y_{ij} - 1/(P1+P2) \sum_i (Yi + Y_{ii} + Y_g + Y_{ij}) + 2/(P+1)\ (P+2).Y$

The variance of GCA and SCA were,

$Var\ (g_i) = (P-1)/P(P+2).\ \sigma^2_e$

$Var\ (S_{ij}) = 2(P-1)/(P+1)\ (P+2).\ \sigma^2_e$

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

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

3.12.9 Estimation of heterosis:

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

Heterosis over better parent (heterobeltiosis in %) = ($\overline{F1}$-$\overline{B.P}$/ $\overline{B.P}$) × 100

Where,

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

$\overline{B.P}$ = Mean of better parent

Heterosis over check variety was calculate by the same was,

Heterosis over check variety (Standard heterosis in %) = ($\overline{F1}$- $\overline{CV}$/ $\overline{CV}$) × 100

Where,

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

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

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

Critical differences (CD) = t × √2EMS/√r

Here,

EMS = Error mean sum of squares

r = Number of replications

t = Tabulated t value at error d.f

CD values were compared with the values obtained from (F_1-B.P) and (F_1-C.V) to test the significance of respective heterotic effects.

3.14.11 Fatty acid content analysis

Seed oil of 18 *Brassica juncea* L. samples viz. BINA7, BARI sharisha11 and BARI sharisha16 among the parental lines and F_1 hybrids of BINA7 × BJ00-S1, BINA7 × BJ00-S2, Rye5 × BJ00-S1, Rye5 × BJ00-S2, Daulat × BJ00-S1, Daulat × BJ00-S2, BS10 × BJ00-S1, BS10 × BJ00-S2, BS16 × BJ00-S1, BS16 × BJ00-S2, BS16 × BJ00-S3, BS16 × BJ00-S4, BS11 × BJ00-S1, BS11 × BJ00-S2 were used in quality analysis after growing in the field experiment. Chemicals like sodium chloride, nitrogen gas, glacial acetic acid and standard fatty acid methyl esters were used for fatty acid analysis. Determination of fatty acid content in traditional and commercial mustards oil of Bangladesh is done by Gas-Liquid Chromatography (Tanvir, 2014).

3.10.1 Methylation of Fatty Acid

Total lipid (400-600 mg) was taken in a ground joint flask and saponified with 15-30 mL 2M KOH (ethanolic) in water bath at 700 C for 1 hour by joining with a condenser. After cooling, the solution was diluted with equal volume of distilled water and acidified with concentrated HCl to PH<2 as ascertained with a PH meter. The liberated fatty acids (a mixture) were extracted with 30-60 mL of diethyl ether. Small amount of water was also extracted along with free fatty acids. This undesired water was removed by adding anhydrous sodium sulphate. The ether extract devoid of water was collected in another joint flask. The extract was then evaporated to dryness under N2. Dry methanolic HCl (25- 50 mL) prepared as above, was added into the flask containing the fatty acid mixture and the content was heated at 850 C under reflux for 2 hours. After cooling, the fatty acids methyl esters (FAME) were extracted three times with equal volume of petroleum spirit (bp40-600). All extracts were combined and evaporated to a small volume under N2.

3.10.2 Purification of Fatty Acid Methyl Esters

3.10.2.1 Preparation of TLC Plate

A slurry of silica gel G for thin layer chromatography is made with water (2 mL water per gm silica gel G) in a beaker (500mL capacity) and spread on 2 mm thick glass plates 20×20 cm by a TLC spreader. The silica gel coating is 250 µm. The slurry thus spread is kept on the platform for about 10 minutes, transfer to the metal racks and dried in an oven at 1100 C for about an hour. The plates are now ready for use.

3.10.2.2 Thin Layer Chromatographic (TLC) procedure

Standard fatty acids preparation (~3-5 mL) is now spotted on the plates with a glass capillary taking precaution so that not more than 2-3 µL are spotted on the plates at a distance nearly ¾ for an inch from one edge on the plates. The gaps between two spots should be around half an inch and the spots should be as small as possible for better resolution of the fatty acids. The unknown should 50 be spotted on the two locations. After air drying the plate is dipped in the solvents (n- hexane: Diethyl ether: glacial acetic acid 70:30:1) in the TLC jar which is pre-equilibrated with the solvent system for about an hour. The solvent risen up the silica gel (ascending chromatography) and is allowed to rise approximately anywhere between 15-18 cm (nearly one hours) at which point the plate is removed from the jar, air dried, placed in the iodine chamber for 5 minutes. The FAME band in the plate was visualized in the iodine chamber. The FAME in the sample can be identified by their Rf values when compared to standard. After the yellow color vanished the band was scraped into a centrifuge tube and eluted with methanol. The tube was then centrifuged and the supernatant was transferred into a dry flask. The FAME solution was evaporated to dryness under nitrogen. A small volume of dichloromethane solution was added to re-dissolve the FAME band and a 5-10 mm aliquot and analyzed in Gas-liquid chromatography.

3.10.3 Gas-Liquid Chromatographic (GLC) analysis of fatty acid methyl esters

The fatty acid methyl esters, prepared and purified as above, were analyzed by gas-liquid chromatography (GLC). A 2×4 mm inside diameter column (Preferably glass) packed with 12-15 % (w/w) ethylene glycol succinate liquid phase coated on 100/200 mesh Gas-chrom P was used. The temperature was1900 C and the detector temperature was 2600 C. The injector temperature of the column was programmed initially at 1700 C for 8 minutes, then it was allowed to rise to 2000 C at a rate of 10 C/min and the isothermal final period was 55 minutes. Thermal conductivity detectors were excellent. Nitrogen was used as a carrier gas at a flow rate of 11.4 mL/min. Hydrogen flow was 10% above nitrogen flow. Standard fatty acid methyl esters were used for the identification of the sample fatty acid peaks. The following Standard fatty acids were used, the methyl esters of C8:0 C9:0 C10:0 C11:0 C12:0 C14:0 C16:0 C18:0 C18:1 C18:2 C18:3 C20:0 C22:0. The peak area of each component was measured automatically by chromatograph machine. It was also measured by the actual physical measurement by the triangulation method (Tanvir et al, 2014). The 51 total mm of all peak areas were taken as 100% and the percent population of a given fatty acid peak was calculated accordingly. The fatty acids were expressed as weight percentages of total fatty acids.

Brief procedure of determination of Fatty acid composition

- Fiftin mustard seeds were crashed and the powdery samples were put in a 50 ml screw capped pyrex glass tubes having 50 cm in length and 1 cm internal diameter.
- Then 2 ml of methanolic sulphuric acid added in each tube and glass vials were put in pre-heated oven at 80°C for 1 hour and shake after 15 minutes.
- The glass vials taken out, cooled and then 2ml of distil water were added in each tube to stop the reaction.
- Then esterifies fatty acids were extracted with 1ml of petroleum ether (40-60°C) thrice.
- After then the ether content was evaporated and remaining oily surface was injected into gas chromatography for fatty acid profile.

CHAPTER IV

RESULTS AND DISCUSSIONS

The data was collected from seven parental lines and 21 F_1 populations derived from the half diallel crosses of the selected parents of *Brassica juncea* on twelve yield and yield attributing characters and their fatty acid compositions. The data subjected to the biometrical and biometrical analysis and obtained results from varietal performance, correlation among yield attributing variables, combining ability effects among the parents and F_1 hybrids, heterosis effects of the hybrids and fatty acid compositions of the selected samples of parents and the hybrids derived from them were demonstrated below under the following headings:

4.1 Varietal performance and genetic parameters

For the successful crop improvement program, the breeders collected and accumulated the required genetic variability and select yield associated and highly heritable characters after eliminating the environmental components of phenotypic variation (Mather, 1949). Hence, prior information on both phenotypic and genotypic coefficient of variation is requisite for the estimation of heritability in order to predict the expected genetic advance possibly by selection for a character can be evaluated.

The accessibility of transgressive segregants in the breeding methods relies upon the dissimilarities of the parents. The existing variability is useful for developing the new cultivars by combining the desirable genes from the diversified genotypes into the new one. Hence, the obtaining results were referred to analysis of variance (ANOVA), range, mean, coefficient of variations (CV%), mean performance of the selected parents, genotypic variance, phenotypic variance and environmental variance among the variables, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense (h^2_b) and genetic advance and expected genetic advance as percentage of mean for twelve characters of the seven parental genotypes of *Brassica juncea* that were used to do diallel mattings , is illustrated in Table 4, Table 5 and Table 6.

Table 4. Analysis of variance (MS values) of twelve quantitative characteristics of 7 parents of *Brassica juncea*

Sources	d.f	DFF	D 50% F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
Replications	2	4.905	0.191	5.333	6.651	0.089	0.149	0.016	42.576	0.191	0.013	0.046	0.643
Genotypes	6	20.429**	36.048**	20.318**	456.406**	0.691**	0.750**	0.071*	737.741**	0.628*	0.115**	3.539**	11.670**
Error	12	0.571	1.857	4.056	19.153	0.052	0.111	0.019	51.585	0.144	0.008	0.014	0.743

**: Significant at 1% level of probability *: Significant at 5% level of probability

Note:

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

Table 5. Yield and yield related quantitative characters and mean performance of selected *Brassica juncea* varieties

Parents	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
P1	35.67e	43.67d	102.67c	138.11c	4.33b	7.44a	4.36ab	210.33d	13.69a	3.27a	7.18b	29.48b
P2	37.33d	45.00cd	103.33c	143.28c	3.67cd	7.11ab	4.00c	189.67e	13.11abc	2.87c	5.10e	31.82a
P3	39.67b	44.67cd	105.00bc	140.45c	3.89c	6.56b	4.13bc	223.33bc	13.33ab	2.97bc	5.57d	28.66b
P4	39.00bc	43.67d	104.00c	158.89b	3.67cd	6.89ab	4.38a	216.89bcd	13.19abc	3.07b	6.55c	26.19c
P5	42.00a	49.33b	109.67a	170.56a	3.33d	6.89c	4.17abc	238.89a	12.55cd	3.33b	7.32b	29.34b
P6	43.00a	53.00a	108.33ab	162.06b	4.78a	5.89ab	4.01c	228.11ab	12.41d	2.80d	5.54d	26.35c
P7	37.67cd	47.00bc	105.67bc	156.78b	4.00bc	7.11ab	4.25abc	210.56cd	12.72bcd	3.07a	7.99a	29.61b
Min.	35.67	43.67	102.67	138.11	3.33	5.89	4.00	189.67	12.41	2.80	5.10	26.19
Max.	43.00	53.00	109.67	170.56	4.78	7.44	4.38	238.89	13.69	3.33	7.99	31.82
Mean	39.19	46.62	105.52	152.87	3.95	6.84	4.18	216.82	12.99	3.05	6.45	28.78
CV (%)	1.93	2.92	1.91	2.86	5.75	4.87	3.35	3.31	2.92	2.89	1.84	2.99

Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

Among the twelve characters taken for conducting this experiment viz., number of primary branches per plant, number of secondary branches per plant and plant height were considered as growth promoting factors while days to first flowering, days to 50% flowering and days to siliqua maturity were regarded as earliness attributes. Number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua and 1000 seeds weight (g) were the reproductive traits whereas yield per plant (g) and harvest index (%) were considered as economic traits. All the traits were low genotypic and phenotypic coefficient of variations except number of primary branches and yield per plant (Table 6). Similar statement was given by Shekhawat *et al.* (2014) whereas none of the traits were recorded for the highest (>20%) PCV and GCV, however, moderate estimates (10-20%) of PCV and GCV was recorded for 1000-seeds weight (12.13 and 12.11 respectively) and remaining traits showed the lowest estimates (<10%) of PCV and GCV. A similar pattern of results was also noted by the earlier worker Verma (2021). Highly significant variations were estimated for all the traits under studied except seeds per siliqua. Variability among the selected twelve parameters is discussed below in details:

4.1.1 Days to first flowering

Highly significant variation was found among the genotypes in case of days to first flowering with the mean sum of square 20.43 (Table 4). It was varied from 35.67 DAS to 43.00 DAS with a mean value of 39.19 DAS (Table 5). The highest duration for days to first flowering was recorded in BJ-00 (43.00 DAS) followed by BARI sharisha-16 (42.00DAS) and Daulat (39.67 DAS) where BINA-7 required 35.67 DAS to take first flowering, the lowest among the genotypes (Table 5). The phenotypic variance was (7.19) slightly higher than the genotypic variance (6.62) and genotypic and phenotypic coefficient of variations were 6.57 and 6.84, respectively. This minor difference between phenotypic and genotypic coefficient of variation explored that the present variation was mainly contributed by the genotypes as the environmental influences were negligible. The value of GCV and PCV indicated considerable variation was present among the genotypes for the trait. Days to first flowering showed the highest heritability (92.05%) with medium genetic advance as percentage of mean (12.97%) indicated, inheritance of days to first flowering might be controlled by the additive gene effects (Table 6). It was supported by Shekhawat *et al*. (2014) finding in which high

Table 6. Estimation of genetic parameters for twelve yield and yield related characters of selected *Brassica juncea* varieties

Traits	**σ^2p**	**σ^2g**	**σ^2e**	**PCV**	**GCV**	**h^2_b (%)**	**GA**	**GA (% of mean)**
Days to 1st flowering	7.19	6.62	0.57	6.84	6.57	92.05	5.08	12.97
Days to 50% flowering	13.25	11.39	1.86	7.81	7.24	85.99	6.45	13.83
Days to siliqua maturity	9.48	5.42	4.06	2.92	2.21	57.20	3.63	3.44
Plant height (cm)	164.90	145.75	19.15	8.40	7.89	88.39	23.38	15.29
No. of primary branches per plant	0.26	0.21	0.05	13.02	11.68	81.31	0.85	21.58
No of secondary branches per plant	0.32	0.21	0.11	8.31	6.74	65.76	0.77	11.27
Silique Length (cm)	0.04	0.02	0.01	4.57	3.09	46.03	0.18	4.33
Silique per plant	280.30	228.72	51.58	7.72	6.98	81.60	28.14	12.98
Seeds per silique	0.31	0.16	0.14	4.25	3.09	52.95	0.60	4.64
1000 seed weight (g)	0.04	0.03	0.07	6.85	6.21	82.15	0.35	11.59
Yield per plant (g)	1.19	1.18	0.01	16.87	16.77	98.81	2.21	34.35
Harvest index (%)	4.39	3.64	0.74	7.28	6.63	83.07	3.58	12.45

Note:

σ^2p= Phenotypic variance, σ^2g= Genotypic variance, σ^2e= Environmental variance, PCV=Phenotypic coefficient of variation,

GCV= Genotypic coefficient of variation, h^2_b= Heritability in broad sense (%), GA= Genetic advance, GA (%) = Genetic advance as percentage of mean.

heritability (62.05%) with moderate genetic advance (15.36%) was estimated, suggested that high to moderate heritability with high to moderate genetic advance was due to additive gene action and simple selection may be effective.

4.1.2 Days to 50% flowering

Highly significant variation was found among the genotypes with the mean sum of squares 36.05 (Table 4). Days to 50% flowering ranged from 43.67 DAS to 53.00 DAS with a mean value of 46.62 DAS. The maximum duration was observed in BARI sharisha-16 (53.00 DAS) followed by BJ-00 (49.33 DAS) while the minimum days required for BINA-7 (43.67 DAS) and BARI sharisha-10 (43.67 DAS) in case of days to 50% flowering (Table 5). Similar range of flowering duration was found by Shekhawat *et al.* (2014) who found, most of the *Brassica juncea* species required 40.66 DAS to 61.33 DAS with an average of 53.09 DAS for days to flowering. Obtained results expressed that the genotypic variance (11.39) was lower than the phenotypic variance (13.25) indicating environmental factors slightly influenced the expression of this trait (Table 6). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 7.81 and 7.24, respectively indicating considerable variability was exist within the genotypes. High heritability (85.99%) was observed for this trait with a low genetic advance (6.45) and a moderate genetic advance as percentage of mean (13.83), indicating, selection for the improvement of this trait will be rewarded (Table 6). Akoju *et al.* (2020) found moderate PCV (10.51%) and the lowest GCV (8.54%) for days to 50% flowering. Jahan (2014) and Hussain *et al.* (2014) observed high heritability couple with moderate genetic advance as percentage of mean for this trait. The case study also revealed that the flowering traits of the genotypes was moderate sensitive and influenced by the environmental temperature fluctuation as well as the expression of the traits was controlled by the additive gene action.

4.1.3 Days to siliqua maturity

The mean sum of squares for days to siliqua maturity was 20.32 with a high amount of variation (Table 4). The average days required to be matured of the siliqua was 105.52 DAS ranged from 102.67 DAS to 109.67 DAS (Table 5). For siliqua maturity, 109.67 DAS were required for BARI sharisha-16 which was the highest duration for days to siliqua maturity followed by BJ-00 (108.33 DAS), however, the lowest days to siliqua maturity was observed in BINA-7 (102.67) followed by Rye-5, BARI sharisha-10 and

Daulat required 103.33, 104.00, 105.00 respectively (Table 5). Days to siliqua maturity exhibited low genotypic variance (9.48) and phenotypic variance (5.42) along with lower phenotypic coefficient of variation (2.92) and genotypic coefficient of variation (2.21). Difference between phenotypic variance and genotypic variance indicating environmental factors slightly influenced in the expression of this trait. (Table 6). A moderate heritability was observed for the trait including, lower value of genetic advance (3.63) and genetic advance as percentage of mean (3.44) indicated non-additive gene action was involved in the inheritance of this trait. Ara *et al.* (2010), Jahan (2008) and Hussain *et al.* (2014) found high heritability with low genotypic advance in percent of mean for days to siliqua maturity, therefore, selection for this trait might not be rewarding. It was also supported by Tewachew and Mohammed (2018), who estimated heritability for days to siliqua maturity was moderate.

4.1.4 Plant height (cm)

Considerable variation among the genotypes was observed in plant height. ANOVA revealed the mean sum squares for plant height was 456.41 where, the maximum plant height was 170.56 cm and the lowest was 138.11 cm (Table 5) with a mean value of 152.87 cm. The highest plant height was observed in BARI sharisha-16 (170.56 cm) followed by BJ-00 (162.06 cm), BARI sharisha-10 (158.89 cm) and BARI sharisha-11 (156.78 cm). The lowest plant height was found in BINA-7 (138.11 cm) followed by Daulat (140.45 cm) and Rye-5 (143.28 cm) (Table 5). For plant height, genotypic and phenotypic variance was recorded as 164.90 and 145.75 respectively (Table 6) with a moderate environmental variance (19.15). Differences between these two variances indicated environmental factors influence in the expression of this trait. The highest genotypic, phenotypic and environmental variances were observed in plant height as reported by Khan *et al.,* (2013). Phenotypic and genotypic coefficient of variation for trait was lower 8.40 and 7.89 respectively, (Table 6). On the contrary, moderate genotypic and phenotypic coefficient of variations (14.22 and 15.89 respectively) was found by Nagoo *et al.,* (2021). High heritability (88.39%) with the highest value of genetic advance (23.38) and moderate genetic advance as percentage of mean (15.29) were observed for plant height. Similar results were found in Patel *et al.* (2019) findings, revealed plant height was expressed high heritability (89.72%) with moderate genetic advance as per cent of mean (14.62%). Mekonnen *et al.* (2014), Bibi *et al.* (2016) and Gupta *et al.* (2019) reported high heritability with high genetic advance as percentage of mean for plant height. High heritability with moderate genetic advance as percent of mean revealed that expression of plant height was controlled by additive genetic action, hence, selection for this trait may be effective to get shorter plant of *Brassica juncea*.

4.1.5 Number of primary branches per plant

The mean sum square value for number of primary branches per plant was 0.69 (Table 4) revealed highly significant variation was existed among the genotypes. Number of primary branches per plant ranged from 3.33 to 4.78 among the different genotypes with an average of 3.95 (Table 5). The maximum number of primary branches holding plant was found in BJ-00 (4.78) followed by BINA-7 (4.33) and BARI sharisha-11 (4.00). However, in case of BARI sharish-16, Rye-5, BARI sharisha-10 and Daulat exhibited the minimum number of primary branches per plant that were 3.33,3.67,3.67 and 3.89, respectively (Table 5). The genotypic variance (0.21) and phenotypic variance (0.26) were the least diverse to each other. Moderate genotypic coefficient of variation (11.68) and phenotypic coefficient of variation (13.02) was observed for this trait indicating considerable variation was present among the genotypes (Table 6). Czern (2020) also observed moderate GCV (17.97) and PCV (19.17) for primary branches. The lowest disparity between the genotypic coefficient of variation and phenotypic coefficient of variation indicated that minor environmental effects were attributed on the expression on this trait. High heritability (81.31%) coupled with minor genetic advance and a higher genetic advance as percentage of mean (21.58) indicated heritability is due additive genetic action and selection for the trait might be effective. Singh *et al.* (2010) and Rout *et al.* (2019) estimated high heritability with high genetic advance as percentage of mean for this trait. However, Alamerew and Woyessa (2017) found low heritability (34.20%) with high genetic advance as percentage of mean (30.10%) for the selected trait.

4.1.6 Number of secondary branches per plant

The mean sum of square (0.75) for number of secondary branches per plant was significant (Table 4) and number of secondary branches varied from 5.89 to 7.44 (Table 5). The maximum number of secondary branches per plant was found in BINA-7 (7.44) which was statistically similar with Rye-5 (7.11) and BARI sharisha-11 (7.11). The lowest number of secondary branches per plant was observed in BJ-00 (5.89). Number of secondary branches per plant in Daulat (6.56), BARI sharisha-10 (6.89) and BARI sharisha-11 (6.89) were statistically similar (Table 5). The genotypic and phenotypic variance was recorded as 0.21 and 0.11, respectively. Moderate genotypic coefficient of variation (11.68) and phenotypic coefficient of variation (13.02) was found for the trait (Table 6). Patel *et al*. (2021) estimated low genotypic and phenotypic coefficient of variations (5.12 and 8.04) for secondary branches whereas Iqbal *et al.* (2015) and Rout *et al*. (2019) observed moderate GCV and PCV for this trait. It indicated that existing variation was useful in selecting the segregants for number of secondary branches per plant. High heritability (65.76%) with lower genetic advance (0.77) and moderate genetic advance as percent of mean (11.27) indicating that genes responsible for the expression of the trait was controlled by the additive genetic action. This research findings was supported by Afrin *et al.* (2017) and Mishra and Nath (2022), who observed high heritability (82.51%) with moderate genetic advance as per cent of mean (12.92%) in 10 varieties of *Brassica juncea* L. while Singh *et al*. (2011) found low heritability (24.15%) for this traits.

4.1.7 Siliqua length (cm)

The mean sum square for siliqua length (cm) was 0.07 (Table 4). Siliqua length (cm) of the selected genotypes ranged from 4.00 cm to 4.38 cm (Table 5) with an average of 4.18 cm. The longest siliqua was observed in BARI sharish-10 (4.38 cm) followed by BINA-7 (4.36 cm) and BARI sharisha-11 (4.25 cm) whereas the shorter siliqua was found in Rye-5 (4.00 cm) and it was statistically similar with BJ-00 (4.01 cm), Daulat (4.13 cm). Lower value of genotypic variance (0.04) and phenotypic variance (0.02) was observed for siliqua length whereas the environmental variance was negligible (Table 6). It also exhibited low genotypic coefficient of variation (4.57) as well as phenotypic coefficient of variation (3.09). Similar value was reported by Khan *et al.* (2013). A moderate heritability (46.03%) was estimated with low genetic advance (0.18) and a low genetic advance as percentage of mean (4.33) for the trait (Table 6). Low GCV (7.16) and PCV (7.84) was estimated by Ali *et al.* (2013) and Khan *et al.* (2015) found high heritability with low genetic advance (%) mean. Whereas Yadava *et al*. (2011) revealed high heritability (88.50%) with moderate genetic advance as per cent of mean (17.71%) for siliqua length. Moderate heritability coupled with low genetic advance as percent of mean given an assumption on the presence of non-additive gene effects on the expression of this trait.

4.1.8 Number of siliquae per plant

The mean sum of squares for number of siliquae per plant was 737.74 revealed that highly significant variation was present among the selected genotypes (Table 4). The maximum siliqua production was recorded as 238.89 while the lowest value was 189.67 with a mean value of 216.82 siliqua per plant. The highest number of siliquae was observed in BARI sharisha-16 (238.89) which was statistically similar with BJ-00 (228.11) and Daulat (223.33) whereas the lowest number of siliquae was found in Rye-5 (189.67) followed by BINA-7 (210.33), BARI sharisha-11 (210.56) and BARI sharisha-10 (216.89) (Table 5). In case of *Brassica juncea* species siliqua number was ranged from 215.66 to 350.66, estimated by Patel *et al*., (2021). The phenotypic variance (280.30) and genotypic variance (228.72) was higher with a large environmental variance (51.58) was found for the selected trait. However, the lower genotypic coefficient of variance (6.98) and phenotypic coefficient of variance (6.98) was recorded (Table 6). For number of siliquae per plant, the lower GCV (7.49) and moderate PCV (11.38) was supported by Yadava *et al.*, (2011). The larger difference between phenotypic variance and genotypic variance indicates higher environmental influences on the expression of the trait. Similar results were observed by Khan *et al.*, (2013). The heritability estimated for this trait was higher (81.60%) along with higher genetic advance (28.14) and a moderate genetic advance as per centage of mean (12.98), (Table 6). Mandal *et al.* (2022) similarly observed high heritability (80.61%) with moderate genetic advance (14.36%). So, this trait could be exploited for further improvement by the selection procedure. Mekonnem *et al.* (2014) and Alam (2010) estimated that siliquas per plant had moderately high GCV and genetic advance and high heritability.

4.1.9 Seeds per siliqua

Number of seeds per siliqua ranged from 12.41 to 13.69 with an average of 12.99 among the different varieties (Table 5). The maximum number of seeds was found in BINA-7 (3.69) which was statistically similar with Daulat (13.33), BARI sharisha-10 (13.19) and Rye-5 (13.11) while the lowest number of seeds were estimated in BJ-00 (12.41) followed by BARI sharisha-16 (12.55) and BARI sharisha-11 (12.72). The mean sum square for the trait was recorded as 0.628 (Table 4). According to Patel *et al*. (2021) seeds per siliqua was varied from 11.80 to 16.46. The genotypic and phenotypic variance for the trait was 0.31 and 0.16, respectively with an environmental variance 0.14 (Table 6). Lower case of genotypic coefficient of variance (4.25) and phenotypic coefficient of variance (3.09) was observed for the trait. Yadava *et al*. (2011) revealed the similar genotypic and phenotypic coefficient of variance (1.11 and 2.03, respectively). Higher phenotypic variance with considerable environmental variance indicated that expression of the character was also associated with the environmental interaction. A moderate heritability (52.95%) besides lower genetic advance (0.60) and genetic advance as percentage of mean (4.64) indicating, the character is governed by both additive and non-additive gene actions. Improvement of the character required further selection procedure to the extended generations. High heritability (86.00%) and moderate genetic advance (10.81%) was narrated by Hussain *et al.* (2014) and Czern (2020).

4.1.10 Thousand seed weight (g)

Significant variation was found for the character with the mean sum of square was 0.12 (Table 4). Thousand seed weight extended from 2.80 g to 3.33 g with the mean value was 3.05 g. The highest value was observed in BARI sharisha-16 (3.33 g) followed by BINA-7 (3.27 g), BARI sharisha-10 (3.07 g) and BARI sharisha-11 (3.07 g). Whereas variety BJ-00 (2.80 g) was recorded as the minimum seed weight followed by Rye-5 (2.87 g) and Daulat (2.97 g) (Table 5). The least value of phenotypic variance and genotypic variance for the selected character was recorded as 0.04 and 0.03, respectively with the larger value of environmental variance (0.07). The recorded phenotypic coefficient of variance (6.85) and genotypic coefficient of variation (6.21) was low (Table 6). Similar observations were also found in Hussain *et al.* (2014) and Amsalu (2020), observed low GCV and PCV (0.062 and 0.131, respectively) for 1000 seed weight. All these factors strongly indicated the expression of this character was largely influenced by the environment. While the estimated heritability (82.15%) was higher with low genetic advance (0.35) as well as moderate genetic advance as percentage of mean (11.59) suggested that character was governed by additive gene actions. Hence, improvement of the lines by selection procedure might be effectsive for this trait. The results were sorted with similar findings of Patel *et al*. (2019) who stated that heritability was high (96.65%) with moderate genetic advance as percentage of mean (18.61%). Yadav *et al*. (2011) reported high heritability (96.00%) with low genetic advance (2.30%) for test weight.

4.1.11 Yield per plant (g)

Significant variation was observed among the varieties and the mean sum of square for yield per plant was 3.53 (Table 4). The estimated result revealed that yield per plant was varied from 5.10 g to 7.99 g with an average 6.45 g (Table 5). The highest value was observed in BARI sharisha-11 (7.99 g) which was statistically similar with BARI sharisha-16 (7.32 g) and BINA-7 (7.18 g). However, variety Rye-5 was recorded for the lowest yield value as 5.10 g followed by BJ-00 (5.54 g) and Daulat (5.57 g). Yield per plant exhibited the lowest value for genotypic (1.19) and phenotypic variance (1.18) whereas the environmental variance was negligible. The estimated phenotypic coefficient of variance (16.87) and genotypic coefficient of variance (16.77) was moderate (Table 6), indicating considerable variations were exhibited by yield per plant that could be beneficial for selecting the segregating lines in next. The highest heritability (98.81%) was recorded for this character along with low genetic advance (2.21) and high genetic advance as percentage of mean (34.35%). Therefore, selection might be effective as the expression was controlled by the additive genetic effects. Yadava *et al.* (2011) recorded the maximum GCV and PCV for seed yield per plant (51.46 and 55.64) followed by biological yield per plant (48.98 and 52.27), harvest index (24.20 and 36.70), test weight (25.64 and 26.17) and siliqua on main primary. While Patel *et al.* (2019) found moderate phenotypic coefficient of variation seed yield per plant (16.42) and total number of branches per plant (11.58). Afrin *et al.* (2017), Rout *et al.* (2019) and Aktar *et al.* (2019) observed high heritability coupled with high genetic advance as percentage of mean for seed yield of *Brassica juncea*.

4.1.12 Harvest index (%)

Highly significant variations were recorded for the trait being studied. The mean sum of square for harvest index was 11.67 (Table 4). The obtained values for yield were ranged from 26.19(%) to 31.82(%) with the mean value of 28.78 in percentage (Table 5). The highest value was found in Rye-5 (31.82 in %) which was statistically similar with BARI sharish-11 (29.61 in %), BINA-7 (29.48 in %) and BARI sharisha-16 (29.34 in %). While the lowest value was observed in BARI sharisha-10 (26.19 in %) followed by BJ-00 (26.35 in %) and Daulat (28.66 in %). (Table 5). Bhuiyan (2015) revealed that harvest index was varied from 16.53% to 28.94% for different species of *Brassica juncea*. The recorded phenotypic variance (4.39) and genotypic variance (3.64) was low for the selected trait with lower phenotypic coefficient of variation (4.39) and genotypic coefficient of variation (3.64). Phenotypic variance was higher than the genotypic variance indicated that the exhibited variation was not only due to the genotypes but also environmental factors influence its phenotypic expression (Table 6). However, high heritability (83.07%) was estimated. High heritability with low genetic advance (3.58) and moderate genetic advance as percentage of mean (12.45) revealed that phenotypic expression was controlled by the additive genetic effects. Ahmad (2013) and Sikarwar *et al.* (2017) found high heritability with moderate genetic advance for this trait.

4.2 Correlation analysis among the variables of different parental lines of *B. juncea*

In all breeding programs a specific trait can be improved by indirect selection via other characters. A proper understanding of different characters with the target trait and among the different characters themselves is needed for the estimation of correlation of yield with their related characters. Two types of correlation viz., positive correlation which indicating the change of the two traits be in the same direction (increase or decrease) while the negative correlation which means the increase in the first trait combined with a decrease in the second trait (or reverse).The phenotypic and genotypic correlation demonstrated the extent of association among different characters, hence, it assists to base selection procedure to a required balance, when two opposite characters affecting the main characters are being selected. Coupling phase of linkage is responsible for positive correlation whereas repulsion phase of linkage of genes arisen the negative correlation for different characters. No correlation reveals that the concerned genes are located far apart on the same chromosome or on the different chromosomes. As yield is a complex trait, governed by many genes, the influence of each character on yield could be determined through correlation analysis in order to estimate the extent and nature 0f relationship prevailing among yield and yield related characters. Therefore, the correlation coefficient values of twelve selected traits in *Brassica juncea*. genotypes are evaluated and estimated results revealed that genotypic correlations were greater than the phenotypic correlation coefficients. Research findings are illustrated in Table 7.

Table 7. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for selected *Brassica juncea* L. varieties

Traits		DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW
D50%F	r_g	0.835*									
	r_p	0.787**									
DSM	r_g	0.989**	0.899**								
	r_p	0.762**	0.824**								
PH	r_g	0.751	0719	0.973**							
	r_p	0.699**	0.604**	0.641**							
NPB	r_g	0.089	0.411	-0.083	-0.178						
	r_p	0.044	0.361	0.038	-0.228						
NSB	r_g	-0.925**	-0.804*	-0.692	-0.419	-0.502					
	r_p	-0.747**	-0.634**	-0.485**	-0.353	-0.375					
SL	r_g	-0.525	-0.688	-0.592	-0.023	-0.251	0.699				
	r_p	-0.457*	-0.451*	-0.177	-0.096	-0.375	0.467*				
SPP	r_g	0.829*	0578	0.914**	0.692	-0.008	0.632	-0.031			
	r_p	0.689**	0.506*	0.661**	0.558**	0.026	-0.359	0.138			
SPS	r_g	-0.904**	-0.992**	-0.998**	-0.981**	0.009	0673	0.555	-0.587		
	r_p	-0.629**	-0.710**	-0.643**	-0.671**	-0.139	0.518**	0.455*	-0.315		
TSW	r_g	-0.224	-0.269	0.085	0.181	-0.457	0.699	0.814*	0.399	0.271	
	r_p	-0.188	-0.238	0.098	0.153	-0.404	0.491*	0.509*	0.255	0.166	
YPP	r_g	-0.226	-0.058	0.167	0.343	-0.177	0.539	0.807*	0.253	-0.086	0.791*
	r_p	-0.227	-0.065	0.117	0.317	-0.152	0.458*	0.569**	0.245	-0.049	0.722**

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

Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

4.2.1 Day to 50% flowering

Day to 50% flowering is strongly significant and positively correlated with days to first flowering (0.835, 0.787) and days to siliqua maturity (0.899, 0.824) at both genotypic and phenotypic levels but plant height (0.604) and siliqua per plant (0.506) is strongly and positively correlated with days to 50% flowering at only phenotypic level (Table 7). Maurya *et al.* (2012, Jamali *et al.* (2016) and Tadesse and Alemu (2019), who also reported that days to first flowering had highly significant and positive correlation with days to 50% flowering, plant height, siliqua per plant and seed yield while he reported negative association with secondary branches per plant. Positive but non-significant correlation with number of primary branches per plant (0.411, 0.361) was found at both genotypic and phenotypic level whereas positive correlation was found with plant height (0.719) at genotypic level only. However, strongly significant and negative correlation was found with days to 50% flowering with number of secondary branches per plant (-0.804,-0634) and number of seeds per siliqua (-0.992, -0.710) at both genotypic and phenotypic levels (Table 10) while 1000 seed weight (-0.269, -0.238) and yield per plant (-0.058, -0.065) and harvest index (-0.328, -0.282) showed negative correlation with days to 50% flowering at both levels. Agricultural *et al.* (2020) found negative association with seeds per siliqua, siliqua length, 1000 seed weight and number of siliqua per plant was present for days to first flowering both at genotypic and phenotypic levels.

4.2.2 Days to siliqua maturity

Both at genotypic and phenotypic levels, days to siliqua maturity was highly significant and positively correlated with days to first flowering (0.989, 0.762), days to 50% flowering (0.899, 0.824), plant height (0.973, 0.641) and siliqua per plant (0.914, 0.661) whereas 1000 seed weight (0.085, 0.098) and yield per plant (0.167, 0.117) showed positive direction but non-significant association at both levels towards days to siliqua maturity (Table 7). Mekonnen *et al.* (2014), Naznin *et al.* (2015) and Kumari *et al.* (2017) suggested that days to siliqua maturity had positive and non-significant association with seed yield per plant. Tadesse and Alemu (2019) reported that all the traits were positively and strongly correlated with siliqua maturity both at genotypic and phenotypic levels. On the contrary, negative association with strong significance was observed in number of seeds per siliqua (-0.998, -0.643) and number of secondary branches per plant (-0.692) with days to siliqua maturity at genotypic level while siliqua length (-0.592, -0.177) expressed negative association with days to siliqua maturity at both genotypic and phenotypic levels (Table 10). Prakash (2014) found days to siliqua maturity was negatively correlated with secondary branches per plant, seeds per siliqua, 1000 seed weight and yield per plant.

4.2.3 Plant height (cm)

Plant height was strongly significant and positively correlated with days to siliqua maturity (0.973, 0.641) at both genotypic and phenotypic levels where, with days to first flowering (0.699), days to 50% flowering (0.604) and siliqua per plant (0.558) was strongly significant and positively associated at only phenotypic level (Table 7). This findings were supported by Prakash (2014), Afrin *et al.* (2011), Ali *et al*. (2013) and Jamali *et al.* (2016) who found that plant height was significantly associated with days to flowering, days to ripening, siliqua per plant, yield per plant and harvest index. However, 1000 seed weight (0.181, 0.153) and yield per plant (0.343, 0.317) were positively but non-significantly associated with plant height at both genotypic and phenotypic levels (Table 10). Number of seeds per siliqua (-0.981, -0.671) was negatively and strongly correlated with plant height both at genotypic and phenotypic levels. On the contrary, number of primary branches per plant (-0.178, -0.228), number of secondary branches per plant (-0.419, -0.353) and siliqua length (-0.023, -0.096) were non-significantly and negatively associated with plant height (Table 7). Kumar *et al.* (2016) and Siddique *et al.* (2017) estimated that plant height was negatively associated with days to flowering, primary branches, secondary branches, umber of seeds per siliqua, siliqua length and harvest index at genotypic level while he found negative correlation with number of siliquae per plant, 1000 seed weight and harvest index at phenotypic level.

4.2.4 Number of primary branches per plant

Among all the traits, days to first flowering (0.089, 0.044) and days to 50% flowering (0.411, 0.361) showed positive correlation with number of primary branches per plant at both genotypic and phenotypic levels (Table 7). At the phenotypic level, days to siliqua maturity (0.038) and siliqua per plant (0.026) expressed positive correlation with number of primary branches per plant. Similar findings were sported by Gangapur *et al*. (2009), Naznin *et al*. (2015) and Singh *et al*. (2017) reported that primary branches had positive relationship with number of siliqua per plant, yield per plant and 1000 seed weight at both index. On the other hand, plant height (-0.178, -0.228), number of secondary branches per plant (-0.502, -0.375), siliqua length (-0.251, -0.375), 1000 seed weight (-0.457, -0.404) and yield per plant (-0.177, -0.152) had negative correlation with number of primary branches per plant at both levels (Table 7). Kumar *et al*. (2017) revealed that seed yield and 1000 seed weight had non-significant negative association with number of primary branches per plant.

4.2.5 Number of secondary branches per plant

At phenotypic level siliqua length (0.467), number of seeds per siliqua (0.518), 1000 seed weight (0.491) and yield per plant (0.438) was significantly correlated with positive direction with number of secondary branches per plant while these traits were positive but non-significantly correlated at genotypic index (Table 7). Halder *et al*. (2014), Afrin *et al*. (2017) and Devi *et al.* (2018) observed that number of secondary branches had positive correlation with days to maturity, siliqua length and 1000 seed weight. Strongly significant and negative correlation for days to first flowering (-0.925, -0.747) and days to 50% flowering (-0.804, -0.634) was observed with number of secondary branches per plant at both genotypic and phenotypic levels while at phenotypic levels days to siliqua maturity (-0.485) showed strong association with number of secondary branches per plant. Plant height (-0.419, -0.353) and number of primary branches (-0.502, -0.375) showed negative and non-significant correlation at both levels whereas days to siliqua maturity (-0.692) was negatively associated at only genotypic level (Table 7). Malik *et al.* (2000) and Mekonnen *et al.* (2014) revealed that correlation between number of secondary branches and days to flower completion, day to maturity, siliqua length, seeds per siliqua and 1000-seed weight was negative and non-significant both at genotypic and phenotypic levels.

4.2.6 Siliqua length (cm)

Siliqua length (cm) was positively and significantly correlated with 1000 seed weight (0.814, 0.569) and yield per plant (0.807, 569) at both genotypic and phenotypic index while number of secondary branches per plant (0.467) and number of seeds per siliqua (0.455) had significant only at phenotypic level and positively but non-significantly at genotypic index towards siliqua length (Table 7). This findings were supported by Hussain *et al.* (2014), Siddique *et al*. (2017) and Kumar *et al.* (2021) where, they observed siliqua length had significant and positive correlation with seeds per siliqua, siliqua per plant, 1000 seed weight and seed yield per plant. Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. Rashid *et al.* (2015) also reported that siliqua length had a positive and insignificant effects on seed yield. Significant negative correlation was found for siliqua length with days to first flowering (-0.457) and days to 50% flowering (-0.451) at phenotypic level only. However, negative association was also found in days to siliqua maturity (-0.592, -0.177), plant height (-0.023, -0.096) and number of primary branches per plant (-0.251, -0.357) with siliqua length at both level (Table 10). According to Jamali *et al.* (2016) Agricultural *et al.* (2020), siliqua length was negatively associated with days to flowering, days to maturity, number of primary branches per plant and number of siliquae per plant that was similar to the research findings be undertaken.

4.2.7 Siliqua per plant

Siliqua per plant showed strong significance and positive attitudes towards days to first flowering (0.829, 0.689) and days to siliqua maturity (0.914, 0.661) at genotypic and phenotypic levels while days to 50% flowering (0.506) and plant height (0.558) showed positive and significant association towards siliqua per plant at phenotypic level only (Table 7). It was supported by Gangapur *et al*. (2009) and Kumari *et al.* (2017) who reported that number of siliqua per plant had positively and strongly correlated with number of seeds per siliqua and yield per plant at both genotypic and phenotypic levels. Negative correlation was found with harvest index (-0.214, -0.285) for siliqua per plant both at the genotypic and phenotypic levels. Again, number of primary branches per plant (-0.008,0.026) and siliqua length (-0.031, 0.138) expressed negative association at genotypic level with siliqua per plant but positive at phenotypic index while number of secondary branches per plant (-0.359) showed negative correlation at phenotypic level. Siddique *et al.* (2017) and Devi *et al.* (2018) also reported on negative association of siliqua per plant with siliqua length, 1000 seed weight and harvest index at both levels.

4.2.8 Number of seeds per siliqua

In case of number of seeds per siliqua, number of secondary branches (0.518) and siliqua length (0.455) showed positive significance at phenotypic level. Positive association was found with 1000 seed wight (0.271, 0.166) and harvest index (0.305, 0.130) at both genotypic and phenotypic levels which was non-significant whereas number of primary branches (0.009), number of secondary branches (0.673) and siliqua length (0.555) showed positiveness only at genotypic level (Table 7). Jamali *et al*. (2016) and Rauf and Rahim, (2018) similarly estimated positive and strong significance with yield per plant both at genotypic and phenotypic level. Strong significance and negative correlation were observed in days to first flowering (-0.904, -0.629), days to 50% flowering (-0.992, -0.710), days to siliqua maturity (-0.998, -0.643) and plant height (-0.981, -0.671) with number of seeds per siliqua both at genotypic and phenotypic index. Number of seeds per siliqua was negatively but non-significantly associated with siliqua per plant (-0.587, -0.315) at both levels. Dawar *et al.* (2018) reported negative association was present in case of seeds per siliqua with days to 50% flowering, plant height, siliqua length, number of siliqua and 1000 seed weight.

4.2.9 Thousand seed weight (g)

In case of thousand seed weight, siliqua length (0.814, 0.509) and yield per plant (0.791, 0.722) showed positive and significant correlation at both genotypic and phenotypic levels while number of secondary branches (0.491) expressed positive and significant correlation with thousand seed weight only at phenotypic levels. Positive and non-significant association was also found in days to siliqua maturity (0.085, 0.098), plant height (0.181, 0.153), number of seeds per siliqua (0.271, 0.166) and harvest index (0.171, 0.109) at both levels (Table 7). Similarly, Yadava *et al*. (2011), Maurya *et al.* (2012) and Kumari *et al*. (2017) observed that thousand seed weight exhibited significant positive correlation with siliqua length and number of seeds per siliqua. Negative correlation was observed in days to first flowering (-0.224, -0.188), days to 50% flowering (-0.269, -0.238) and number of primary branches per plant (-0.457, -0.404) at both genotypic and phenotypic levels with thousand seed weight. Negative association with days to flowering, number of branches per plant, number of siliqua per plant and seeds per siliqua for thousand seed weight was supported by May and Jetir, (2022).

4.2.10 Yield per plant (g)

Yield per plant was significantly and positively correlated with siliqua length (0.807, 0.569) and 1000 seed weight (0.791, 0.722) both at genotypic and phenotypic levels

(Table 7). However, positive but non-significant correlation was also observed in days to siliqua maturity (0.167, 0.117), plant height (0.343, 0.317), number of secondary branches (0.539, 0.458), siliqua per plant (0.253, 0.245) and thousand seed weight (0.171, 0.109) with yield per plant at both genotypic and phenotypic levels. These positive association indicating, increasing siliqua length and 1000 seed weight was highly attributed to the improvement of yield per plant. Jamali *et al*. (2016) and Siddique *et al.* (2017) reported seed yield per plant had positive association with strong significance with plant height and number of siliquae per plant. Yield per plant was negatively correlated with days to first flowering (-0.226, -0.227), days to 50% flowering (-0.058, -0.065), number of secondary branches (-0.177, -0.152) and number of seeds per siliqua (-0.086, -0.049) at both levels (Table 10). Jahan (2006) studied correlation and revealed that yield per plant showed negative association with non-significance with days to 50% flowering while Halder *et al.* (2014) reported that seed yield had significant negative correlation with days to flowering.

4.3 Mean performance of F_1 hybrids derived from 7x7 half diallel mating design

Morphological characterization of 21 F_1 hybrids along with their parents was carried out to distinguish among the populations. 12 quantitative characters were chosen to select the best suited lines. The results of characterization of each genotype obtained from the half diallel mattings of the selected varieties of *Brassica juncea* based on the selected parameters are represented in Table 8 and Table 9.

4.3.1 Days to first flowering

Significant variation was observed for days to first flowering with a mean sum of square 19.68 (Table 8). Duration for first flowering ranged from 33.33 DAS to 43.67 DAS with an average value of 37.88 DAS. In case of crossings, the minimum value was observed in hybrid G3 (33.33 DAS), nearly similar value was also observed in G6 (34.33 DAS), G8 (35.33 DAS) and G1(35.67 DAS) whereas among the parental line P1 (35.67 DAS) required the minimum duration for flower initiation (Table 9). On the contrary, the maximum duration was seen in G20 (43.67 DAS) followed by G17 (40.33 DAS) and G18 (40.33 DAS) in cross combinations and among parents, P6 (43.00 DAS) was the highest in first flowering (Table 9). The result was almost similar with Patel *et al*. (2019) who observed days to first flowering for different line and varieties of *Brassica juncea* ranged from 35.33 to 49.00 days after sowing.

Table 8. Analysis of variance (ANOVA) for twelve yield attributing traits of 21 F_1 hybrids with their parents

Sources	d.f	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
Replications	2	1.15	4	6.87	13.02	0.02	0.10	0.01	419.10	0.09	0.05	0.50	0.53
Genotypes	27	19.68**	16.68**	21.19**	261.44**	4.23**	17.03**	0.39**	5884.04**	2.66**	0.42**	38.03**	12.39**
Error	54	1.79	2.04	9.17	18.85	0.05	0.24	0.03	139.99	0.24	0.02	0.32	1.43

****: Significant at 1% level of probability** ***: Significant at 5% level of probability**

Note:

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

Table 9a. Mean performance of yield and yield contributing traits of 21 F_1 hybrids with their 7 parents of *Brassica juncea*.

Genotype	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
Parents												
P1	35.67GHI	43.67E-J	102.67I	138.33M	4.33P	7.44OP	4.36F-I	210.33KL	13.69CDE	3.27DEF	7.18NO	29.48E-H
P2	37.33E-H	45.00C-G	103.33HI	143.28I-M	3.67QR	7.11PQ	4.01KL	189.67M	13.11D-J	3.87I-L	5.10P	31.82ABC
P3	39.67CD	44.67C-H	105.00E-I	140.45KLM	3.89Q	6.56QR	4.12I-L	223.33I-L	13.33D-G	2.97HIJ	5.57P	28.66F-I
P4	39.00CDE	43.67E-J	104.00GHI	158.89BCD	6.67QR	6.89PQ	4.38F-I	216.89JKL	13.19D-I	3.07F-I	6.55O	26.19JK
P5	42.00AB	49.33B	109.67A-E	170.56A	3.33R	6.89PQ	4.17I-L	238.89HI	12.55G-J	3.33DE	7.32NO	29.35E-H
P6	43.00A	53.00A	108.33A-G	162.06BC	4.78O	5.89R	4.00KL	228.11IJK	12.41IJ	2.80JKL	5.54P	26.35JK
P7	37.67D-G	47.00BC	105.67D-I	156.78CDE	4.00PQ	7.11PQ	4.25H-K	210.56KL	12.72F-J	3.07F-I	7.99N	29.61E-H
Cross combinations												
G1	35.67GHI	42.00IJ	111.33AB	143.56I-M	5.11MNO	10.11H-K	4.28G-J	265.67EFG	12.92E-J	3.27DEF	15.27CD	30.92B-E
G2	36.00F-I	43.67E-J	108.00A-H	137.33M	4.89NO	10.33G-J	4.500D-H	248.78GH	13.63CDE	2.67LM	14.87C-F	30.81B-E
G3	33.33J	41.67J	108.33A-G	150.33E-I	5.67JKL	9.89I-L	5.03B	294.33CD	13.37DEF	3.67AB	13.95F-I	29.30E-H
G4	37.00E-H	44.33D-I	107.67A-H	139.33KLM	5.33LM	10.67F-I	3.95L	262.44EFG	10.99K	2.73KLM	12.22LM	28.02HIJ
G5	36.00F-I	43.00F-J	112.00A	138.45LM	6.00G-J	12.00CD	4.56DEF	301.22C	12.81F-J	3.20D-G	12.31LM	25.58K
G6	34.33IJ	41.67J	110.67ABC	146.00H-K	5.44KLM	10.11H-K	4.33F-I	268.22EF	12.29K	3.57BC	11.83M	26.18JK
G7	39.00CDE	44.00D-J	105.67D-I	148.78G-J	6.56DEF	10.78E-H	4.54D-G	340.44AB	13.22D-H	2.53M	16.89A	33.53A
G8	35.33HIJ	42.33HIJ	106.00C-I	149.11F-J	7.56A	8.22NO	4.47E-H	211.00JKL	14.74AB	3.80A	13.43IJK	28.46GHI
G9	37.67D-G	44.33D-I	108.67A-G	153.22D-G	7.22AB	11.55CDE	4.66DE	272.78EF	13.11D-J	2.87I-L	15.52BC	31.70A-D

Genotype	DFF	D50%F	DPM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
G10	40.33BC	42.33HIJ	112.33A	142.78J-M	6.89BCD	12.22C	4.75D	357.33A	12.37J	2.90IJK	14.20E-I	29.88C-H
G11	40.33BC	46.33CD	109.33A-F	163.00BC	6.70D	14.72A	4.51D-H	310.78C	12.68F-J	3.27DEF	16.31AB	32.68AB
G12	36.00F-I	42.67G-J	104.67F-I	142.11J-M	5.11MNO	9.22L	4.76CD	261.89FG	13.63CD	3.00G-J	13.52HIJ	28.73F-I
G13	36.00F-I	46.00CDE	106.00C-I	164.11AB	6.33EFG	13.11B	5.31A	333.00B	12.59F-J	3.67AB	13.91GHI	29.76D-H
G14	38.00DEF	44.67C-H	107.00B-I	141.67KLM	5.89HIJ	8.33MN	4.57DEF	230.33HIJ	13.78CD	2.87I-L	14.01F-I	29.58E-H
G15	35.67GHI	44.67C-H	107.00B-I	145.22I-L	6.78CD	11.11EFG	4.03JKL	296.22CD	13.11D-J	3.37CD	14.43D-H	30.22C-G
G16	37.67D-G	43.67E-J	108.67A-G	152.67D-H	5.22MN	9.11LM	4.72DE	299.22CD	13.22D-H	3.77AB	12.54KLM	27.14IJK
G17	36.00F-I	44.00D-J	110.33A-D	157.56BCD	6.22FGH	15.11A	3.91L	305.55C	14.30BC	3.03GHI	12.02LM	26.35JK
G18	39.67CD	45.33C-F	104.33GHI	163.00BC	6.67DE	9.56JKL	5.07AB	281.56DE	13.23D-H	3.70AB	15.11CDE	30.32C-G
G19	40.33BC	44.33D-I	110.67ABC	156.11C-F	6.11GHI	9.44KL	5.02BC	205.78LM	15.11A	3.13E-H	14.83C-G	30.43C-F
G20	43.667A	43.67E-J	109.33A-F	154.37D-G	7.11BC	11.01EFG	4.57DEF	274.67EF	11.04K	2.87I-L	12.80JKL	28.06HIJ
G21	38.33CDE	44.00D-J	108.00A-H	143.67I-M	6.78IJK	11.33DEF	4.66DE	264.22EFG	12.44HIJ	3.87A	14.04F-I	30.36C-G
Min.	33.33	41.67	102.67	137.33	3.33	5.89	3.91	189.67	10.99	2.53	5.10	25.58
Max.	43.67	53.00	112.33	170.56	7.56	15.11	5.31	357.33	15.11	3.87	16.89	33.53
Mean	37.88	44.46	107.67	150.09	5.58	9.85	4.48	264.40	13.02	3.18	12.12	29.27
CV (%)	3.54	3.22	2.81	2.89	3.98	4.99	3.66	4.47	3.73	3.89	4.70	4.09
LSD	2.19	2.34	4.95	7.11	0.36	0.81	0.27	19.37	0.79	0.20	0.93	1.96

Note:

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

4.3.2 Days to 50% flowering

Days to 50% flowering showed significance variation with the mean sum of square was 16.68 (Table 8). The estimated value varied from 41.67 DAS to 53.00 DAS with a mean value of 44.46 DAS. Mishra and Nath (2022) reported days to fifty percent flowering extended from 47 to 57.33 days in *B. juncea* species. The estimates showed that G3 (41.67 DAS) and G6 (41.67 DAS) in crossings required minimum time for 50% flowering. Statistically similar value was also found in G1 (42.00 DAS), G8 (42.33 DAS) and G10 (42.33 DAS) among the cross combinations and P1 (42.67 DAS) in parental lines. On the contrary, P6 (53.00 DAS) then P5 (49.33 DAS) and in F_1 hybrids, G16 (46.67 DAS) followed by G11 (46.33 DAS) and G13 (46.00 DAS) had taken the longest duration for covering 50% flowering in the field (Table 9). Shahina (2015) and Nagoo *et al.* (2021) worked with 60 advanced lines of Indian mustard with 3 checks while they found flowering coverage of fifty percent plants need 48.00 to 69.00 days after sowing.

4.3.3 Days to siliqua maturity

The mean sum of square for this trait was 21.19 (Table 8). Duration for days to siliqua maturity among the genotypes extended from 102.67 DAS to 112.33 DAS with an average 107.67 DAS (Table 9). The minimum value was estimated in P1 (102.67 DAS) followed by P2 (103.33 DAS) and P4 (104.00 DAS) in case of parents however, cross combinations G18 (104.33 DAS) which was statistically corresponding to G12 (104.67 DAS) and G7 (105.67 DAS) showed the minimum duration. Shekhawat *et al.* (2014) estimated that 80% plants in a line became matured within 121.00 to 141.00 days after sowing. While Shahina (2015) and Nagoo *et al.* (2021) found *Brassica juncea* species required 196.00 to 228.00 DAS for days to maturity. On the contrary, F_1 lines G10 (112.33 DAS) need the maximum duration which was statistically corresponding to G5 (112.00 DAS), G1 (111.33 DAS) and P5 (109.67 DAS) followed by P6 (108.33 DAS) in parents for days to siliqua maturity.

4.3.4 Plant height (cm)

Plant height showed strong significance with a mean sum square of 261.44 (Table 8). The estimates for plant height were ranged from 137.33 cm to 170.56 cm with a mean value of 150.09 cm (Table 9). The highest plant height was found in P5 (170.56 cm) preceded by P6 (162.06 cm) and P4 (158.89 cm) among the parental lines. In cross combinations, G13 (164.11 cm) followed by G11 (163.00 cm) and G18 (163.00 cm) also indicated that they were nearly similar with the highest value. Akoju *et al.* (2020) carried out an experiment with 38 genotypes of Indian mustard who found plant height was ranged from 108.00 to 168.00 cm. However, the lowest value was estimated in G2 (137.33 cm) which was corresponding to G5 (138.45 cm), G4 (139.33 cm) and G14 (141.67 cm) and in parents P1 (138.33 cm) among the crossings. These estimations were also supported by Patel *et al.* (2019) who reported that plant height of *Brassica juncea* species ranged from 142.00 cm to 165.00 cm.

4.3.5 Number of primary branches per plant

The number of primary branches per plant was ranged from 3.33 to 7.56 with an average 5.58. In crossing lines, G8 (7.56) was recorded for holding the highest number of primary branches per plant followed by G9 (7.22), G20 (7.11), and G10 (6.89) while parental lines P4 (6.67) was the maximum in primary branch production (Table 9). On an average 5.78 to 10.67 primary branches was observed by Mishra and Nath (2022) for different lines and their parents of *Brassica juncea*. The lowest value was found in P5 (3.33) which was similar with P2 (3.67). Among the crossings, G2 (4.89) preceded by G1 (5.11) and G12 (5.11) was the lowest in number of primary branches per plant. The mean sum square for the trait was 4.23 (Table 8). Similar range of primary branches was also observed in Gangapur *et al.* (2009a) findings.

4.3.6 Number of secondary branches per plant

Data revealed significant variation was present in number of secondary branches per plant with the mean sum square of 17.03 (Table 8). The estimated value was varied from 5.89 to 15.11 with an average 9.85. In crossings, G17 (15.11) possessed the highest secondary branches. Furthermore, hybrids G11 (14.72), G13 (13.11) and G5 (12.00) as well as parental line P1 (7.44) showed that their values were also higher in case of number of secondary branches per plant (Table 9). Yadava *et al.* (2011) found that secondary branches per plant ranged from 11.95 to 17.73. The lowest value was found in P6 (5.89) followed by P3 (6.56) in parents whereas in cross combinations, it was the lowest in G8 (8.22), G14 (8.33) and G16 (9.11). It was supported by Akoju *et al.* (2020) who narrated, each plants of *Brassica juncea* genotypes produced 6.00 to 17.00 secondary branches per plant.

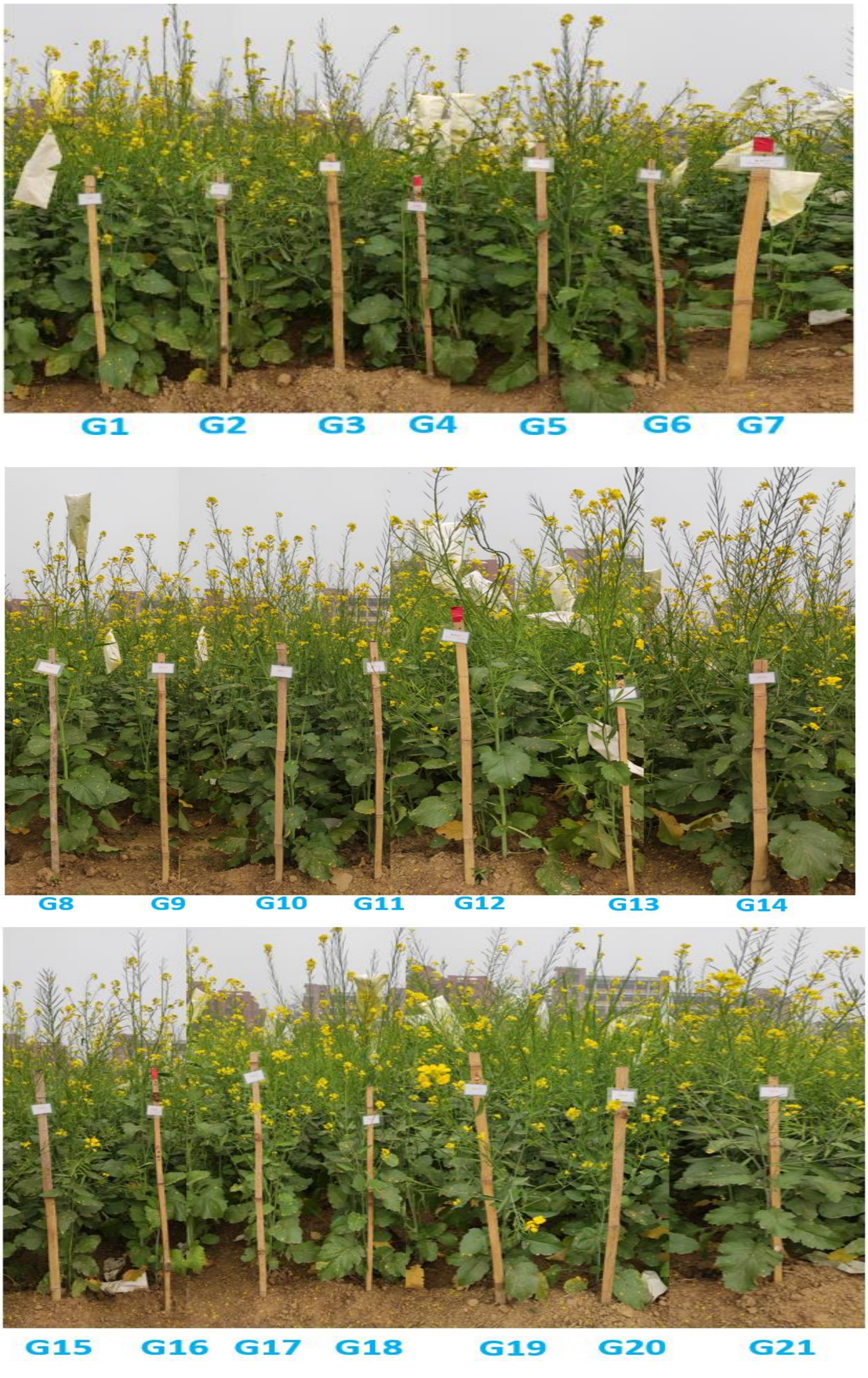
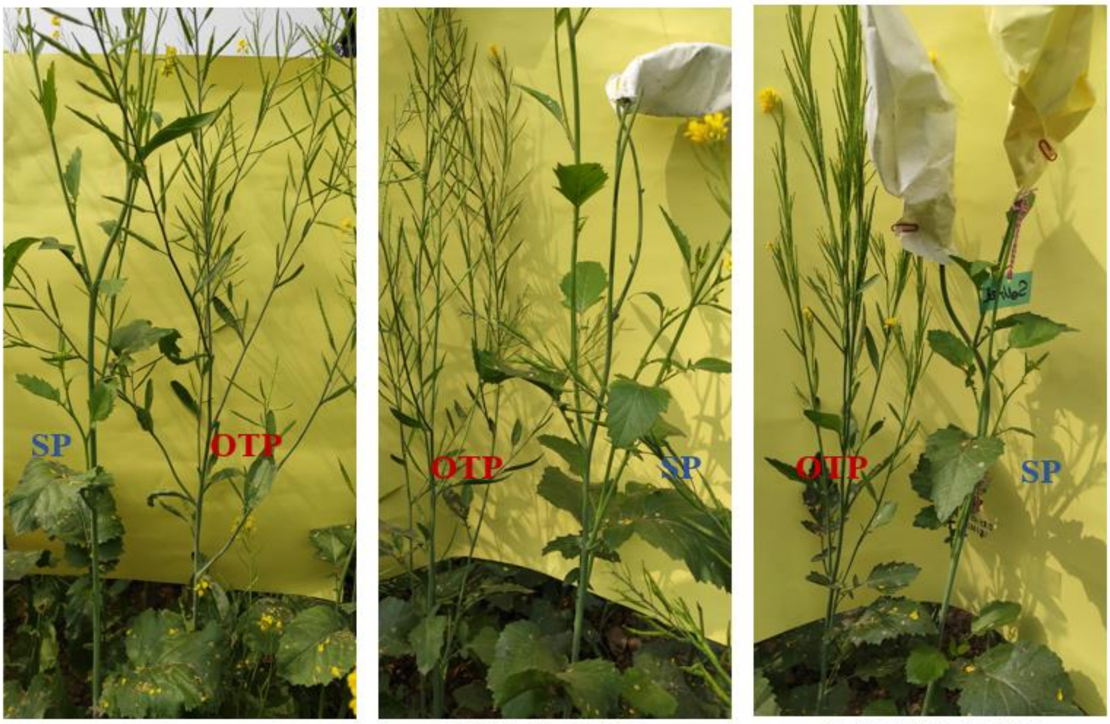
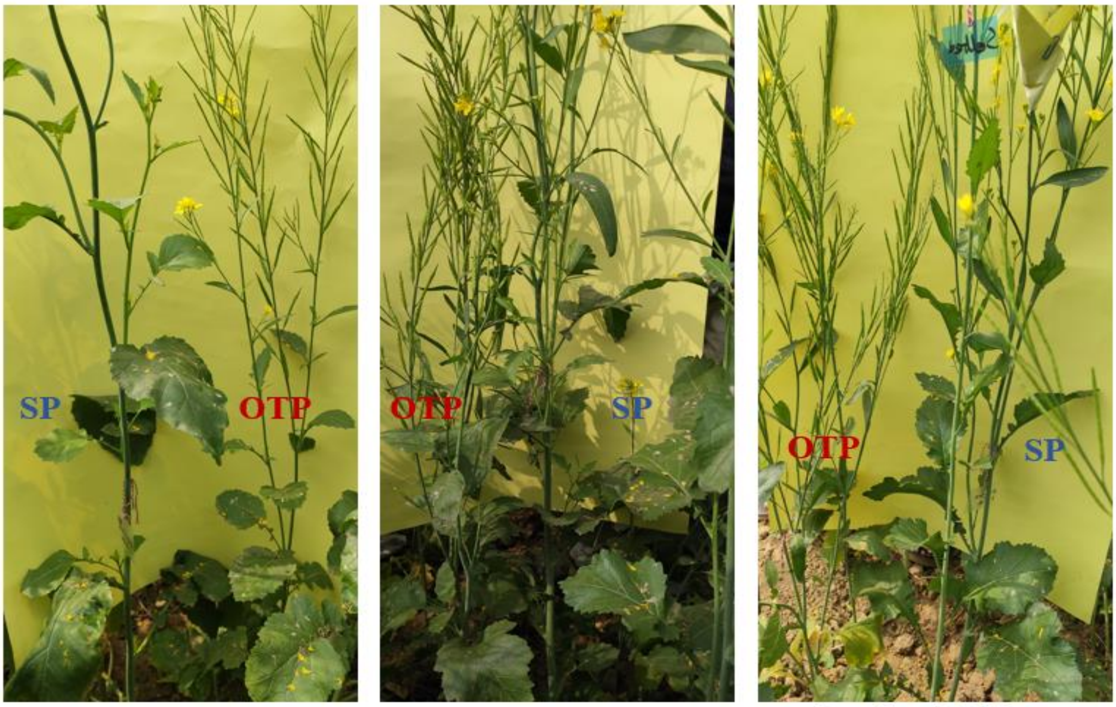


Plate 7: Growing stage of 21 F_1 lines obtained from the seed of 7×7 half diallel crosses.



BARI16×BJ00 BINA7×BJ00 BARI10×BJ00



Rye5×BJ00 BARI11×BJ00 Daulat×BJ00

Plate 8: Selection of F_1 hybrids plants based on stem vigor, color and leaf shape.

Note: SP- Selected plant, OTP- Off type plant.

4.3.7 Siliqua length (cm)

The estimated mean sum square for siliqua length was 0.342 (Table 8). Siliqua length (cm) of different lines ranged from 3.91 cm to 5.31 cm with a mean value of 4.48 cm. The highest siliqua length was observed in hybrids G13 (5.31 cm) which was statistically similar with G18 (5.07 cm), G3 (5.03 cm) and G19 (5.02 cm) while parent P4 (4.38 cm) and P1 (4.36 cm) had longer siliqua. Patel *et al.* (2021) estimated length of siliqua for different F_2 lines was extended from 3.68 to 5.46 cm. Whereas the lowest value was found in G17 (3.91 cm) followed by G4 (3.95 cm) and P2 (4.00 cm) and P6 (4.01 cm) among parents in case of siliqua length (Table 9). Gangapur *et al*. (2009a) and Dawar *et al.* (2018) also reported siliqua length lies between 3.00 to 6.00 cm. Siliqua length (cm) of different individuals were shown in Plate 10.

4.3.8 Siliqua per plant

In case of siliqua per plant, significant variation was found among the genotypes with mean sum of square 5884.04 (Table 8). Siliqua number ranged from 189.67 to 357.33 whereas the average number was 264.40. Among the cross combinations, the maximum siliquae were found in G10 (357.33), similar results were also observed in G7 (340.44), G13 (333.00) and G11 (310.78). Parents, P5 (238.89) followed by P6 (228.11) showed the highest in siliqua yielding per plant that indicated good yielding capacity of a plant. Obtained research findings were sorted by Yadava *et al.* (2011) who found each plant generated 223.23 to 482.60 siliqua. The lowest number was estimated in P2 (189.67) followed by P1 (210.33) and P7 (210.56) besides, hybrids G19 (205.78), (211.00) and G14 (230.33) similarly showed the lowest content in siliqua production (Table 9). Siliqua number ranged from 212.26 to 293.25 estimated by Yadava *et al*. (2004) in *Brassica juncea* species and the derived F_1 lines.

4.3.9 Seeds per siliqua

Seeds per siliqua extended from 10.99 to 15.11 with a mean value of 13.02 (Table 9). Czern (2020) observed seeds per siliqua varied from 11.90 to 14.05 among the genotypes and their derived lines of *B. juncea* species. Among the cross combinations, the maximum number of seeds was observed in G19 (15.11) which was statistically corresponding to G8 (14.74), G13 (14.30), G14 (13.78) and parent P1 (13.89). On the

Plate 9a: Plant height of different parents (P) of *Brassica juncea* L. (P1-P4)

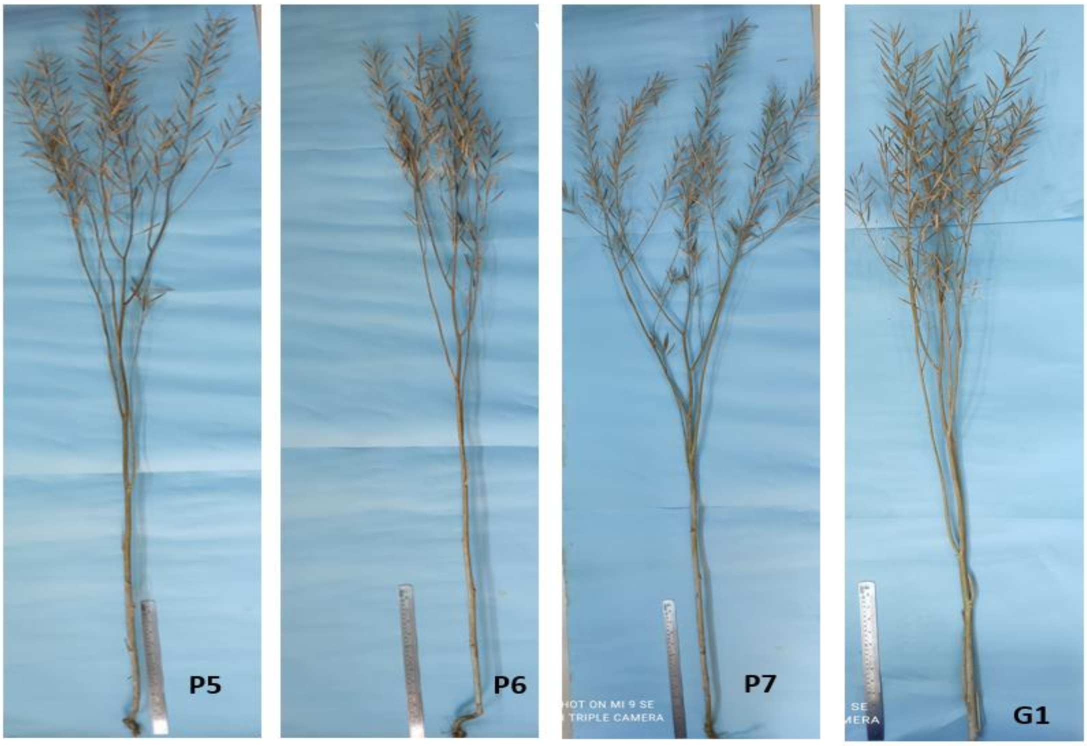


Plate 9b: **Plant height of different parents (P) of *Brassica juncea* (P5-G1)**

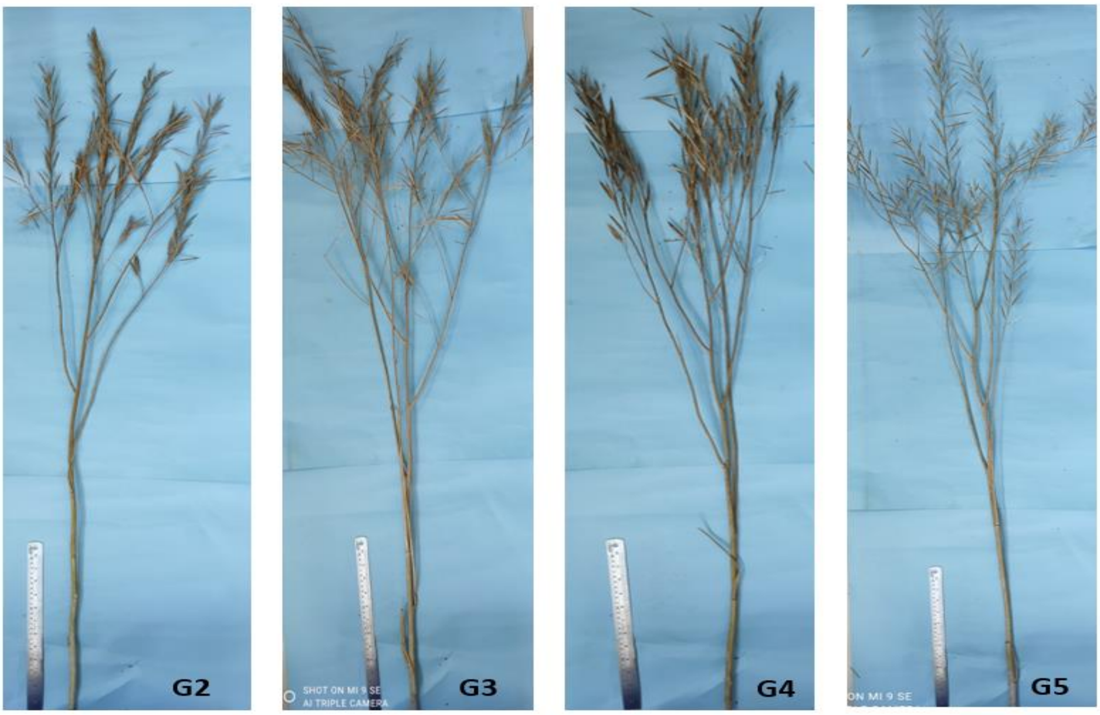


Plate 9c: Plant height of different F$_1$ hybrid lines (G) of *Brassica juncea* (G2-G5)

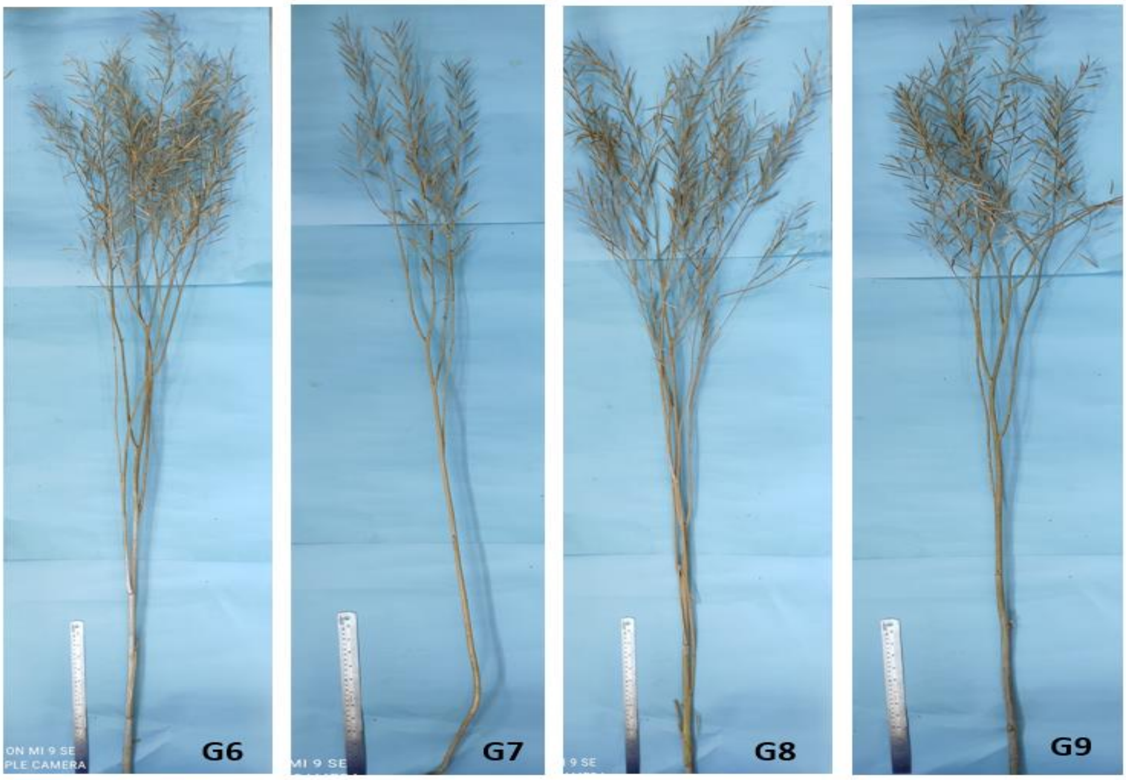


Plate 9d: Plant height of different F$_1$ hybrid lines (G) of *Brassica juncea* (G6-G9)

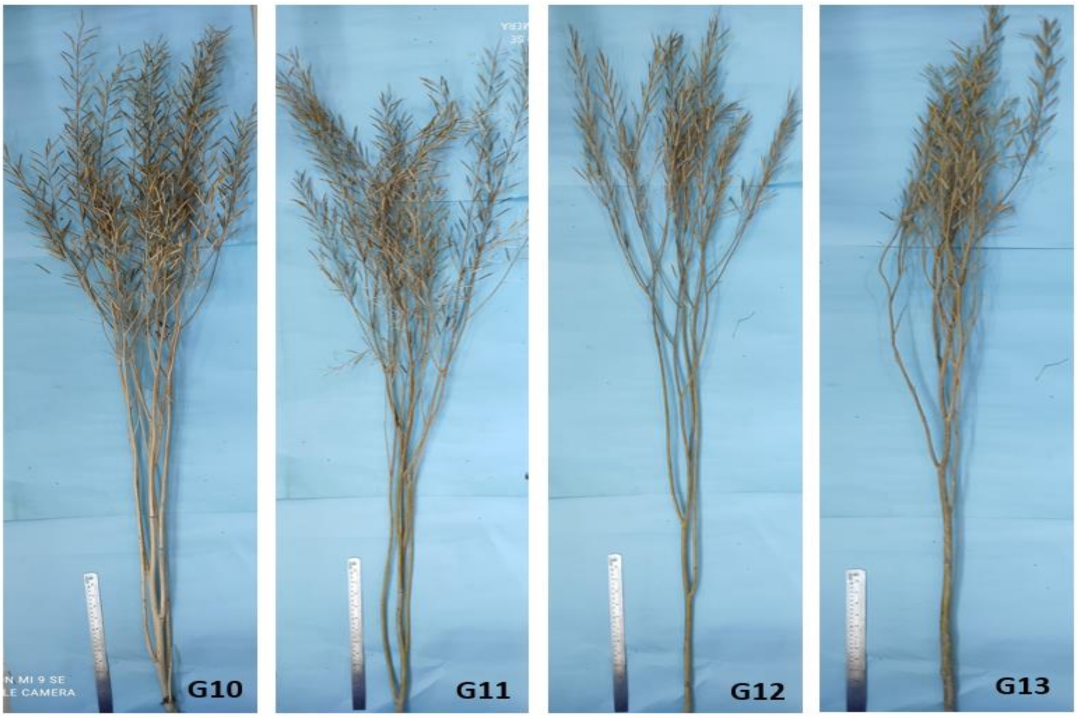


Plate 9e: Plant height of different F₁ hybrid lines (G) of *Brassica juncea* (G10-G13)

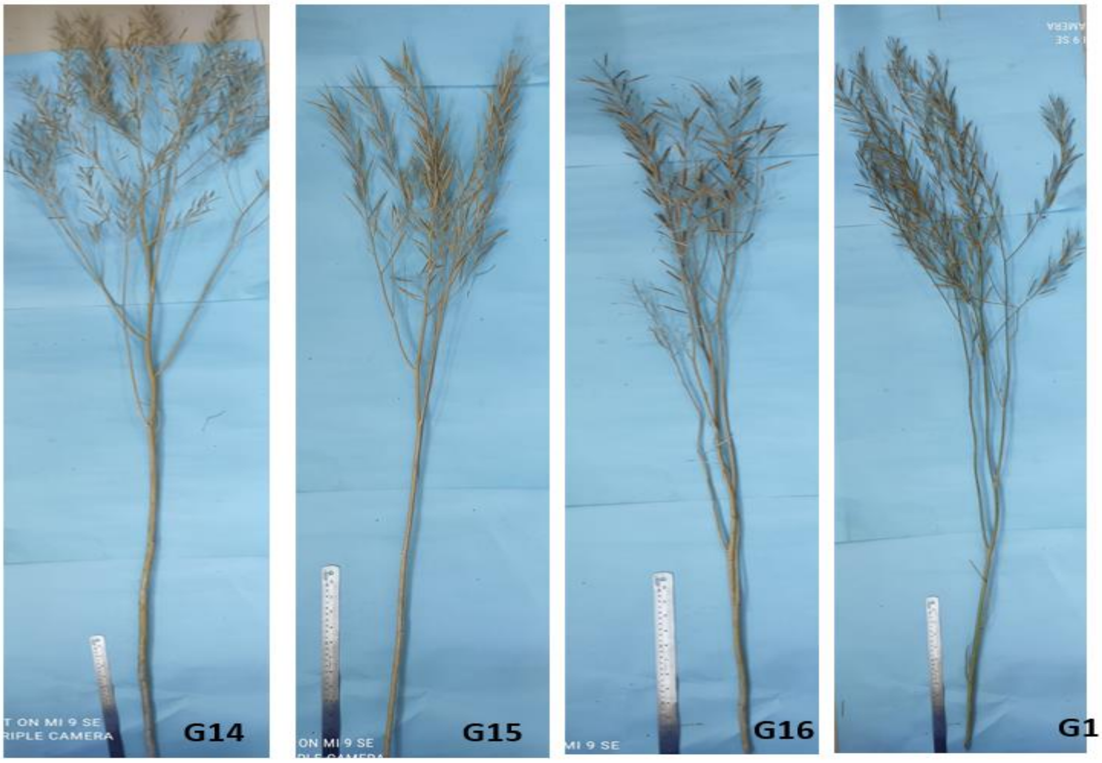


Plate 9f: Plant height of different F₁ hybrid lines (G) of *Brassica juncea* (G14-G17)

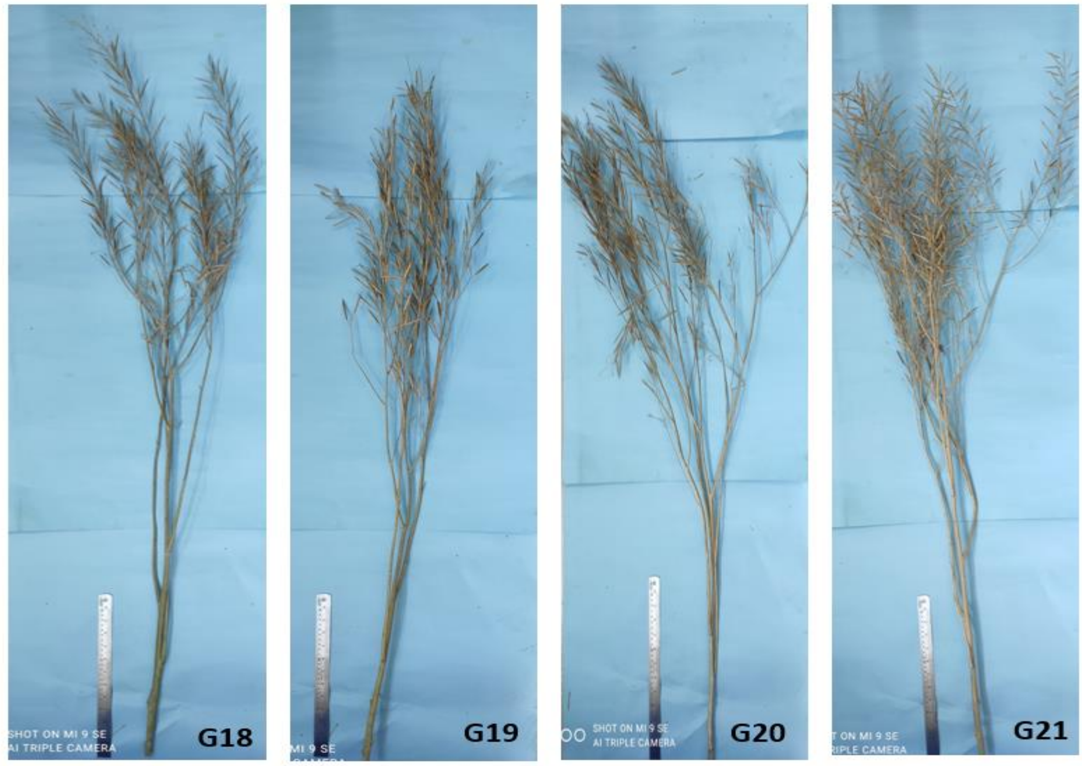


Plate 9g: Plant height of different F$_1$ hybrid lines (G) of *Brassica juncea* (G18-G21)

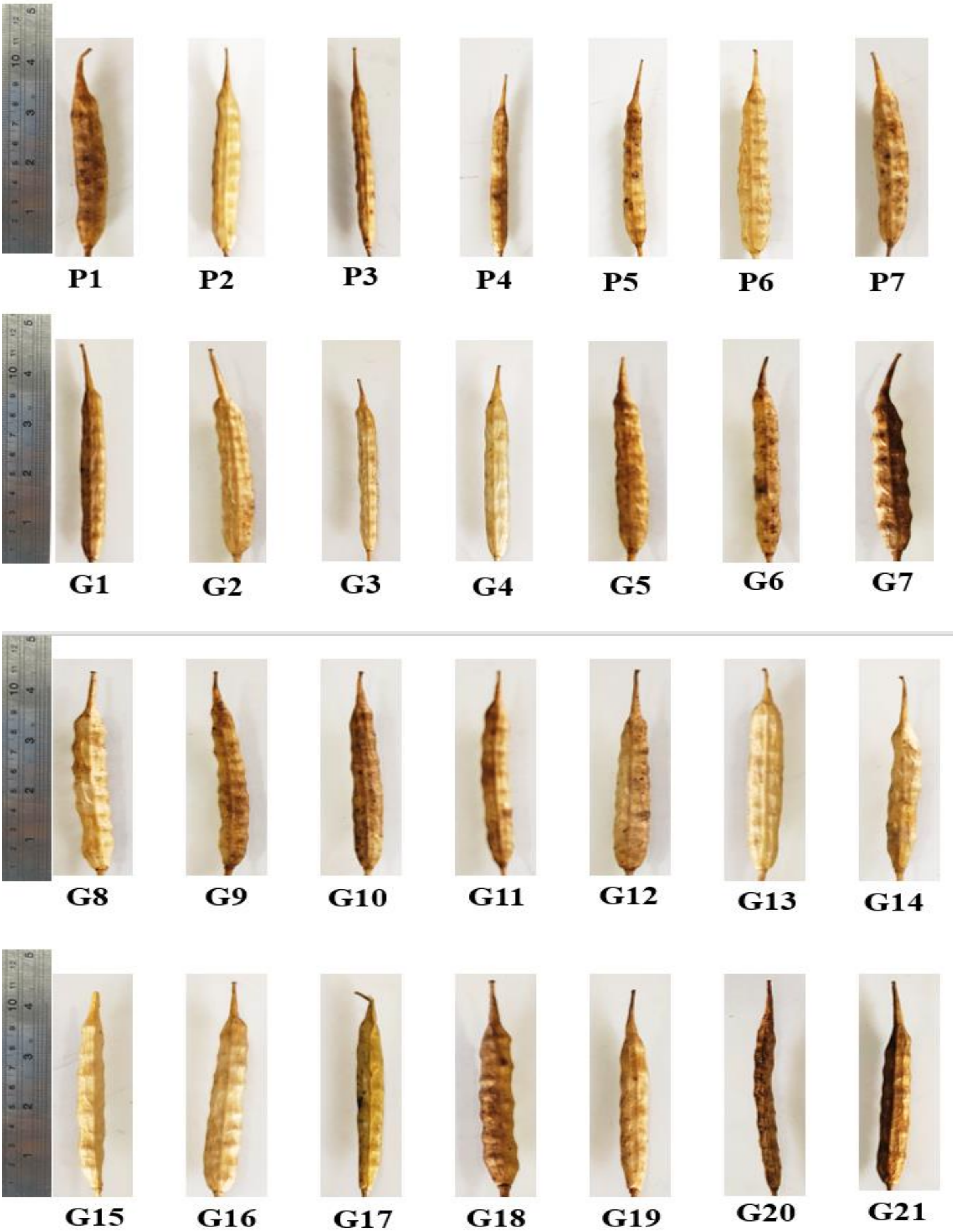


Plate 10: Siliqua length variation among the 21 F_1 lines (G1-G21) and their 7 parents (P1-P7) of *Brassica juncea*.

other hand, the minimum value was found in G4 (10.99) followed by G20 (11.04), G6 (12.29) and P6 (12.41) for seeds per siliqua (Table 9). Mean sum square for the trait was 2.66 (Table 8). Ali *et al*. (2013) and Tripathi *et al*. (2019) also reported that seeds per siliqua in *Brassica juncea* species ranged from 11.6 to 16.2.

4.3.10 Thousand seed weight (g)

Significant variations were observed in 1000 seed weight with the mean sum of squares 0.05 (Table 8). Seed weight among the populations were ranged from 2.53 g to 3.87 g and the average 1000 seed weight was 3.18 g (Table 9). The highest value for thousand seed weight was estimated in G21 (3.87 g) followed by G8 (3.80 g), G16 (3.77 g) and G18 (3.70 g) whereas the lowest value was observed in G7 (2.53 g) preceded by G2 (2.67 g) and G4 (2.73 g) in case of F_1 hybrids. Patel *et al.* (2019) estimated 1000 seed weight ranged from 4.13 g to 5.97 g per plant while 1000 seed weight ranged from 1.25 to 6.25 g was found by Czern (2020). Among the parental lines, P2 (3.87 g) and P5(3.33 g) had the maximum value for 1000 seed weight. (Table 12). Similar statement was reported by Patel *et al*. (2021) where 1000 seed weight was ranged from 3.59 g to 6.14 g per plant.

4.3.11 Yield per plant (g)

The estimates for yield per plant revealed significant variation was present among the genotypes where the mean sum of square was 38.03 (Table 8). The yield per plant ranged from 5.10 g to 16.89 g with mean 12.12 g. The highest yield was observed in G7 (16.89 g) which was statistically similar with G11 (16.31 g), G9 (15.52 g) and G1 (15.27 g) among F_1 populations and P7 (7.99 g) in parents (Table 9). This report was supported by Mandal *et al.* (2022) who estimated seed yield per plant was ranged from 6.58 to 14.48 g. The lowest value was found in P2 (5.10 g) followed by P6 (5.54 g) and P3 (5.57 g) in parental lines and in case of crossings, G6 (11.83 g), G17 (12.02 g) and G4 (12.22 g) also showed the lowest value for yield per plant. Statistically similar results were found in Shekhawat *et al*. (2014) who revealed seed yield of each plant of different varieties of *Brassica juncea* and their derivatives were varied from 14.56 g to 19.74 g.

4.3.12 Harvest index (%)

Significant variations were observed in harvest index with mean sum of squares 12.39 (Table 8). Variations among the data varied from 25.58% to 33.53% with an average 29.27%. Among the crossings, the highest value of harvest index was found in G7 (33.53%) which was statistically similar with G11 (32.68%), G9 (31.70%) and G1 (30.92%) and within the parents, P2 (31.82%) had the maximum in harvest index. G5 (25.58%) indicated the lowest value followed by G6 (26.18%) and G17 (26.35%) while P4 (26.19%) and P6 (26.35%) showed the lowest harvest index in terms of percentage value (Table 9). This findings were supported by Mishra and Nath (2022) who found harvest index ranged from 24.55% to 34.16% for different F_1 populations of *Brassica juncea*.

4.6 Combining ability analysis

4.6.1 Genetic components for combining ability effects

A parent with higher significant general combining ability (GCA) was considered as a good general combiner, that will provide a scope to transmit the positive heredity to its off springs while specific combining ability (SCA) effects signify the action of non-additive gene action in the expression of the traits. SCA acted as a source of variance with crosses and high SCA effects indicating the exploitation of heterosis (Singh *et al.,* 2011). Negative direction of combining effects were desirable for earliness and short plant. Broad sense heritability defined the proportion of phenotypic variance that was contributed to the genetic causes within the populations (Schmidt *et al.,* 2019b). High narrow sense heritability provides selection facilities on the contrary, low heritability in narrow sense indicated dominance variance which was responsible for superiority of heterozygotes. The results of different genetic components of the parents and their hybrids are presented in Table 10 and Table 11.

4.6.1.1 Days to first flowering

Analysis of variance revealed significant variation was present among GCA and SCA components. Variance of GCA (6.62) was higher than the SCA variance (2.67) indicating additive gene action was involved in the expressions of the trait (Table 11). Ratio of GCA and SCA variance (2.48) also expressed the predominance of additive gene effects. Higher heritability in broad sense (76.9%) indicating observable

Table 10. ANOVA of combining ability for twelve plant characters in 7×7 half diallel of *Brassica juncea*.

Sources	d.f	DFF	D50F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
GCA	6	42.91**	27.88**	17.33**	672.58**	1.63**	2.54**	0.12**	338.16*	2.34**	0.41**	4.17**	30.90**
SCA	21	13.05**	13.47**	34.67*	143.97**	4.98**	21.16**	0.47**	7468.58**	3.77**	0.47**	48.05**	7.10**
Error	54	1.80	2.05	9.17	18.85	0.05	0.24	0.03	139.99	0.24	0.02	0.32	1.43
GCA: SCA		3.29	2.07	0.50	4.67	0.33	0.12	0.26	0.05	0.62	0.87	0.09	4.35

****: Significant at 1% level of probability** ***: Significant at 5% level of probability**

Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, PH= Plant height (cm), DSM=Days to siliqua maturity, NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

Table 11: Genetic components of GCA and SCA in *Brassica juncea*

Genetic components	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
σ^2gca	6.62	2.61	0.36	88.54	0.40	0.56	0.02	34.62	0.80	0.10	1.06	3.04
σ^2sca	2.67	1.20	1.42	32.49	1.05	5.10	0.12	1938.16	1.45	0.12	9.42	1.43
σ^2gca/ σ^2sca	2.48	2.17	0.25	2.73	0.38	0.11	0.17	0.02	0.03	0.83	0.11	2.12
σ^2A	3.31	1.31	0.18	44.27	0.20	0.28	0.01	17.31	0.40	0.05	0.53	1.52
σ^2D	2.67	1.20	1.42	32.49	1.05	5.10	0.12	1938.16	0.55	0.12	9.42	1.43
$(\sigma^2D/\sigma^2A)^{1/2}$	0.90	0.96	2.81	0.86	2.29	4.29	3.48	8.42	1.18	1.58	5.13	0.97
h^2_b (%)	76.90	61.17	92.21	80.27	96.18	95.71	82.99	93.35	80.17	91.38	96.84	67.28
h^2_n (%)	42.52	32.80	51.02	46.28	15.43	4.98	4.94	1.31	33.56	26.75	5.13	34.72

Note:

σ^2gca= Variance of general combining ability, σ^2sca=Variance of specific combining ability, σ^2A= Additive genetic variance, σ^2D= Dominance variance, $(\sigma^2D/\sigma^2A)^{1/2}$=Mean degree of dominance, h^2_b= Broad sense heritability (%) and h^2_n (%)= Narrow sense heritability (%).

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

phenotypic expression was solely due to genetic causes along with a moderate narrow sense heritability (42.52%) was associated with this trait (Table 11). So, selection will be possible for the improvement of days to first flowering. This results were related to the findings by Sabaghnia *et al.* (2010) who reported days to flower starting was controlled by additive variance.

4.6.1.2 Days to 50% flowering

Both GCA and SCA showed significant variations among the individuals for days to 50% flowering. GCA variance (2.61) was higher than SCA variance (1.20) and their ratio (2.17) was higher than the unity level. Furthermore, additive variance (1.31) was higher than the dominance variance (1.20), hence, additive gene effects was linked for the expression of the trait. Moderate broad sense heritability and narrow sense heritability was 61.17% and 32.80%, respectively (Table 11). So, there will be a chance to maintain the uniformity of flowering over the generations. Akabari *et al*. (2017) also found higher GCA value than the SCA value while Singh *et al.* (2022) reported higher unity level in case of flowering.

4.6.1.3 Days to siliqua maturity

From the estimation of ANOVA, strong and positive significance was observed in GCA value (17.35**) while SCA (34.67*) component showed positive value for the trait (Table 10). Higher variance of SCA indicated non-additive gene action was present as well as dominance variance (1.42) was greater than the additive variance (0.18). High broad sense heritability (92.21%) was found for days to siliqua maturity means, genetic variables played a strong role in expressing the traits and high narrow sense heritability (51.02%) indicated the possibility of gene transferring that controlled the trait hence, selection might be possible based on days to siliqua maturity (Table 11). Maurya *et al*. (2014) also estimated higher SCA variance than the GCA variance, indicating additive variance was responsible for the inheritance of the trait. Opposite findings were reported by Pethe *et al.*, (2018).

4.1.6.4 Plant height (cm)

In case of plant height, higher significant variations were observed for GCA and SCA. GCA variance (88.54) was greater than that of SCA variance (32.49) and the ratio was higher than the unity which indicated the trait was controlled by additive gene effects.

Moreover, additive variance (44.27) was higher than dominance variance (Table 11). A moderate heritability in narrow sense (46.28%) was observed for plant height indicating, it is possible to bring out the dwarf plant by selection procedure, in addition to this, higher broad sense heritability (80.27%) was also estimated for plant height. Shrimali *et al.* (2016) and Meena (2017) observed both additive and non-additive gene action was predominated in plant height while Choudhary *et al.* (2000) reported maximum value for SCA variance.

4.6.1.5 Number of primary branches per plant

Estimated SCA variance (1.05) was larger than the GCA variance (0.40). So, non-additive gene action was controlled the expression of the trait and greater dominance variance (1.05) was prominent for this this trait. Number of primary branches possessed the highest value for broad sense heritability (96.18%), hence, arisen phenotypic variance was due to genetic causes (Table 11). A lower value of narrow sense heritability (15.43%) was estimated. The insignificant differences between broad and narrow sense heritability indicated dominance variance was high and heterozygotes would be superior over homozygotes. Similar results were found by Kumar *et al.* (2021) and Maurya *et al.* (2014) reported, SCA variance was larger than the GCA variance (7.19>0.765).

4.6.1.6 Number of secondary branches per plant

Significant variations were observed among the genetic components estimated in ANOVA analysis. The ratio of GCA and SCA variance was less than the unity that indicated predominancy of non-additive gene action (Table 11). Dominance variance (5.10) was larger than the additive variance (0.28). Number of secondary branches possessed higher value for broad sense heritability (95.71%), hence, arisen phenotypic variance was due to genetic causes. Singh *et al*. (2019) estimated higher SCA effects than the GCA and suggested, generating of secondary branches was controlled by the dominant genetic effects. A lower value of narrow sense heritability (4.98%) indicated dominance variance was high and heterozygotes would be superior over homozygotes suggested by Singh *et al.,* (2019).

4.6.1.7 Siliqua length (cm)

Variance of specific combining ability (0.12) was higher than the variance of general combining ability (0.02), thereby, the ratio was less than the unity indicating the predominance of non-additive gene actions. The calculated dominance variance was 0.12 (Table 11). High heritability in broad sense (82.99%) was observed in siliqua length whereas narrow sense heritability was 4.94% and heterozygotes showed the superiority over their homozygotes as the gene controlled the trait was non-fixable. So selection based on the trait was difficult for crop improvement. Maurya *et al*. (2014) and Afrose *et al*. (2019) supported this statement as they found higher SCA value for siliqua length.

4.6.1.8 Siliqua per plant

Significant and positive variations were observed within the genetic components of combining ability effects. GCA variance (34.62) was lower than the SCA variance (1938.16) and the ratio of GCA and SCA was less than the unity (Table 10). The variance effects pointed out that the expression of siliqua number was totally controlled by both additive and non-additive gene effects. High broad sense heritability (93.35%) was associated with the minimum narrow sense heritability (1.29%) that indicated cross combination had a chance to show high heterotic effects (Table 11). High broad sense coupled with low narrow sense heritability indicating negative dominance variance was predominant in controlling siliqua production. Unity level less than 1 was also reported by Akabari *et al.* (2017) indicating dominance variance was responsible for the trait while Singh *et al.* (2022) observed siliqua per plant was determined by additive gene actions.

4.6.1.9 Number of seeds per siliqua

Higher SCA variance (1.45) was found in seeds per siliqua and the unity of GCA and SCA was less than 1.00 that revealed non-additive gene action was involved in the expression of the selected trait (Table 11). Heritability in broad sense (80.17%) was higher whereas narrow sense heritability (33.56%) was moderate indicating, there will be a better chance of selecting superior individuals in next generations, so improvement of this trait will be possible in future. This was supported by Shrimali *et al.* (2016) and

Afrose *et al.* (2019) who found higher SCA variance than GCA variance for seeds per siliqua.

4.6.1.10 Thousand seed weight (g)

In case of thousand seed weight, greater SCA variance (0.12) was observed than the GCA variance (0.10) and the proportion was 0.83 that revealed both additive and non-additive gene effects were involved in thousand seed weight (Table 11). Estimated data also revealed high heritability in broad sense (91.38%) with low narrow sense heritability (26.75%). Findings were supported by Gul *et al.* (2019) who reported additive and non-additive effects were involve in 1000 seed weight expression. However, Kumar *et al.* (2021) found greater GCA than the SCA effects for the trait (Table 12).

4.6.1.11 Yield per plant (g)

Significant variation was observed among the GCA and SCA components for yield per plant. SCA variance (9.42) was greater than the GCA variance (1.06). The ratio GCA and SCA variance was less than the unity (0.11) (Table 11). Hence, dominance effects were prominent in case of yield producing ability of the individuals. In addition to this, the highest heritability in broad sense (96.84%) along with the lowest narrow sense heritability (5.13%) was estimated (Table 11). High dominance with low narrow sense heritability indicated heterozygote individuals were superior in case of yield per plant. Choudhary *et al.* (2000) and Singh *et al*. (2019) observed that seed yield was controlled by both additive and non-additive gene effects. On the contrary, Meena (2017) reported additive variance was responsible for the performance of seed yield production.

4.6.1.12 Harvest index (%)

In case of harvest index, GCA variance (3.04) was higher than the SCA variance (1.43). The proportional ratio of GCA and SCA was 2.12 that revealed additive gene effects were predominant to express the trait. High heritability in broad sense (67.28%) with moderate narrow sense heritability (34.72%) was also observable in harvest index (Table 11). This facilitated selection procedure that can be used for the improvement of the selected trait. Effects of additive gene action was reported by Sabaghnia *et al.* (2010) whereas harvest index controlled by dominance variance was reported by Singh *et al.*, (2022).

4.6.2 Analysis of general combining ability (GCA) effects

In a series of crossings, general combining ability denotes the average performance of the parents. Furthermore, the variance of GCA is due to the additive genetic variance and additive × additive gene actions. Parents having higher GCA variance is useful for generating high specific combinations. Positive and significant GCA values of a parent is considered as a good general combiner for yield and yield related improvement, in contrast, negative general combining ability effects are desirable for earliness and shorten plants. The estimated GCA effects were represented in (Table 12).

4.6.2.1 Days to first flowering

Negative GCA effects was expected for days to first flowering. Among the selected parents P1 (-2.15) possessed the highest negative significant GCA effects, regarded as the best combiner for flower initiation followed by P4 (-0.78). On the contrary, P5 (1.48) followed by P6 (1.33) had the highest positive value in case of days to first flowering (Table 12). Singh *et al.* (2019) found 2 lines among the 6 lines as good general combiners for days to first flowering in his experiment.

4.6.2.2 Days to 50% flowering

Early flowering indicated plant became matured earlier. In case of days to 50% flowering negative effects of general combining ability was desirable as it was assumed that this behavior of parents was transmitted to the off springs. Four parents showed the expected negative GCA effects, among them P1 (-1.34) was reported the best combiner line as it had the highest negative value with strong significance followed by P4 (-0.97) whereas P6 had the highest positive significant value for days to 50% flowering (Table 12). Aghao *et al.* (2010), Singh *et al.* (2010) and Nasrin *et al.* (2011) reported negative significant GCA effects for days to maturity in *Brassica juncea*.

4.6.2.3 Days to siliqua maturity

Again, negative significant GCA effects was useful for getting early matured plants. Among the parental material, four parents showed negative GCA effects however, only P3(-1.44) showed the desired negative GCA effects with strong significance and considered as best general combiner for days to siliqua maturity (Table 12) while the maximum positive and significant value was observed in P6 (1.74). Verma (2011),

Table 12. Estimates of general combining ability (GCA) for twelve characters in 7×7 half diallel population of *Brassica juncea*.

Parents	DFF	D50F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
P1	-2.15**	-1.34**	0.22	-7.72**	-0.39**	-0.09	-0.05	-5.99*	-0.20*	0.02	-0.24*	-0.49
P2	-0.01	-0.49	-0.15	-1.52	0.30**	0.34**	-0.07*	2.46	0.12	-0.12**	0.54**	1.85**
P3	-0.34	-0.08	-1.44*	-4.51**	-0.15**	-0.31*	0.01	4.68*	0.27*	-0.16**	0.20	0.65*
P4	-0.78**	-0.97**	-1.22	3.54**	-0.10*	-0.44**	0.12**	-3.10	0.52**	0.18**	-0.36**	-1.27**
P5	1.48**	1.03**	1.00	6.69**	-0.07	-0.02	0.06*	1.16	-0.33**	0.03	-0.05	-0.04
P6	1.33**	1.40**	1.74**	0.40	0.20**	0.16	-0.04	0.61	0.16	-0.10**	-0.49**	-1.02**
P7	0.48	0.44	-0.15	3.12**	0.20**	0.36**	-0.02	0.18	-0.55**	0.15**	0.40**	0.32
SE (gij)	0.24	0.26	0.54	0.77	0.04	0.09	0.03	2.11	0.09	0.02	0.10	0.21
SE (gi-gi)	0.37	0.39	0.82	1.18	0.06	0.13	0.05	3.22	0.13	0.03	0.16	0.33

**: Significant at 1% level of probability *: Significant at 5% level of probability

Note:

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

Horisaki and Niikura (2007), Shrimali *et al*. (2016) and Saeidi *et al.* (2018) found negative GCA for earliness in *B. juncea*.

4.6.2.4 Plant height (cm)

Plant height is one of the important traits for getting shorter plant. Hence, negative GCA effects was desirable. Strong significance and negative direction were found in P1 (-7.72) and P3 (-4.51). On the other hand, P5 (6.69), P4 (3.54) and P7 (3.12) showed the highest positive value with strong significance (Table 12). Similar finding for GCA effects were also reported by Atikunnahe *et al.* (2017), Singh *et al*. (2010) and Aghao *et al.*, (2010).

4.6.2.5 Number of primary branches per plant

Positive GCA effects of parent was desired to get highest number of branches per plant in cross combinations. In this sense, P2 (0.30) was considered as the best general combiner which possessed the highest positive and significant value preceded by P6 (0.20) and P7 (0.20). In contrast, 4 parents had negative value for primary branches per plant (Table 12). Choudhary *et al*. (2000) reported GCA effects of primary branches per plant was the lowest in different genotypes of *B. juncea*. However, the highest positive GCA effects for this trait was observed by Singh *et al*., (2015).

4.6.2.6 Number of secondary branches per plant

In considering to get the best general combiner for number of secondary branches per plant, the parental material P7 (0.36) showed the strong significance with positive direction which was statistically similar with P2 (0.34) while P4 (-0.44) was regarded as poor general combiner followed by P3 (-0.31). Chowdhury *et al*. (2004) estimated the highest number of parental lines as a good combiner for secondary branches in *B. juncea* and Gupta *et al.* (2011) reported different varieties of *Brassica juncea* showed significant GCA effects for this trait (Table 12).

4.6.2.7 Siliqua length (cm)

For siliqua length, three parents had positive general combining ability effects but, positive GCA effects along with strong significance was found only in P4 (0.12) that was considered as best general combiner for siliqua length. However, P2 (-0.07) followed by P6 (-0.04) was reported as the highest negative GCA effects (Table 12).

So, the improvement of the trait was difficult for the parent that containing undesired GCA effects. In case of F_1 line for siliqua length the highest positive and significant GCA effects were found by Meena (2017) while Turi *et al.* (2011) estimated the non-significant GCA effects in *Brassica juncea*.

4.6.2.8 Number of siliquae per plant

Positive and significant general combining effects was desirable for siliqua per plant as it is thought to be one of the important traits for getting high yield. Among the parent materials, five parents showed positive GCA effects and P3 (4.68) was reported as the best combiner as it possessed the highest positive and significant GCA effects and P2 (2.46) followed by P5 (1.16) showed high positive but non-significant GCA effects. So, it facilitates great opportunity for improving the yield and yield contributed traits by selecting the parents in hybridization program. On the other hand, P1 (-5.99) was poor combiner because it possessed the maximum undesired effects for number of siliqua (Table 12). Kumar *et al.* (2021) and Grace (2007) found significant variations among the parental lines where, they observed the maximum parents had positive and significant GCA effects. Gupta *et al.* (2011) and Rameeh (2011d) reported that GCA effects for number of siliquae per plant was highly significant.

4.6.2.9 Seeds per siliqua

Parent P4 (0.52) exhibited the highest positive and highly significant general combining effects followed by P3 (0.27) for the selected trait. Hence, the parent P4 can be selected as the suitable parent for getting the desirable cross combinations. Whereas P7 (-0.55) preceded by P5 (-0.33) had the highest negative GCA effects for seeds per siliqua (Table 12). Singh *et al*. (2019) found four lines that had good combining ability for seed number while Arifullah *et al*. (2012) and Atikunnahar *et al*. (2017) observed significant GCA effects in 3 lines that were good in seed production whereas Singh *et al.* (2019) found only 1 line among the 6 as a good combiner for seeds per siliqua.

4.6.2.10 Thousand seed weight (g)

The estimated result revealed that parental line P4 (0.18) exhibiting positive significance of GCA followed by P7 (0.15) and positive but non significance in P1 and P5 (Table 12) implying the tendency of the parental lines to increase the yield. However, negative and significant GCA effects were also observed in parental line P3

(-0.16) that was corresponding to P2 (-0.12). In case of 1000 seed weight Maurya *et al*. (2014) and Gul *et al*. (2019) observed most of the varieties had negative and significant GCA effects whereas Nasrin *et al*. (2011) and Turi *et al*. (2011) reported positive GCA and significant effects for majority of the line.

4.6.2.11 Yield per plant (g)

In case of yield per plant, parents having positive GCA will be selected as a promising general combiner. Among the selected parents, P2 (0.54) had the positive significant values which was considered as superior combiner for producing high yielding cultivars followed by P7 (0.40). However, P6 (-0.49) and P4 (-0.36) showed highly significant but negative GCA effects indicating, these parents were not good combiner for improving this trait (Table 12). Inayat *et al*. (2019) reported seed yield per plant among four out of eight varieties had positive effects, furthermore, Atikunnaher *et al*. (2017) and Singh *et al.* (2019) estimated 5 lines had good combining ability effects on seed yield.

4.6.2.12 Harvest index (%)

The highly significant and positive GCA effects were observed in P2 (1.85) and P3 (0.65) in addition, P7 (0.32) showed positive but non-significant GCA effects (Table 12). While little scope was found for the improvement of this trait in P4 (-1.27) followed by P6 (-1.02). Shrimali *et al.* (2016) found 4 varieties out of 10 that could be used in breeding program for improving this trait and Singh *et al*. (2019) found 2 within 5 as a good harvest index combiner.

4.6.3 Analysis of specific combining ability (SCA) effects

Specific combining ability (SCA) effects was denoted to hybrid combination that is better or worse than expected. Effects of SCA was arisen due to dominance and all the three types of gene actions viz, dominance, additive x dominance, dominance x dominance effects responsible for high performance of a specific cross combinations. The magnitude and direction of the significant effects for the selected parents given meaningful comparisons and a notion to the future breeding program. Estimated specific combining ability effects for twelve characters of the parental lines are presented in Table 13.

Table 13. Estimates Specific Combining Ability (SCA) for twelve characters in 7×7 half diallel populations of *Brassica juncea*.

F_1 Hybrids	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
G1	-0.056	-0.639	3.593*	2.712	-0.38**	0.013	-0.075	4.794	-0.024	0.186**	2.848**	0.294
G2	0.611	0.62	1.556	-0.525	-0.153	0.884**	0.063	-14.316*	0.536*	-0.377**	2.785**	1.383*
G3	-1.611*	-0.491	1.667	4.426*	0.575**	0.565*	0.482	39.017**	0.023	0.282**	2.435**	1.792**
G4	-0.204	0.176	-1.222	-9.726**	0.218	0.922**	-0.534	2.867	-1.496**	-0.495**	0.392	-0.722
G5	-1.056	-1.528*	2.37	-4.325*	0.612**	2.082**	0.173**	42.203**	-0.174	0.094	0.925*	-2.168**
G6	-1.87**	-1.898**	2.926*	0.509	0.051	-0.012	-0.076	9.631	-0.979**	0.219**	-0.449	-2.968**
G7	1.463*	0.102	-0.407	4.725*	0.819**	0.901**	0.118	68.902**	-0.192	-0.369**	4.029**	1.759**
G8	-1.759**	-0.676	-0.296	-2.993	1.77**	-1.528**	0.136	-52.762**	1.075**	0.559**	1.135*	-1.388*
G9	-1.685*	-0.676	0.148	-2.036	1.41**	1.382**	-0.003	4.756	0.302	-0.221*	2.909**	0.614
G10	1.13	-3.046**	3.074*	-6.192**	0.807**	1.879**	0.377	89.868**	-0.935**	-0.066	2.032**	-0.211
G11	1.981**	1.917*	1.963	11.313**	0.613**	4.175**	0.125	43.746**	0.086	0.06	3.258**	1.239*
G12	-0.759	-0.75	-0.333	-7.007**	-0.23	0.117	0.148	-4.095	-0.185	-0.206**	1.56*	0.088
G13	-3.019**	0.583	-1.222	11.841**	0.97**	3.59**	0.756**	62.759**	-0.368	0.616**	1.643**	-0.117
G14	-0.87	-1.12	-0.963	-4.315	0.254*	-1.363**	0.116	-39.355**	0.321	-0.062	2.182**	0.695
G15	-2.352**	-0.157	0.926	-3.478	1.14**	1.213**	-0.44**	26.966**	0.366	0.197**	1.715**	-0.012
G16	-0.907	-0.86	1.222	-7.651**	-0.192	-0.289	0.067	36.755**	0.013	0.375**	0.84*	-0.821
G17	-2.426**	-0.898*	2.148	3.526	0.535**	5.538**	-0.649**	43.644**	0.592*	-0.236**	0.759*	-0.62
G18	2.093**	1.398**	-1.963	6.25**	0.981**	-0.219	0.492**	20.079**	0.23	0.19**	2.958**	2.007**
G19	-0.352	-2.565**	0.259	-1.069	0.401**	-0.549*	0.525**	-60.392**	2.259**	0.019	3.259**	2.226**
G20	3.833**	-2.269**	0.815	-5.532*	1.398**	0.804**	0.046	8.929	-1.103**	-0.488**	0.338	-1.491*
G21	-1.352*	-2.306**	-1.259	-9.948**	-0.205	0.964**	0.24*	-0.962	-0.187	0.634**	2.018**	1.804**
SE (sij)	0.695	0.742	1.569	2.25	0.115	0.255	0.085	6.131	0.252	0.064	0.295	0.621
SE (sij-sik)	0.816	0.871	1.842	2.643	0.135	0.299	0.1	7.201	0.295	0.075	0.347	0.729
SE (sij-skl)	0.965	1.031	2.18	3.127	0.16	0.354	0.118	8.52	0.35	0.089	0.41	0.862

****: Significant at 1% level of probability   *: Significant at 5% level of probability**

4.6.3.2 Days to first flowering

In case of days to first flowering, negative estimates of SCA effects were desirable to get early matured plants. Among the F_1 lines derived from the diallel mattings, 16 lines had negative SCA effects in which G13 (-3.02) was noted for the highest value followed by G17 (-2.43), G15 (-2.35), G8 (-1.759), G6 (-1.87) and G3 (-1.61). Hybrid G3 was derived through the combination of high general combiners, G6 and G17 was obtained from high general combiner × low general combiner besides, G8 was attained from high general combiner × average general combiner. However, crossing lines of G13 and G15 was derived from average general combiner × low general combiner Therefore; G3, G13 and G17 was considered as the best specific combiner for early flowering (Table 13). These findings were supported by Sincik *et al.,* (2014), Shrimali *et al.,* (2016) and Kaur *et al.,* (2020).

4.6.3.2 Days to 50% flowering

Days to 50% flowering is assigned as a good indicator for the selection of early matured plant. The estimated data revealed, 15 hybrid lines possessed the negative effects for days to 50% flowering. Among them, hybrid G10 (-3.05) was considered the superior line for early flowering which was statistically identical to hybrids G19 (-2.67) and G21 (-2.31) for their negative and significant values. The hybrids G5, G6 and G17 displayed high SCA effects due to the combination of high general combiner × low general combiner parental lines. While the hybrid G10 was obtained from average general combiner × low general combiner parental lines and the hybrids G19, G20 and G21 had high SCA effects derived from the combination of low general combiners. On the contrary, G11 (1.92) followed by G18 (1.39) was regarded as poor specific combiner (Table 13). Gupta *et al.* (2011) found significant negative SCA effects in hybrids for days to 50% flowering. Atikunnaher *et al.* (2017) estimated out of 12 F_1 hybrids, 8 crosses showed negative significance towards days to flowering.

4.6.3.3 Days to siliqua maturity

For the trait days to siliqua maturity, negative effects were expected for shorter growth duration. In this case, 8 lines showed negative non-significant SCA effects, hence these lines could be used as a promising line for selecting early matured plant in future. None of the hybrids showed significant negative SCA effects. Both the hybrids G18 (-1.96) and G21 (-1.259) was considered as the best specific combiner followed by G13 (-1.222), G4 (-1.222) and G14 (-0.963). Best specific combiners G13 was derived due to the combination of high general combiner × average general combiner, G14 was obtained from high general combiner × low general combiner as well as G18 was obtained from average general combiners besides, G4 and G21 was derived from low general combiner × average general combiner. Rest of the lines showed positive specific combining ability effects indicating majority of the crosses had poor specific combinations for days to siliqua maturity (Table 13). It was supported by Singh *et al.* (2022) who found three F_1 lines having negative significant SCA effects.

4.6.4.4 Plant height (cm)

Out of 21 crosses, the negative estimates were found in 10 cross combinations. Hybrids G21 (-9.95) was a good specific combiner as it had the maximum negative and significant SCA effects followed by G4 (9.73), G12 (-7.01), G20 (-5.53) and G5 (-4.33). So, these crosses could be used as a suitable combination for dwarfness (Table 13). Cross combinations G4, G5 and G12 showed high SCA effects which was obtained from the combination of high general combiner × low general combiner and G5 was obtained due to the combination of average general combiner × low general combiner whereas G16, G20 and G21 derived from low general combiner × low general combiner. However, highly significant and positive SCA effects was observed in G13 (11.84) and G11 (11.31). Meena (2017) similarly reported that F_1 population had larger vegetative growth, hence he obtained two crosses with negative significant SCA effects. Inayat *et al.* (2019) observed desired negative SCA effects for plant height was present in 24 cross combinations derived from 8×8 diallel crosses.

4.6.4.5 Number of primary branches per plant

Among the F_1 progenies, 16 crosses showed the positive specific combining ability effects which was desirable to produce maximum siliqua in a plant. Within the combinations, G8 (1.77), G9 (1.41) and G20 (1.40) reported as the highest positive and significant SCA effects, therefore, treated as the best specific combiner for selection. High SCA effects found in G10 was obtained from the combinations of high general combiners and G8, G15 and G18 derived from high general combiner × low general combiner whereas G9 and G20 was obtained from high general combiner × average general combiner. On the other hand, negative SCA effects was observed in G1 (-0.38), G21 (-0.21) and so on (Table 13). Maurya *et al.* (2014) reported out of 28 crossings, 13 crosses had positive SCA effects however, Chowdhury *et al*. (2004) and Singh *et al.* (2000) reported as most of the lines showed positive SCA effects for primary branches.

4.6.4.6 Number of secondary branches per plant

The positive and strong significance was also desirable for number of secondary branches per plant. Out of 21 crosses, 15 lines possessed the positive specific combining ability effects. Hybrids G17 (5.54) was the best specific combiner which was statistically corresponded to G11 (4.18) and G5 (2.08). However, rest 6 crosses showed negative SCA effects indicating they were poor combiner for the selected trait (Table 13). F_1 G11 obtained from the combinations of high general combiners and G10 from high general combiner × average general combiner whereas G13, G17 and G21 derived from average general combiner × low general combiner besides, G2, G4 and G5 was attained from the combination of low general combiner × low general combiner, all of them had high SCA effects for number of secondary branches. Grace (2007) and Kaur *et al*. (2020) observed number of secondary branches per plant had positive specific combining ability for most of the lines in F_1 population. However, Afrose *et al.* (2019) reported negative SCA effects was prominent within the hybrids.

4.6.4.7 Siliqua length (cm)

Out of 21 cross combinations, there were 15 crosses that had positive significant SCA effects for siliqua length (Table 13). The cross combination G13 (0.76) produced the highest significant positive SCA effects followed by G4 (0.48), G18 (0.49) and G19 (0.53) considered as the best specific combiner for the concerned trait. Among the combinations, G18 and G19 was gained due to the combination of high general combiner × low general combiner while G13 was obtained from high general combiner × average general combiner, furthermore, G5 and G21 was obtained from low general combiner × low general combiner which showed high SCA effects. So, for obtaining desirable hybrid with longer siliqua these cross combinations could be selected for future breeding program. However, negative SCA effects for siliqua length was observed in 6 cross combinations. Horisaki and Niikura (2007), Inayat *et al.* (2019) and Singh *et al.* (2019) also reported significant variation was present in siliqua length, where they found majority cross combinations showed positive and significant SCA effects.

4.6.4.8 Siliqua per plant

Siliqua per plant was regarded as one of the important traits for measuring the yield performance of a line. Hence, positive specific combining ability effects was expected for siliqua per plant. Out of 21 hybrids, fifteen crosses showed positive SCA effects (Table 13). The highest SCA effects was found in G10 (89.87) preceded by G7 (68.90) and G13 (62.76). For siliqua per plant, G7, G13 and G15 was derived from high general combiner × average general combiner and G3 from high general combiner × low general combiner whereas hybrids G10, G16, G17 and G18 was attained due to the combination of average general combiners and G5 from low general combiner × average general combiner showed high SCA effects. Whereas G19 (-60.39) was considered as poor specific combiner. Yadav *et al.* (2010) and Gupta *et al*. (2015) found 12 crossing lines as a good specific combiner, could be utilized in future breeding program. Singh *et al.* (2022) studied 10 varieties of *Brassica juncea* and 45 F_1 lines derived from them, he reported 28 F_1 liens had higher SCA effects with positive direction that was similar with the present research findings.

4.6.4.9 Seeds per siliqua

There were 12 crosses from which hybrid G19 (2.26) found to have highly positive significant SCA effects followed by G8 (1.08) and G17 (0.59), therefore, they could be selected for yield improvement and nine crosses showed negative SCA effects for 1000 seed weight, indicating they were poor in combining with each other (Table 13). High SCA effects of G2 was obtained by the combination of high general combiners whereas hybrids G8 and G17 was obtained from high general combiner × average general combiner and G19 was attained from the combination of average general combiner × low general combiner. Horisaki and Niikura (2007), Meena (2017) also reported significant variation on seed number, where they found majority of the cross combinations showed positive and significant SCA effects for seeds per siliqua whereas Inayat *et al.* (2019) and Singh *et al.* (2019) found half of the crossing lines had negative SCA effects for seeds per siliqua.

4.6.4.10 Thousand seed weight (g)

Higher 1000 seed weight is one of the most important yield contributing traits for getting higher yield. Out of 21 hybrids, 12 cross combinations were recorded as good specific combiner in which G21 (0.63) possessed the highest value followed by G13 (0.62) and G8 (0.60). Crosses having the highest negative SCA effects was observed in both G4 (-0.49) and G20 (-0.49). For 1000 seed weight, high SCA effects of G18 was obtained by the combination of high general combiners and G16 was gained from high general combiner × average general combiner while hybrids G3, G6, G8 and G21 was obtained from high general combiner × low general combiner. Furthermore, crossings G1 and G13 was attained from the combination of average general combiner × low general combiner. Atikunnaher *et al*. (2017) suggested that most of the combinations had negative SCA effects, they found 2 combinations had positive significant SCA effects among 15 crosses. Gul *et al.* (2019) also estimated negative effects for most of the lines. While Maurya *et al.* (2014) found 16 positive lines that could be used as a good specific combiner derived from half 8×8 diallel crosses.

4.6.4.11 Yield per plant (g)

For yield per plant all the cross combinations except G6 (-0.45) showed positive specific combining ability effects. Out of 21 hybrids, 18 crosses had positive and significant SCA effects (Table 13). The highest SCA effects were observed in G7 (4.03) preceded by G19 (3.26), G11 (3.29) and G18 (2.96). The high SCA effects of G1 and G11 was obtained from the combination of high general combiners and G2 with G7 was obtained from high general combiner × average general combiner combinations while hybrids G3, G9 and G18 was attained due to the combination of high general combiner × low general combiner. Again, G14 was derived from average general combiner × low general combiner and G19 obtained from low general combiner × low general combiner. So, these crosses can be selected as a superior specific combiner for yield and can be incorporated to obtain heterotic hybrid combinations. Gul *et al.* (2019) and Maurya *et al.* (2014) reported that the optimum lines in F_1 populations had positive significant on yield per plant while Inayat *et al.* (2019) reported non-significant SCA effects for yield per plant.

4.6.4.12 Harvest index (%)

In case of harvest index, the highly significant and positive SCA effects were observed in 11 crosses, out of them, G19 (2.23) was the best specific combiner, in addition, G18 (2.01), G21 (1.80) and G3 (1.79) also showed positive significant SCA effects (Table 13). High SCA effects of G7 was attained by the combination of high general combiners and G11 from high general combiner × average general combiner besides, G3 was obtained from high general combiner × low general combiner. Furthermore, G18, G19 and G21 was attained due to the combination of low general combiner × low general combiner. While G15 (-2.97) followed by G5 (-2.17), G20 (-1.49) and the rest six crosses offered minor scope for the improvement of this trait. Sabaghnia *et al.* (2010) found 22 out of 36 crossing had negative significant effects for harvest index.

4.5. Analysis of heterosis

Heterosis is one of the important aspects for measuring the hybrid performance. Standard heterosis is used to exploit the superior lines (F_1) over a commercially popular variety. In this study BARI sharrish-11 was employed as a check variety to evaluate the F_1 populations for twelve yield and yield related components**.** Percent heterosis for different characters of the F_1 hybrids over better parent (BP) and standard check values are shown in Table 14.

4.5.1 Days to first flowering

In order to develop early matured variety negative heterosis is desirable for days to first flowering. Among all the F_1 lines, eighteen lines manifested the negative heterotic effects. The highest negative heterotic effects with strong significance over better parent was found in G3 (-14.53**) whereas G1(-4.46**) was showed the lowest effects for days to first flowering. Hybrid G5 (-16.28) showed the highest negative but non-significant value and G7 (-1.68) was recorded as the lowest one in comparing better parent (Table 14). Heterotic effects for standard heterosis revealed that G3 (-11.50**) manifested the highest and G4 (-1.77**) the lowest effects. On the contrary, positive heterosis was also observed for days to first flowering. High significance with positive direction of heterobeltiosis and standard heterosis was found in G11 (7.08** and 7.08**, respectively). Hybrid G18 (1.71*) showed the lowest value in comparing better parent and G16 (0.05**) indicated the lowest value for standard heterosis. Wolko *et al.* (2019) studied with 12 F1 lines to evaluate heterosis who reported 7 crosses showed negative and significant hetrosis over mid parent.

Table 14: **Estimation of Heterosis (heterobeltiosis, HB) over better parent (BP) and standard heterosis (SH) over the check varieties (BARI Sharisha-11) in 21 F_1 hybrids derived from 7×7 half diallel cross in *Brassica juncea*.**

F_1 Hybrids	H (%)	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
G1	HB	-4.46*	-6.67**	7.74*	0.20**	17.92**	35.84**	-1.76	26.31**	-5.56	0.41*	112.82**	-2.82
	SH	-5.31	-10.64**	5.36**	-8.43	27.78**	42.19**	0.80	26.17**	1.63*	6.96	91.24**	4.42
G2	HB	-9.24	-2.24**	2.86	-2.22**	12.82**	38.83**	3.28*	11.39**	-0.38**	-18.37**	107.18**	4.50
	SH	-4.42**	-7.09	2.21	-12.40	22.25**	45.31**	5.97	18.15**	7.21	-13.04**	86.17**	4.03
G3	HB	-14.53**	-4.58**	4.17	-5.38*	30.76**	32.87**	15.30**	35.71**	-2.31*	12.24**	94.43**	-0.62
	SH	-11.50**	-11.35*	2.52	-4.11**	41.69**	39.08**	18.30**	39.79**	5.14	19.57**	74.71**	-1.07
G4	HB	-11.90	-10.14*	-1.82	-18.31**	23.05**	43.30**	-9.33*	9.86**	-19.65**	-18.00**	66.92**	-4.96*
	SH	-1.77**	-5.67**	1.89	-11.13**	33.33**	50.00**	-6.96**	24.64*	-13.53**	-10.87**	52.99**	-5.39
G5	HB	-16.28	-18.87**	3.38*	-8.37**	25.52**	61.22**	4.57**	32.05**	-6.38	-2.04	71.59**	-13.22**
	SH	-4.42**	-8.51**	5.99	-5.28**	50.00**	68.75**	7.30	43.06**	0.76*	4.35	54.19**	-13.61**
G6	HB	-8.85**	-11.35**	4.73*	-6.87**	25.61**	35.83**	-0.61	27.39**	-17.46**	9.18**	48.09**	-11.77**
	SH	-8.85	-11.35**	4.73*	-6.87**	36.11**	42.17**	1.98	27.39**	-11.17**	16.30**	48.09**	-11.77**
G7	HB	-1.68	-2.22**	0.63	3.84*	68.52**	51.50**	10.07*	52.44**	-0.77	-14.61**	203.49**	5.36**
	SH	3.54	-6.38	0.02	-5.10	63.89**	51.55**	6.84**	61.69**	3.99	-17.39**	111.53**	13.21*
G8	HB	-9.40*	-5.93**	1.92	-6.15*	106.00**	15.60**	6.52**	-2.71	11.75**	23.91**	105.19**	-10.56
	SH	-6.19**	-9.93*	0.32	-4.89**	88.94**	15.64**	9.72*	0.21	15.92**	23.91**	68.20**	-3.89**
G9	HB	-10.32	-10.14*	-0.91	-10.16	96.91**	62.43**	7.13*	14.19**	0.10	-14.00*	111.96**	-0.39*
	SH	0.01**	-5.67**	2.84	-2.27**	80.50**	62.48**	5.11*	29.55**	3.11	-6.52**	94.27**	7.04
G10	HB	-6.20**	-20.13**	3.69**	-11.90**	44.12**	71.84**	18.53**	56.65**	-5.66	1.16*	156.16**	-6.09
	SH	7.08**	-9.93**	6.31*	-8.93**	72.22**	71.89**	11.74**	69.71**	-2.73*	-5.43	77.80**	0.91*

F_1 Hybrids	**H (%)**	**DFF**	**D50%F**	**DSM**	**PH**	**NPB**	**NSB**	**SL**	**SPP**	**SPS**	**TSW**	**YPP**	**HI**
G11	HB	7.08**	-1.42	3.47	3.97*	67.50**	107.05**	6.26*	47.60**	-3.29	6.52*	104.27**	2.70**
	SH	7.08*	-1.42	3.47	3.97*	67.50**	107.05**	6.26*	47.60**	-0.29	6.52*	104.27**	10.35
G12	HB	-7.69	-4.48**	0.64	-10.56**	31.39**	33.84**	8.68**	17.26**	2.27**	-2.17	106.45**	0.23
	SH	-4.42**	-9.22*	-0.95	-9.36**	27.78**	29.66**	11.94**	24.38**	7.18	-2.17	69.23**	-2.98
G13	HB	-14.29	-6.76	-3.34	-3.78*	62.81**	90.32**	21.25**	39.40**	-5.50	10.00**	90.04**	1.41
	SH	-4.42**	-2.13**	0.32	4.68*	58.33**	84.41**	24.88**	58.15**	-0.97*	19.57**	74.18**	0.50
G14	HB	-11.63	-15.72*	-1.23	-12.58**	23.22**	27.10**	10.71**	0.98**	3.38**	-3.37*	151.66**	3.21
	SH	0.88**	-4.96**	1.26	-9.64**	47.25**	17.19**	7.47**	9.39*	8.34	-6.52	75.40**	-0.10
G15	HB	-10.08*	-4.96*	-2.43	-8.60**	69.47**	56.28**	-5.06*	32.64	-1.62	9.78**	80.69**	2.05
	SH	-5.31**	-4.96*	1.26	-7.37**	69.47**	56.28**	-5.06*	40.69**	3.10	9.78**	80.69**	2.05
G16	HB	-10.32	-11.49**	-0.91	-10.49	42.28**	32.24**	7.95**	25.26**	0.24	13.00**	71.31**	-7.53**
	SH	0.05**	-7.09**	2.84	-2.62**	30.50**	28.11**	11.18**	42.11**	3.98	22.83**	57.01**	-8.36*
G17	HB	-16.28	-16.98**	1.85*	-2.78	30.13**	119.34**	-10.77**	33.95**	8.38**	-1.09	83.60**	-0.01**
	SH	-4.42**	-6.38**	4.42	0.50	55.50**	112.48**	-8.10**	45.12**	12.42**	-1.09	50.50**	-11.02
G18	HB	1.71*	-3.55	-1.26	2.59*	66.72**	34.39**	15.83**	29.82**	0.26	20.65**	89.13**	2.39
	SH	5.31	-3.55	-1.26	3.97	66.72**	34.39**	19.31**	33.72**	4.00	20.65**	89.13**	2.39
G19	HB	-6.20**	-16.35*	0.91*	-8.47	27.82**	37.07**	20.50**	-13.86	20.37**	-6.00	102.60**	3.69
	SH	7.08**	-5.67**	4.73	-0.42**	52.75**	32.81**	18.22**	-2.27**	18.82**	2.17**	85.68**	2.76
G20	HB	3.97**	-11.49**	-0.30	-9.49	77.83**	54.70**	7.47**	14.98**	-13.21**	-14.00*	60.24**	-5.26
	SH	15.93	-7.09**	3.47	-1.53**	77.83**	54.70**	7.47**	30.45**	-13.21**	-6.52**	60.24**	-5.26
G21	HB	-10.85	-16.98**	-0.31	-11.35**	44.50**	59.38**	9.67**	15.83**	-2.14	26.09**	75.75**	2.53
	SH	1.77**	-6.38**	2.20	-8.36**	44.50**	59.38**	9.67**	25.49**	-2.14	26.09**	75.75**	2.53

****: Significant at 1% level of probability   *: Significant at 5% level of probability**

Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, SL=Siliqua length (cm), SPP=Siliqua per plant, SPS=Seeds per siliqua, TSW=1000 seed weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

4.5.2 Days to 50% flowering

Diversified heterotic effects were estimated for days to 50% flowering. In this case, negative heterosis is also expected to get early matured plant. Data from the standard heterosis indicated that both G3(-11.35**) and G6 (-11.35**) was recorded for its highest negative heterotic effects followed by G1 (-10.64**) and G10 (-9.93**) for days to 50% flowering. Among the lines, G13 (-2.13**) manifested the lowest value for standard heterosis (Table 14). When compared with better parent, G10 (-20.13**) showed the highest negative significant effects which was statistically similar with G5 (-18.87**), G17 (-16.98**) and G21 (-16.98**), while G7 (-2.22**) expressed the lowest effects (Table 14). Nassimi *et al.* (2006), Gupta *et al.* (2010) and Ferdous (2019) observed the expected negative heterosis over mid parent and better parent for most of the genotypes for this trait whereas Singh *et al.* (2012) found positive heterosis over mid parent and better parent.

4.5.3 Days to siliqua maturity

The estimated heterosis for days to siliqua maturity indicated that F_1 population of *Brassica juncea* required longer period during its reproductive stage as most of the data were in positive direction. Only 8 genotypes had negative heterotic effects over better parent while only 2 genotypes manifested the negative heterosis over check variety with non-significant effects. The highest negative heterotic effects were observed in G13 (-3.34) followed by G15 (-2.43) and G4 (-1.82) and G21 (-0.31) showed the lowest heterotic effects over check variety whereas only G18 (-1.26) was manifested the negative standard heterosis (Table 14). When compared with better parent, the maximum positive heterotic effects were observed in G1 (7.74*) followed by G6 (4.73*) and G3 (4.17*). Hybrid G7 (0.02) showed the lowest heterobeltiosis. Data for standard heterosis revealed, G10 (6.31*) hold the highest value for days to siliqua maturity that was identical to G1 (5.36*) and G6 (4.73*). Hybrids G8 (0.32) was recorded for its lowest value over check variety (Table 14). Barfa *et al.* (2017) found negative heterosis over better parent and check variety for five crosses out of six crosses, Similar findings are in accordance with Thanmichon *et al*. (2015), Patel *et al.* (2012) and Gami *et al*. (2018). On the contrary, Kumar *et al.* (2017) observed positive heterotic effects over mid parent for 42 crosses out of 50 crosses and 35 crosses among 50 F_1's for better parent.

4.5.4 Plant height (cm)

Strong significance with higher variation on heterotic effects were observed in plant height. The highest negative heterosis over better parent with strong significance was found in G4 (-18.31**) followed by G14 (-12.58**) and G10 (-11.90**). Moreover, higher negative but non-significant heterotic effects was also found in G16 (-10.49) and the lowest heterotic effects was found in G1 (-0.20). Considering standard heterosis, the highest negative effects was observed in G4 (-11.13**) which was statistically corresponding to G14 (-9.64**) and G12 (-9.36**) but, G9 (-2.27) indicated the minimum heterosis over check variety. Negative heterosis for plant height was expected to develop dwarf mustard variety. Positive heterosis was also observed for plant height. Hybrids G11 (3.97*) showed the highest result when compared with better parent. On the other hand, standard heterosis revealed, G13 (4.68*) possessed the highest value and G17 (0.50) indicated the lowest one for plant height (Table 14). Gul *et al*. (2019) and Wolko *et al.* (2019) observed positive heterobeltiosis and mid parent heterosis for most of the traits under being studied. However, Turi *et al.* (2006) estimated negative and significant heterosis for plant height in hybrids of *Brassica juncea*.

4.5.5 Number of primary branches per plant

All the F_1 lines showed strong significance and positive effects for both standard and heterobeltiosis. Cross combinations G8 (106.0**) indicated the maximum value followed by G9 (96.91**) and G20 (77.83**) while G2 (12.88**) showed the minimum value over better parent. On the other hand, data obtained from standard heterosis revealed that G8 (88.94**) was the highest in heterotic effects which was statistically similar with G9 (80.50**) and G20 (77.83**). Cross combination G2 (22.25**) showed the lowest effects over check variety (Table 14). According to Nassimi *et al*. (2006) among 56 crosses, 28 crosses had positive heterotic effects over mid parent and 27 crosses had positive effects over better parent. Research findings were supported by Singh *et al.* (2012) and Ferdous (2019) found positive heterotic effects over better parent and mid parent for all the selected traits.

4.5.6 Number of secondary branches per plant

In case of secondary branches, again all the F_1 lines showed strong significance and positive effects for both standard heterosis and heterobeltiosis. Data obtained from standard heterosis revealed that G17 (119.34**) was the highest in heterotic effects which was statistically similar with G11 (107.05**) and G13 (90.32**) whereas G8 (15.64**) showed the lowest value over BARI sharisha-11. On the other hand, G17 (112.48**) indicated the maximum value followed by G11 (107.05**) and G13 (84.41**), while G9 (15.60**) showed the minimum value over better parent (Table 14). Gupta *et al.* (2010) found 7 crosses out of 12 that showed positive and significant effects over mid parent and better parent. Turi *et al*. (2006) estimated 17 out of 28 crosses had positive heterotic effects over better parent and Barfa *et al.* (2017) estimated heterosis effects of 16 characters for 6 crosses, among them 4 crosses showed positive and significant effects.

4.5.7 Siliqua length (cm)

The highest heterotic effects with positive direction were found in G13 (21.25**) followed by G18 (15.83**) and G3 (15.30**) while G2 (3.28*) indicated the lowest value over better parent for siliqua length. Hybrids G13 (24.88**) manifested the highest positive effects similar with G18 (19.31**) and G3 (18.30**) in comparison with check variety. The lowest value was found in G1 (0.80) for standard heterosis. Negative heterosis for standard heterotic effects was found in hybrid G17(-10.77*) and G4(-9.33*) which was also the highest over check variety among the cross combinations. Crossing of G6 (-0.61) and G5 (-1.25) expressed the lowest negative value for heterobeltiosis and standard heterosis respectively (Table 14). Kumar *et al.* (2009) and Wolko *et al.* (2019) reported positive heterosis for siliqua length over better parent in F_1 of *B. juncea* and *B. napus* while Bhinda *et al.* (2020) studied with 36 F_1 lines and evaluated heterosis for siliqua length, he found 12 crosses had positive and significant heterotic effects for siliqua length while remaining showed negative heterotic effects.

4.5.8 Siliqua per plant

In order to get a satisfactory yield from a plant, higher number of siliqua production is obligatory. Hence, positive heterosis is expected in this case. The estimated data indicated that G10 (56.65**) followed by G7 (52.44**) and G11 (47.60**) showed strong significance along with positive heterotic effects over better parent and G14 (0.98**) expressed the lowest effects over better parent (Table 14). In case of standard heterosis, G10 (69.71**) followed by G7 (61.69**) and G13 (58.15**) indicated the highest value for siliqua number. Research findings were supported by Bhinda *et al.* (2020) who observed 32 out of 36 crosses had significant positive heterotic effects over check variety. On the contrary, only two genotypes viz. G8 and G19 (-2.71, 0.21 and -13.86, -2.27, respectively) had indicated the negative effects on siliqua per plant (Table 14). According to Breeding *et al.* (2015), siliqua per plant showed high significance and positiveness with all the traits for 44 crosses among 45 over mid parent and 42 showed positive heterobeltiosis and Rameeh (2019) estimated significant positive heterotic effects over mid parent in case of *Brassica napus.*

4.5.9 Number of seeds per siliqua

In case of seeds per siliqua, the highest standard heterotic effects were found in G19 (18.82**) followed by G8 (15.92**) and G17 (8.38**) with positive direction and the lowest heterotic effects over check variety was observed in G9 (0.10). Hybrids G19 (20.37**) manifested strong significance and positive heterotic effects over better parent followed by G8 (15.92**), G17 (12.42**) and G3 (12.24**). Among the F_1 's, G9 (0.30) showed the minimum positive effects over better parent. The highest negative effects was estimated in G4 (-19.65**) over BARI sharisha-11 while G2 (-0.38**) and G11 (-0.29) showed the lowest negative value for heterobeltiosis and standard heterosis, respectively (Table 14). Shehzad *et al.* (2015) and Ferdous (2019) reported that most of the F_1's displayed positive heterosis over both check variety and better parent whereas Breeding *et al.* (2015) reported 18 F_1 lines had negative mid parent heterotic effects and 20 F_1 populations over standard heterosis.

4.5.10 Thousand seed weight (g)

Thousand seed weight is one of the important parameters to develop higher yielding variety. In this sense, positive heterosis is desirable for thousand seed weight. Prominent positive heterotic effects over check variety with higher significance was observed in G21 (26.09**) preceded by G8 (23.91**) and G18 (20.65**) where, G19 (2.17**) showed the lowest value (Table 14). Positive heterosis over better parent was also observed in G21 (26.09**) indicating the highest value which was statistically similar with G8 (23.90**) and G18 (20.65**). Hybrid G1 (0.41*) was recorded as for the lowest heterobeltiosis effects. The maximum negative heterosis over check variety was found in G2 (-18.37**) preceded by G4 (-18.00**) where, G17 (-1.09) indicated the lowest negative effects. G8 (-17.39**) expressed the highest value and G15 (-2.17) was the lowest in negative effects on thousand seed weight over better parent (Table 14). Meena *et al.* (2014) reported, all the cross combinations except one showed negative heterobeltiosis, on the contrary, Gupta *et al.* (2011) and Kumar *et al*. (2017) found majority of the crosses among 50 crosses had positive heterobeltiosis had positive heterotic effects for 1000 seed weight.

4.5.11 Yield per plant (g)

In case of yield per plant, all the F_1 lines represented highly significant and positive heterosis value for heterobeltiosis and standard heterosis. Among the combinations, G7 (203.49**) followed by G10 (156.16**) and G14 (151.66) manifested better heterotic effects over the check variety BARI sharisha-11 and G6 (48.09**) was recorded for its lowest value. On the other hand, hybrids G7 (111.53**) showed the highest heterotic effects which was statistically corresponding to G11(104.27**) and G9 (94.27**) when compared with better parent while G6 (48.09%) also showed the lowest value for heterobeltiosis (Table 14). Meena, (2017), Ali *et al*. (2003) and Singh *et al*. (2017) found all traits of F_1 hybrid's showed positive heterotic effects over better parent and mid parent as opposite effects was observed in Barfa *et al.* (2017) where he found all traits displayed negative heterotic effects on seed yield per plant.

4.5.12 Harvest index (%)

A few genotypes manifested positive and significant heterotic effects for harvest index (%). Significant positive heterosis over better parent was found in cross combination G7 (5.36**) followed by G11 (2.70*) while non-significant positive heterotic effects over better parent were observed in G2 (4.50) preceded by G19 (3.69) and G14 (3.21). Whereas G12 (0.23) showed the lowest positive effects over better parent. Moreover, G7 (13.21*) and G10 (0.91*) showed positive and significant heterotic effects over check variety. Hybrids G11 (10.35) followed by G9 (7.04) and G1 (4.42) showed positive non-significant effects over BARI sharisha-11. Furthermore, G5 (-13.22** and -13.61**) followed by G6 (-11.77** and -11.77**) revealed the highest negative significant heterotic effects over both better parent and check variety while G14 (-0.10) and G17 (-0.01*) showed the lowest negative effects over better parent and check variety respectively (Table 14). It was supported by Gupta *et al.* 2010) who estimated heterosis for harvest index. Results revealed that among 12 crosses, 5 lines showed positive heterotic effects over mid parent while 5 crosses had positive effects over better parent.

4.9 Fatty acid compositions analysis

Brassica species contain a diversified composition of fatty acids, among them seven major fatty acids viz. palmitic acid (C16:0), stearic acid (C18:0), oleic acid (C18:1), linoleic acid (C18:2), linolenic acid (C18:3) eicosenoic acid (C22:0) and erucic acid (C22:1) were extracted from *Brassica juncea*. Oils that contain high erucic acid are used for industrial purposes, considering health issues oils extracted from *Brassica* species need to contain low erucic acid. Therefore, developing lines having low erucic acid content along with increasing oleic acid, linoleic acid and linolenic acid is one of the promising objectives of this breeding program. Oils containing high oleic acid are greatly resistant to heating and oxidation whereas erucic acid is one of the most beneficial fatty acids in mostly found within *Brassica* species. In general, zero fatty acid genotypes are belonged to *Brassica napus*, *Brassica juncea* and *Brassica rapa*. For human nutrition oleic acid, linoleic acid, linolenic acid and erucic acid plays an important role. Sharafi *et al*. (2015) reported that high oleic acid has cholesterol lowering properties that helps to maintain blood cholesterol level.

In order to develop a short durable variety along with improving the oil content, fatty acids of the selected parents and lines that had crossed with BJ-00, 18 samples viz. BINA7, BARI sharisha11, BARI sharisha16 and BJ00 among the parental lines and F_1 hybrids of BS16×BJ00-S1, BS16×BJ00-S2, BJ00×BS16-S1, BJ00×BS16-S2, BINA7×BJ00-S1, BINA7×BJ00-S2, BS10×BJ00-S1, BS10×BJ00-S2, Rye5×BJ00-S1, Rye5×BJ00-S2, BS11×BJ00-S1, BS11×BJ00-S2, Daulat×BJ00-S1 and Daulat×BJ00-S2 samples were analyzed by gas-liquid chromatography. The fatty acid compositions of different samples were represented in Table 15 and Table 16. Estimated fatty acids were categorized into two groups: saturated fatty acids and unsaturated fatty acids. Myristic acid, palmitic acid, stearic acid, arachidic acid were belonging to the saturated fatty acids and palmitoleic acid, oleic acid, linoleic acid, linolenic acid, eicosenoic acid and erucic acid were into unsaturated fatty acids. Chromatogram of 10 fatty acids content of 18 samples were presented in Appendix 4.

Table 15: Saturated and unsaturated fatty acid content in the selected samples of F_1 hybrids with their parents

	Saturated fatty acids (%)				**Unsaturated fatty acids (%)**					
Treatment	Myristic acid	Palmitic acid	Stearic acid	Arachidic acid	Palmitoleic acid	Oleic acid	Eicosenoic acid	Erucic acid	Linoleic acid	Linolenic acid
	(C14:0)	(C16:0)	(C18:0)	(C20:0)	(C16:1)	(C18:1)	(C20:1)	(C22.1)	(C18:2)	(C18:3)
P1	0.33	4.98	0.88	6.12	0.11	21.53	0.35	29.13	23.82	12.59
P-5	0.71	4.75	0.98	6.51	0.12	15.72	0.81	31.62	23.19	15.26
P-6	0.22	3.85	2.07	1.04	0.1	53.08	0.08	0.81	31.15	7.4
P-7	0.1	2.4	0.8	7.18	0.09	11.85	0.73	48.58	16.73	11.08
G5-S1	0.08	3.97	1.15	8.76	0.1	23.36	0.79	27.52	19.69	10.44
G5-S2	0.17	4.69	1.1	5.23	0.09	16.69	0.71	34.82	25.11	11.01
G10-S1	0.19	6.28	1.3	6.97	0.08	17.59	0.71	35.72	19.82	11.23
G10-S2	0.09	4.92	1.02	6.98	0.18	14.29	0.98	35.86	20.61	14.9
G14-S1	0.53	6.4	1.44	4.59	0.23	15.73	0.61	33.85	23.8	12.74
G14-S2	0.41	4.88	1.02	5.71	0.18	13.66	0.93	32.36	24.8	15.79
G17-S1	0.57	7.36	0.98	5.41	0.24	16.2	0.62	27.8	28.59	12.2
G17-S2	0.02	3.36	1.05	9.93	0.09	22.16	0.68	31.38	21.9	9.34
G19-S1	0.19	3.99	1.16	5.47	0.09	13.9	0.66	44.53	18.74	10.94
G19-S2	0.22	5.16	1.08	8.59	0.26	23.45	0.78	22.14	27.29	10.93
G19-S3	0.32	4.58	1.22	9.04	0.18	24.16	0.55	24.36	25.52	9.67
G19-S4	0.12	4.26	1.28	9.48	0.08	27.81	0.59	22.19	26.54	7.42
G21-S1	0.28	4.87	0.99	10.39	0.16	21.39	0.71	23.47	22.74	14.9
G21-S2	0.11	4.73	0.88	9.77	0.25	15.88	0.94	23.53	25.2	18.63
Min	0.02	2.40	0.80	1.04	0.08	11.85	0.08	0.81	16.73	7.40
Max	0.71	7.36	2.07	10.39	0.26	53.08	0.98	48.58	31.15	18.63

Table 16: Total fatty acid content in percentage among the selected samples of F_1 hybrids with their parents.

Treatment	TSFA	MUFA	PUFA	Oleic/Linoleic acid	Omega-6/Omega-3
P1	12.31	51.12	36.41	0.90	1.89
P5	12.95	48.27	38.45	0.68	1.52
P6	7.18	54.07	38.55	1.70	4.21
P7	10.48	61.25	27.81	0.71	1.51
G5-S1	13.96	51.77	30.13	1.19	1.89
G5-S2	11.19	52.31	36.12	0.66	2.28
G10-S1	14.74	54.10	31.05	0.89	1.76
G10-S2	13.01	51.31	35.51	0.69	1.38
G14-S1	12.96	50.42	36.54	0.66	1.87
G14-S2	12.02	47.13	40.59	0.55	1.57
G17-S1	14.32	44.86	40.79	0.57	2.34
G17-S2	14.36	54.31	31.24	1.01	2.34
G19-S1	10.81	59.18	29.68	0.74	1.71
G19-S2	15.05	46.63	38.22	0.86	2.50
G19-S3	15.16	49.25	35.19	0.95	2.64
G19-S4	15.14	50.67	33.96	1.05	3.58
G21-S1	16.53	45.73	37.64	0.94	1.53
G21-S2	15.49	40.60	43.83	0.63	1.35
Min	7.18	40.60	27.81	0.55	1.35
Max	16.53	61.25	43.83	1.190	4.21
Mean	13.20	50.72	35.65	0.852	2.12

Note:

TSFA=Total saturated fatty acid, MUFA=Monounsaturated fatty acid, PUFA=Polyunsaturated fatty acid, omega-6=linoleic acid, omega-3= linolenic acid, G5=BINA7×BJ00, G10=Rye5×BJ00, G14=Daulat×BJ00, G17=BARI10×BJ00, G19=BARI16×BJ00, G21=BARI11×BJ00; S indicates different plant selection.

4.9.1 Saturated fatty acids

Total saturated fatty acid (TSFA) was estimated through gas chromatography analysis for 18 samples of *Brassica juncea*. Among the saturated fatty acids myristic, palmitic, stearic and arachidic acid was estimated. TSFA ranged from 7.18% to 16.53%. Among the samples P6 (7.18%) had the lowest percentage of TSFA followed by P7 (10.48%), G19-S1 (10.81%) and G5-S2 (11.19%) while G21-S1 (16.53%) which was statistically similar with G21-S2 (15.49%) and G19-S3 (16.16%) possessed the highest value for TSFA (Table 15). According to Wilson (2004), less than 7% saturated fatty acids in edible oils was acceptable for human consumption. However, oils having higher content of saturated fatty acids was beneficial for industrial purposes.

4.9.1.1 Myristic acid (C14:0)

Estimated myristic acid ranged from 0.02% to 0.71% with a mean value of 0.26%. The maximum value was observed in P5 (0.71%) which was statistically similar with the line G17-S1 (0.57%), G14-S1 (0.53%), G14-S2 (0.41%), P1 (0.33%) and G19-S3 (0.32%). On the other hand, the lowest content of myristic acid was found in G17-S2 (0.03%) followed by G5-S1 (0.08%), G10-S2 (0.09%), P7 (0.10%), G21-S2 (0.11%), G19-S4 (0.12%), G5-S2 (0.17%), G10-S1 (0.19%) and P6 (0.22%). It is represented in Table 15.

4.9.1.2 Palmitic acid (C16:0)

Among the selected samples palmitic acid varied from 2.40-7.36% with an average of 4.75% (Table 15). G19-S1 held the highest value as 7.363% followed by G14-S1 (6.39%), G10-S1 (6.28%), G19-S2 (5.159%), P1 (4.98%), G10-S2 (4.92%), G14-S2 (4.88%), G21-S1 (4.873%), P5 (4.75%), G21-S2 (4.73%), G5-S2 (4.69%) and G19-S3 (4.58). Whereas P7 showed the lowest value (2.40%) for palmitic acid that was statistically similar with G17-S2 (3.364%), P6 (3.85%), G5-S1 (3.97%), G19-S1 (3.99%) and G19-S4 (4.26%). Walczak (2014) supported these findings who estimated palmitic acid in different lines of *Brassica juncea* was 3.6 to 4.9% while Chowdhury *et al*. (2010) and Islam *et al.* (2020) reported that palmitic acid content ranged from 1.68-2.68% and 1.77-3.44% among different species in mustard.

4.9.1.3 Stearic acid (C18:0)

Value for stearic acid extended from 0.80% to 2.07% with the average value for the acid was 1.13% (Table 15). The highest percentage among the samples were found in P6 (2.07%). Hybrids G14-S1 (1.44%), G10-S1 (1.30%), G19-S4 (1.28%), G19-S3 (1.22%), G19-S1 (1.16%), G5-S1 (1.15%), G5-S2 (1.10%) and G14-S2 (1.05%) showed the values that were almost similar with the mean value (Table 15). The lowest value was observed in P7 (0.80%) followed by G21-S2 (0.88%), P1 (0.88%), P5 (0.98%) and G14-S1 (0.981%). Beniwal *et al*. (2015) reported that stearic acid varied from 5.4% to 6.5% in Indian mustard, whereas Walczak (2014) found 1.3% to 1.9% of stearic acid content among the 11 cultivars of *Brassica juncea*.

4.9.1.4 Arachidic acid (C20:0)

Arachidic acid was ranged from 1.04% to 10.39% with a mean value of 7.07%. Hybrids G21-S1 (10.39%) was recorded for its highest value followed by G14-S2 (9.93%), G21-S2 (9.77%), G19-S4 (9.48%), G19-S3 (9.04%), G5-S1 (8.76%) and G19-S2 (8.59%) and in parents P5 (6.51%) and P1 (6.12%). The lowest value was observed in P6 (1.04%) followed by G14-S1 (4.59%), G17-S1 (5.41%), G19-S1 (5.47%) and G14-S2 (5.71%). Wijesundera *et al.* (2008) found 0.7% arachidic acid content in *B. juncea.* Obtained data was shown in Table 15.

4.9.2 Unsaturated fatty acids

Among the unsaturated fatty acids palmitolic, oleic, eicosenoic and erucic acid was considered for calculating total monounsaturated fatty acids (MUFA). MUFA was varied from 40.60% found in G21-S2 to 61.25% in P6. Among the cross combinations G19-S1 (59.18%), G17-S2 (54.31%) and G10-S1 (54.10%) contained the highest amount of monounsaturated fatty acids (Table 16). However, the lowest erucic acids was observed in G5-S1(22.14%), G19-02 (22.19%), and G21-S1 (23.53%) within the crossing lines (Table 15). The lowest monounsaturated fatty acid was found in G21-S2 (40.60%). For a balanced diet oils having high oleic acid and low erucic acid percentage was acceptable. While polyunsaturated fatty acids (PUFA) were estimated from linoleic and linolenic acid. PUFA was ranged from 27.81% to 43.83%. The highest PUFA was found in G21-S2 (43.83%) followed by G17-S1 (40.79%) and G14-S2 (40.59%) on the contrary, P7 (27.81%) contained the lowest PUFA that was statistically corresponded to G19-S1 (29.68%) and G5-S1 (30.13%). Linoleic and linolenic acids are considered as an essential fatty acid that acted a as precursors of bioactive long chain fatty acids. Poly unsaturated fatty acids provided up to 10% RDA energy, among them omega-6 provided 4-6% and 2% come from omega-3. Nutrition value of fat was determined by the content of poly unsaturated fatty acids Walczak, (2014).

4.9.2.1 Palmitolic acid (C16:1)

Palmitolic acid was ranged from 0.08 to 0.26% with the mean value was 0.15%. The highest value observed for palmitolic acid was found in G19-S2 (0.26%) which was statistically similar with G21-S2 (0.25%), G17-S1 (0.24%), G14-S2 (0.23%), G10-S2 (0.18%), G19-S3 (0.18%), G14-S2 (0.18%), G21-S2 (0.16%), G5-S1 (0.10%) and in P5 (0.12%) along with P1 (0.11%). Whereas the lowest value was found in G10-S1 (0.08%) followed by G19-S4 (0.08%), G5-S2 (0.08%), P7 (0.09%), G19-S1 (0.09%), G17-S2 (0.09%), and P6(0.10%). It is represented in Table 15.

4.9.2.2 Oleic acid (C18:1)

The estimated oleic acid among the samples were extended from 11.85 to 53.078% with an average value of 20.47%. Oleic acid was higher in P6 (53%). Whereas BJ00×BARI16-S2 (27.81%) preceded by G19-S4 (24.16%), G5-S1 (23.36), G19-S2 (23.45%), G10-S2 (22.18%), G21-S2 (21.39%), P1 (21.53%), G10-S1 (17.59%), G5-S2 (16.99%) and G17-S1 (16.19%) showed medium range of oleic acid (%) through fatty acid profiling (Table 15). The minimum amount of oleic acid was found in P7 (11.85%) followed by G14-S2 (13.66%), G19-S1 (13.89%), G10-S2 (14.82%), G14-S1 (15.73%), and P5 (15.71%). Walczak (2014) reported that oleic acid content extended from 36.3 to 59.1% within 11 advanced lines derived from *Brassica juncea* whereas Ostrikov *et al.* (2020) found an average of 47% oleic acid concentration in 96 lines of *Brassica juncea*. A range of 23.4 to 27.1% oleic acid was estimated in F_1 populations by Iqbal *et al.*, (2006).

4.9.2.3 Linoleic acid (C18:2)

Percentage of linoleic acid showed diversification with a range from 16.77% to 31.15% where, the mean value was 23.62% (Table 12). The highest value was found in P6 (31.15%) followed by G17-S1 (28.59%), G19-S2 (27.29%), G19-S4 (26.54%), G19-S3 (25.52%), G21-S1 (25.20%), G5-S2 (25.11%), G14-S2 (24.80%), P1 (23.82%) and

P5 (23.19%). The lowest value was observed in P7 (16.73%) which was statistically similar with G19-S1 (18.74%), G5-S1 (19.69%), G10-S1 (19.824%) and G10-S2 (20.61%) for linoleic acid (Appendix 4). On an average, 12.53% linoleic acid was estimated by Sawicka *et al*. (2020) whereas Sharafi *et al*. (2015) reported 16.05% linoleic acid present in different cultivars.

4.9.2.4 Linolenic acid (C18:3)

Among the samples, linolenic acid varied from 7.404% to 18.633% with an average value of 12.622%. The maximum value was recorded as G21-S2 (18.63%) followed by G14-S2 (15.79%), P5 (15.26%), G10-S2 (14.89%), G21-S1 (14.90%), G14-S2 (12.74%), P1(12.59%), G17-S1 (12.20%), P7 (11.08%), G5-S2 (11.01%) and G10-S1 (11.23%). Whereas the lowest value was found in P6 (7.40%) which was statistically similar with G19-S4 (7.42%), G17-S2 (9.34%), G5-S1 (10.44%), G19-S1 (10.94%) and G19-S2 (10.93%) for linolenic acid (Table 15). Kumar *et al.* (2018) observed linolenic acid was present in a range from 11.10 to 26.72% while Ali (2017) studied with 20 F_1 lines obtained from *Brassica juncea* and reported that linolenic acid ranged from 9.6 to 12%.

4.9.2.5 Eicosenoic acid (C20:1)

The percentage of eicosenoic acid varied from 0.08% to 0.98% with an average value of 0.68% whereas the maximum value was observed in G10-S2 (0.98%) followed by G21-S2 (0.94%), G14-S2 (0.93%), P5(0.81%), G5-S1 (0.79%), G19-S2 (0.78%), P7 (0.73%), G21-S1 (0.71%) and G5-S2 (0.71%). On the contrary, the lowest value was found in P6 (0.08%). P1 (0.35%), G19-S3 (0.55%), G19-S4 (0.59%), G14-S1 (0.61%), G17-S1 (0.62%), G19-S1 (0.66%) and G17-S2 (0.68%); estimated values of these samples were statistically similar with the mean value of eicosenoic acid (Table 15). Wijesundera *et al*. (2008) found 1.4 to 1.5% eicosenoic acid among the cultivars of *Brassica juncea* on the contrary, Sawicka *et al.* (2020) found 8.64% eicosenoic acid was present in Indian mustard.

4.9.2.6 Erucic acid (C22:1)

The content of erucic acid showed diversification with a range from 0.81% to 48.58% while the mean value was 29.43%. The highest percentage of erucic acid was found in P7 (48.58%) followed by G19-S1 (44.53%), G10-S2 (35.86%), G10-S1 (35.72%), G5-

S2 (34.82%), G14-S1 (33.85%), G14-S2 (32.36%), G17-S2 (31.38%), P1 (29.13%), G17-S1 (27.80%) and G5-S1 (27.52%). On the other hand, P6 (0.806%) showed the lowest value for erucic acid. G5-S1 (22.137%), G19-S4 (22.19%), G21-S1 (23.47%), BARI11×BJ00-S2 (23.53%) and G19-S3 (24.36%); their estimated values were statistically similar around the average value of erucic acid (Table 15). Kumar Rai *et al.* (2018) also supported these statements who estimated 0.80 to 49.40% erucic acid in *Brassica juncea* species. Sharafi *et al*. (2015) reported 31.27% of erucic acid in Indian mustard while Iqbal *et al*. (2011) found 23.21 to 26.81% of erucic acid among different F_1 lines derived from *Brassica juncea* species.

4.9.3 Stability index analysis

The proportion of oleic acid to linoleic acid and linoleic acid to linoleic acid was estimated to obtain the stability index of the edible oils. The proportion of oleic to linoleic acid was ranged from 0.51 to 1.70. The highest proportional value for oleic to linoleic was observed in P6(1.70). In crossings, the highest index was found in G5-01 (1.19), G19-S4 (1.05) and G17-S2 (1.01). The proportional value was lowest in G14-S2 (0.55) (Table 16). Parental line P6 (4.21) possessed the ideal proportional value of omega-6 to omega 3 fatty acids. G19-S4 (3.58), G19-S3 (2.64) and G19-S2 (2.50) had the highest value of ω-6/ω-3 ratio whereas G21-S2 (1.35) possessed the lowest value among the 18 analyzed samples. Polish Organization for Prevention of Cardiovascular Diseases established the ω-6/ω-3 ratio to be equal 4:1 or 5:1. The recent studies revealed that disproportion (excess of ω-6) may result in an inflammatory condition, allergy, proliferation of cancer cells and nipple, prostate and large intestine tumors. Ratio of omega-6 to omega-3 fatty acids estimated by Walczak (2014) ranged from 0.60 to 1.38 and Khan *et al.* (2013) estimated 1.18. Hashempour *et al*. (2016) reported that majority of the currently used vegetable oils fall short of these recommendations. For a balanced diet, the proportion of oleic, linoleic and linolenic acid should be kept at a standard level among the edible oils.

Chapter V

Summary and Conclusion

The present research experiment was conducted on seven *Brassica juncea* varieties with 21 F_1 hybrid's and entitled on "Fatty acid compositions analysis of F_1 populations derived from 7×7 half diallel cross in mustard (*Brassica juncea* L.)". The goal of the undertaken experiment was screening to superior F_1 lines containing low erucic acid content. The genetic variability, heritability, correlation, combining ability, heterosis, and fatty acids compositions were evaluated for the selected varieties was analyzed. As yield is a complex quantitative trait, direct selection may not be effective. Hence, the genotypic and phenotypic correlation coefficients of variation, heritability and genetic gain were estimated for successful breeding program. Seven parents along with 21 F_1 hybrids were evaluated using RCBD design with three replications for 12 quantitative characters in two consecutive rabi season during 2019-20 and 2020-21 at the farm of Sher-e-Bangla Agricultural University, Dhaka-1207.

The estimated phenotypic variance was slightly higher than the genotypic variance for all the traits. The moderate phenotypic and genotypic coefficient of variations were found in number of primary branches per plant (13.02 and 11.68) and yield per plant (16.87 and 16.77) while rest of the traits showed low PCV and GCV respectively (less than 10%). High heritability was observed in all the traits except days to pod maturity (57.20%), siliquae length (46.03%) and seeds per siliquae (52.95%). In breeding programme, heritability coupled with genetic advance is regarded as important selection criteria for selecting the traits. The higher heritability coupled with high genetic advance as percentage of mean was found in number of primary branches per plant (81.31 and 21.58) and yield per plant (98.81 and 34.35).

Correlation coefficients among the different pairs of yield attributing traits indicating, yield per plant was significantly and positively correlated with siliquae length (0.807, 0.569) and 1000 seed weight (0.791, 0.722) both at genotypic and phenotypic levels. However, positive correlation was also observed in days to pod maturity (0.167, 0.117), plant height (0.343, 0.317), number of secondary branches (0.539, 0.458), siliquae per plant (0.253, 0.245) and thousand seed weight (0.171, 0.109) with yield per plant at both genotypic and phenotypic levels. These positive association indicating, increasing siliquae length and 1000 seed weight was highly attributed to the improvement of yield per plant. From the estimation of correlation illustrated that selection for yield improvement should be given emphasizes on the traits viz. plant height, secondary branches per plant, siliquae length, siliquae per plant and 1000 seed weight as these traits were positively associated with yield per plant.

Days to 50% flowering for the selected population extended from 41.67 DAS to 53.00 DAS. Among the crossings, both G3 (41.67) and G6 (41.67) displayed the lowest duration for 50% flowering coverage. In a line, 80% plants became matured between 102.67 to 112.33 DAS. Again, the lowest maturity index was found in hybrid G18 (104.33) followed by G12 (104.67) and G7 (105.67). In general, *Brassica juncea* species required longer period for their vegetative growth. The shortest plant was found in G2 (137.33) followed by G5 (138.45) and G4 (139.33) among the crossings. Siliquae per plant was one of the important yield attributing traits, among the lines it showed diversification which was ranged from 189.67 to 357.33 with an average 274.78. The highest siliquae producing plant was found in hybrids G10 (357.33) followed by G7 (340.44) and G13 (333.00). Again, another important trait, 1000 seed weight, was ranged from 2.57 to 3.87 g. The highest 1000 seed weight producing line was observed in G21 (3.87) followed by G8 (3.80) and G16 (3.77) among the F_1 lines. Furthermore, seed yield per plant was ranged from 5.54 to 16.89 g. The highest seed yield was produced by hybrids G8 (16.89) followed by G11 (16.31) and G9 (15.52). In case of parents, P7 (7.99) produced the highest seed yield per plant.

In order to develop short early matured variety negative heterosis is desirable for days to first flowering, days to 50% flowering, days to pod maturity and plant height. In case of days to 50% flowering all the lines showed negative heterosis over better parent and check variety respectively. Hybrids G10 (-20.13%) and G5 (-18.87%) had the highest negative heterotic effects over better parent and both G3 (-11.35%) and G6 (-11.35%) displayed the highest effects over check variety. Surprisingly, only 8 and 2 lines had negative heterotic effects over better parent and check variety for days to pod maturity respectively. For producing dwarf plant negative heterosis was desirable. In F_1 lines, 17 lines manifested negative heterobeltiosis and standard heterosis. Hybrids G4 (-18.31%, -11.13%) followed by G14 (-12.58%, -9.64%) had the highest negative and significant heterotic effects over better parent and check variety. Again, for yield per plant, all the 21 lines manifested positive and significant heterotic effects. Among the lines, hybrids G7 (203.49% and 111.53%) followed by G9 (111.96% and 94.27%) and G11 (104.27% and 104.27%) had the highest heterotic effects over better parent and check variety respectively.

Analysis of variance for all the traits showed strong significance for general combining ability (GCA) and specific combining ability (SCA). The best suited combiners for yield performance were found in parent P2 (0.54) and P7 (0.40) while P4 (0.18) and P7 (0.15) could be selected for 1000 seed weight. P4 (0.52) and P3 (0.27) for seeds per siliquae and only P3 (4.68) was considered as the good general combiner for siliquae per plant (Table 8). However, to get early matured plant P1 (-2.15 and -1.34) and P4 (-0.78 and -0.97) were considered as good general combiner for days to first flowering and days to 50% flowering respectively besides, parent P3 (-1.44) for days to pod maturity. In case of plant height, inbred P1 (-7.72) followed by P3 (-4.51) could be chosen as the best general combiner, these significant negative estimates were desirable for developing short stature hybrids.

For yield per plant, out of 21 crosses, 18 crosses had positive and significant SCA effects (Table 9). The highest SCA effects for seed yield were observed in G7 (4.03) preceded by G19 (3.26) and G11 (3.29) besides, hybrid G10 (89.87) preceded by G7 (68.90) and G13 (62.76) was showed the highest significant positive SCA effects for siliquae per plant thus, these lines could be selected for yield related improvement. In case of days to 50% flowering, G10 (-3.05) was considered superior line for early flowering followed by G19 (-2.67) and G21 (-2.31) but, unfortunately only 8 lines showed negative non-significant SCA effects for days to pod maturity in which G18 (-1.96) and G21 (-1.259) was noted as the highest SCA effects. For plant height, out of 21 crosses, negative estimates were found in 10 cross combinations. Hybrid G21 (-9.95) was the best specific combiner followed by G4 (9.73) and G12 (-7.01) to obtain the short type of plants.

Maintaining a balanced diet, the edible oils should have contained low saturated fats. For the selected samples, total saturated fatty acids (TSFA) were estimated from myristic, palmitic, stearic and arachidic acid. TSFA within the samples ranged from 7.18% to 16.53%. Among the cross combinations G19-S1 (10.81%) had the lowest TSFA. Among the selected samples, palmitic acid varied from 2.40-7.36% with an average of 4.75% (Table 15). G19-S1 (7.36%) possessed the highest value for palmitic acid whereas the lowest palmitic acid was found in G17-S2 (3.36%) followed by G5-S1 (3.97%) and G19-S1 (3.99%). Content of stearic acid extended from 0.80% to 2.07% with an average 1.13% (Table 15). The highest percentage among the F_1 was found in G14-S1 (1.44%). However, the lowest value for stearic acid was observed in G21-S2 (0.88%) which was statistically similar with G17-S1 (0.98%) and G21-S2 (0.99%).

Among the unsaturated fatty acids palmitolic, oleic, eicosenoic and erucic acid was considered for calculating total monounsaturated fatty acids (MUFA). MUFA was varied from 40.60% (G21-S2) to 61.25% (P6). Among the cross combinations G19-S1 (59.18%), G17-S2 (54.31%) and G10-S1 (54.10%) contained the highest amount of monounsaturated fatty acids. The lowest erucic acids was observed in hybrid G5-S1(22.14%), G19-S4 (22.19%), and G21-S1 (23.53%) and in parents it was found in P6 (0.81%). Increase or decrease in erucic acid is primarily reflected in the content of oleic acid. High oleic acid in oils also contains low erucic acid and vice versa. Hence, oleic acid was also higher in P6 (53%). Whereas hybrid G19-S4 (27.81%) preceded by G19-S4 (24.16%) and G19-S2 (23.45%) showed medium range of oleic acid (%) through fatty acid profiling.

Polyunsaturated fatty acids (PUFA) were estimated from linoleic and linolenic acid. PUFA was ranged from 27.81% to 43.83%. The highest PUFA was found in hybrids G21-S2 (43.83%) followed by G17-S1 (40.79%) and G14-S2 (40.59%). The highest percentage of linoleic was found in hybrids G17-S1 (28.59%) followed by G19-S2 (27.29%) and G19-S4 (26.54%). Among the samples, linolenic acid varied from 7.404% to 18.63% with an average value of 12.622%. The lowest value was found in G19-S4 (7.42%), G17-S2 (9.34%) and G5-S1 (10.44%).

Linoleic acid and linoleic acid are an essential component for edible oils as human body does not synthesize theses type of fats. The proportion of oleic to linoleic acid was ranged from 0.51 to 1.70 and according FAO the ratio should be 2:1. The highest proportional value for oleic to linoleic was observed in P6(1.70). In crossings, the highest index was found in G5-01 (1.19), G19-S4 (1.05) and G17-S2 (1.01). Whereas FAO recommended the linoleic to linolenic acid ratio for edible oils is 4:1. Parental line P6 (4.21) possessed the ideal proportional value of omega-6 to omega 3 fatty acids. Hybrid G19-S4 (3.58), G19-S3 (2.64) and G19-S2 (2.50) had the highest value of ω-

6/ω-3 ratio whereas G21-S2 (1.35) possessed the lowest value among the 18 analyzed samples. Considering the general combining ability P1, P3 and P7 can be used as good inbred lines and hybrids G3, G4, G6, G14, G17 and G21 can be selected for early maturity variety based on the best specific combiner and their heterotic effects. Furthermore, in case of higher yield and yield contributing traits G1, G3, G7, G11 and G13 were recommended for selection. Besides, from the fatty acid analysis, BINA7×BJ00-S1, BARI sharisha-11×BJ00-S1 and BJ00×BARI sharisha-10-S2 can be used as a potential line for selecting plants having low erucic acid in next generations. Hence, these lines that have desirable general combining ability effects, specific combining ability effects and heterotic effects as well as low erucic acid with all other fatty acid compositions at a standard level may be selected for future breeding programme.

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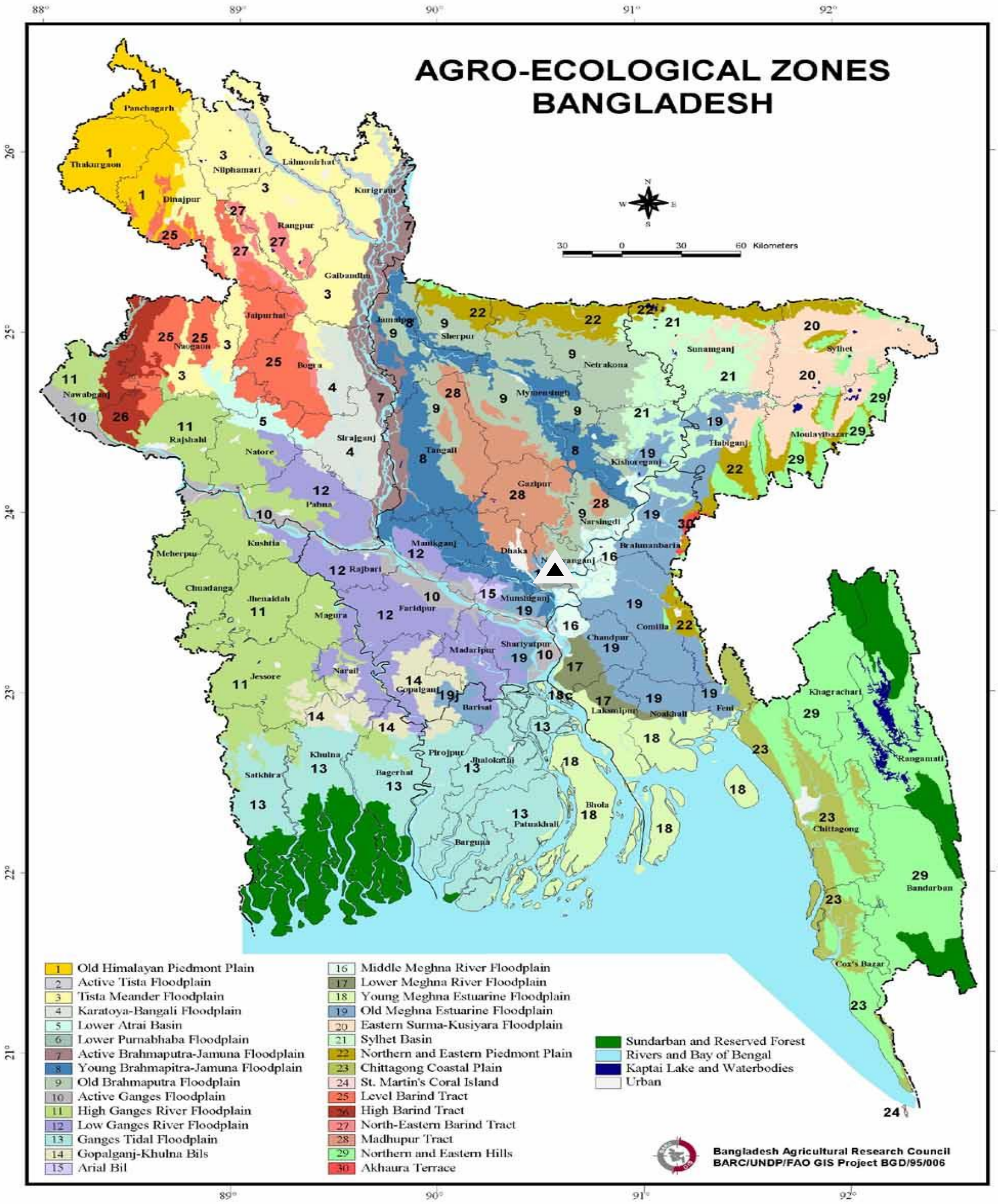
APPENDICES

Appendix 1. Map showing the experimental site of the study



▲ The experimental site under study

Appendix 2a. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from November 2019 to March 2020.

Month	Year	Monthly average air temperature (°C)			Average relative humidity (%)	Total rainfall (mm)	Total sunshine (hours)
		Maximum	Minimum	Mean			
Nov.	2019	31	18	24	63	Trace	216
Dec.	2019	28	16	22	61	Trace	212
Jan.	2020	27	13	20	57	Trace	198
Feb.	2020	29	18	23	70	3	225
Mar.	2020	32	22	25	73	4	231

Source: Bangladesh Meteorological Department (Climate division), Agargaon Dhaka-1212.

Appendix 2b. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from November 2020 to March 2021.

Month	Year	Monthly average air temperature (°C)			Average relative humidity (%)	Total rainfall (mm)	Total sunshine
		Maximum	Minimum	Mean			
Nov.	2020	29.6	19.2	24.40	65	32.4	240
Dec.	2020	26.4	14.1	20.25	61	12.5	248
Jan.	2021	25.4	12.7	19.50	58	8.7	263.5
Feb.	2021	28.7	15.5	22.1	53	28.4	252
Mar.	2021	32.5	20.4	26.45	50	63.8	217

Source: Bangladesh Meteorological Department (Climate division), Agargaon Dhaka-1212.

Appendix 3. Themorphological, mechanical and chemical characteristics of soil of the experimental site as observed prior to experimentation (0 -15 cm depth).

A. Morphological characteristics of the experimental field

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

Mechanical composition:

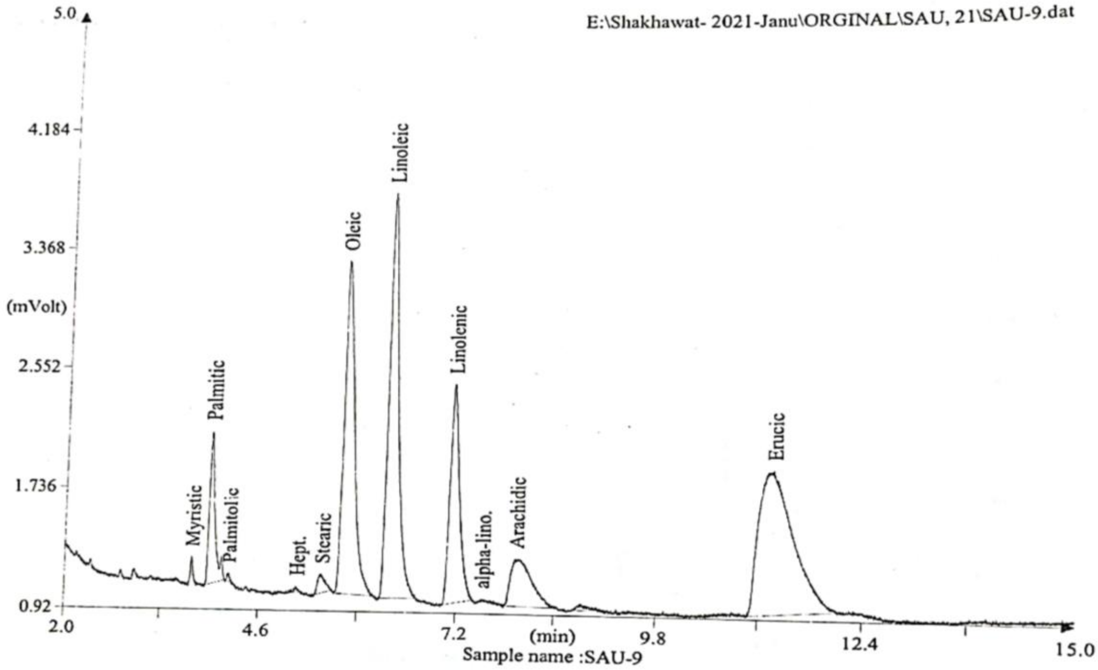
Particle size	Constitution
Texture	**Loamy**
Sand	**40%**
Silt	**40%**
Clay	**20%**

Chemical composition:

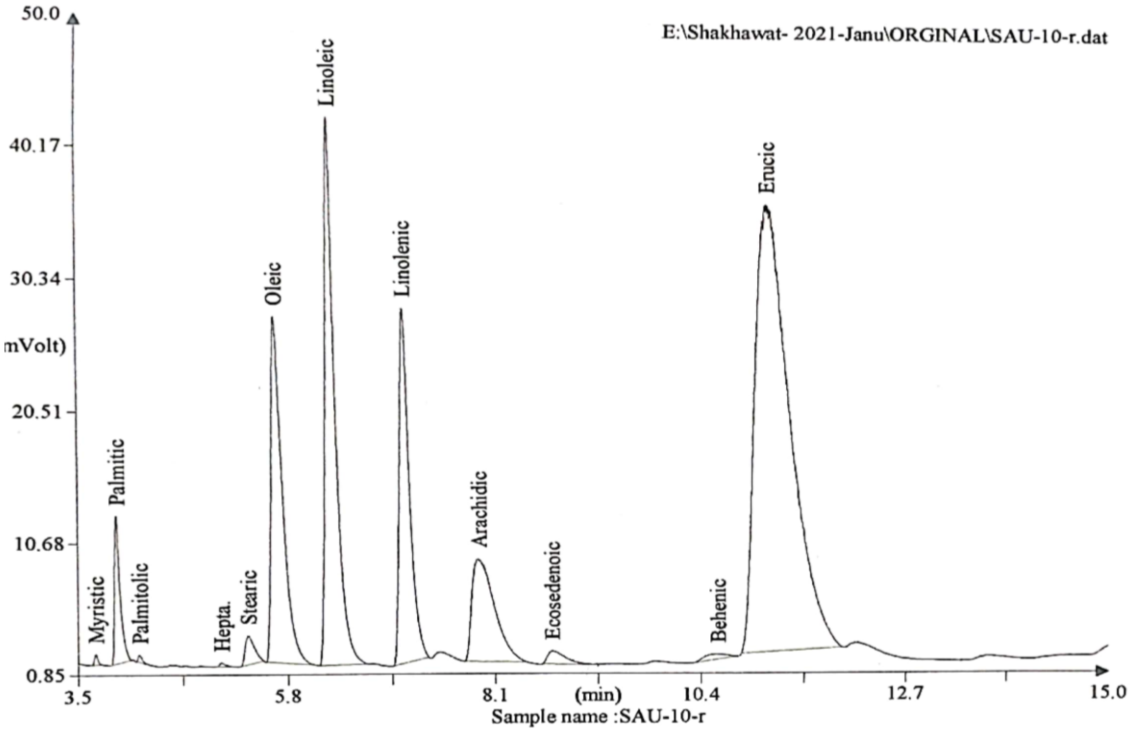
Soil characters	Value
Organic matter	**1.44 %**
Potassium	**0.15 meq/100 g soil**
Calcium	**1.00 meq/100 g soil**
Magnesium	**1.00 meq/100 g soil**
Total nitrogen	**0.072**
Phosphorus	**22.08 µg/g soil**
Sulphur	**25.98 µg/g soil**
Boron	**0.48 µg/g soi**
Copper	**3.54 µg/g soil**
Iron	**262.6 µg/g soil**
Manganese	**164 µg/g soil**
Zinc	**3.32 µg/g soil**

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

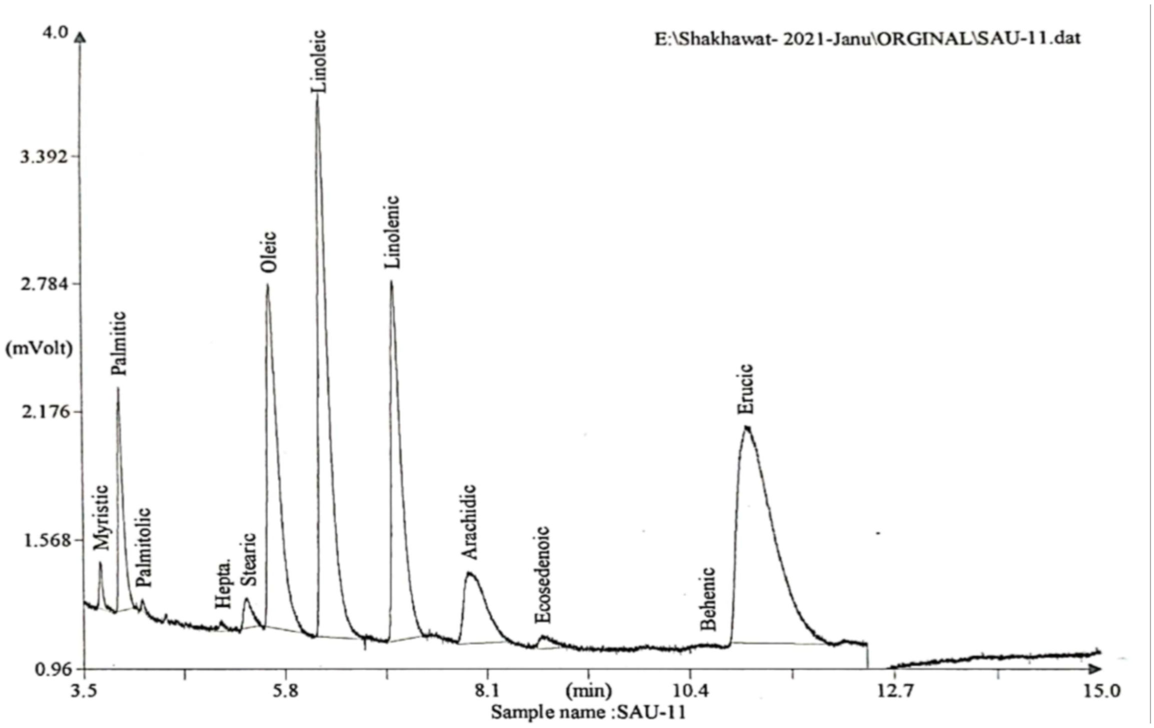
Appendix 4a: Fatty acid compositions in BINA-7



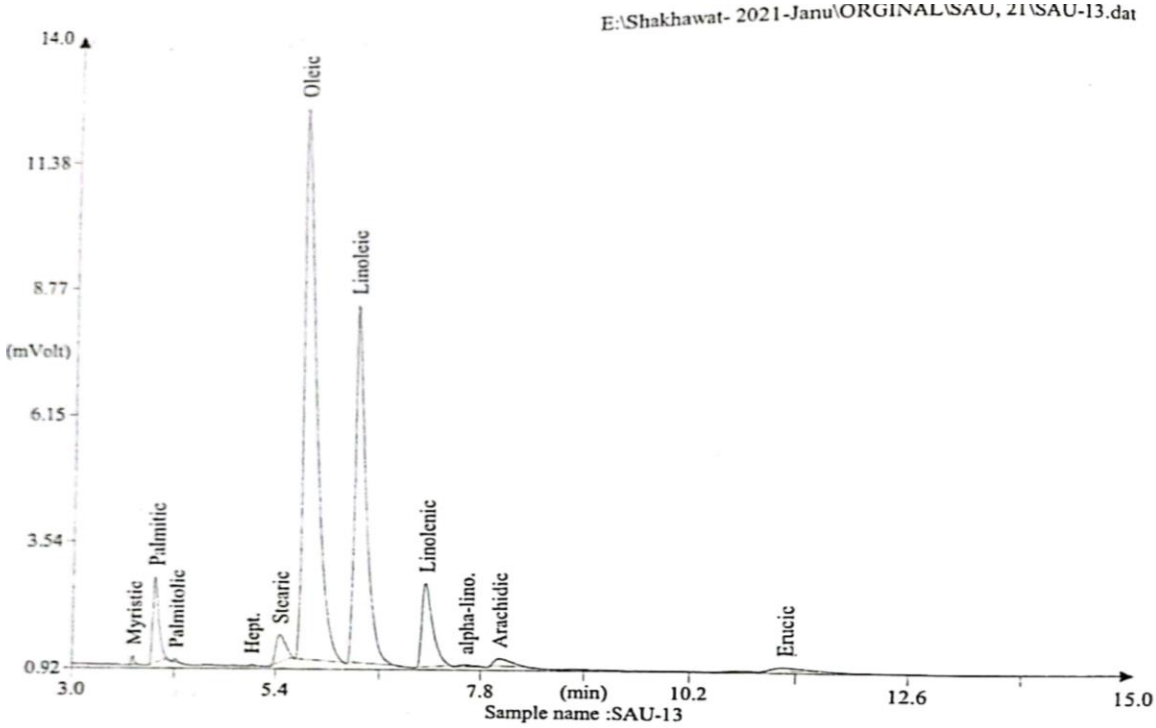
Appendix 4b: Fatty acid compositions in BARI-11



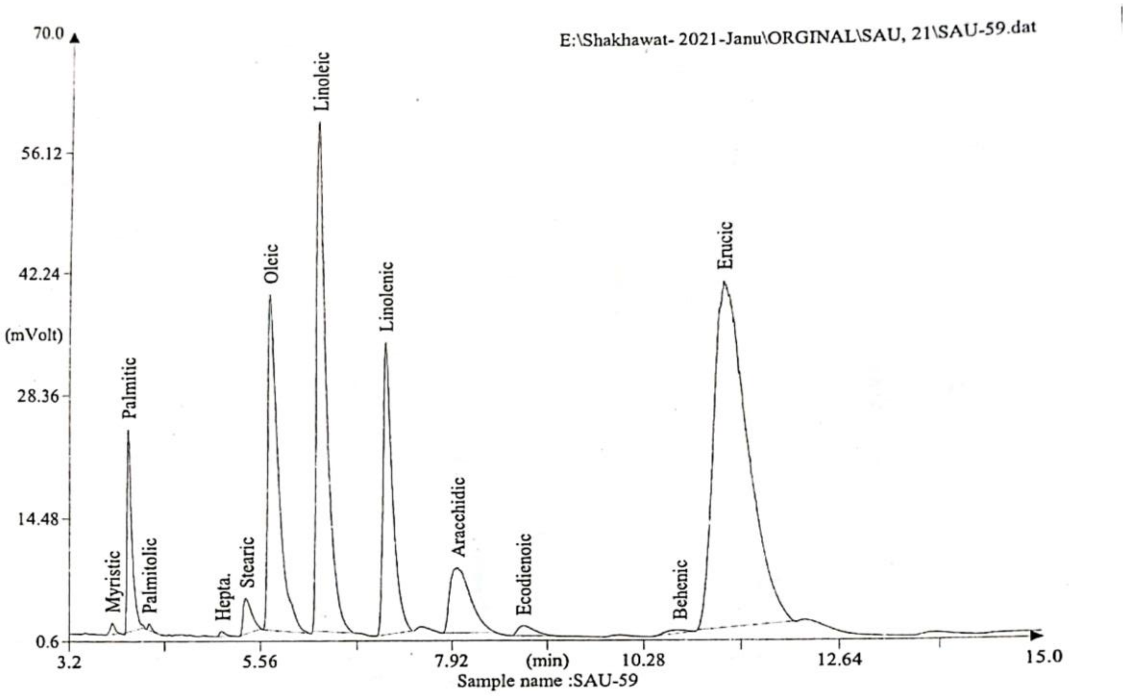
Appendix 4c: Fatty acid compositions in BARI-16



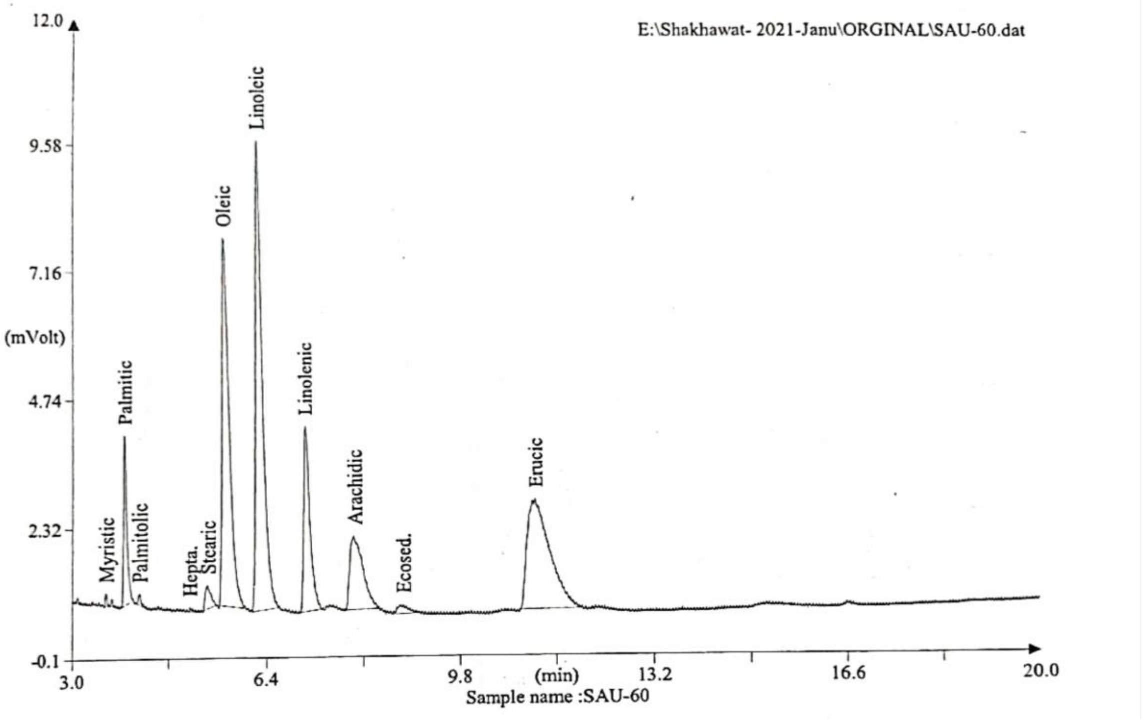
Appendix 4d: Fatty acid compositions in BJ00



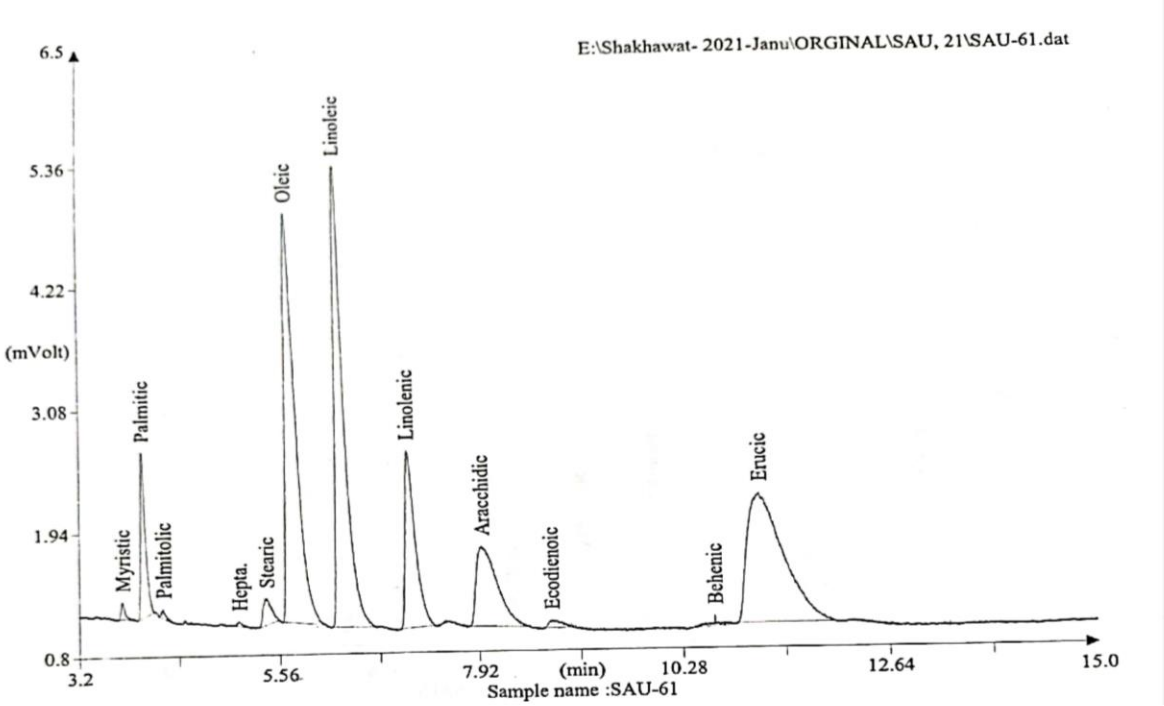
Appendix 4e: Fatty acid compositions in BARI16×BJ00 (Sample 1).



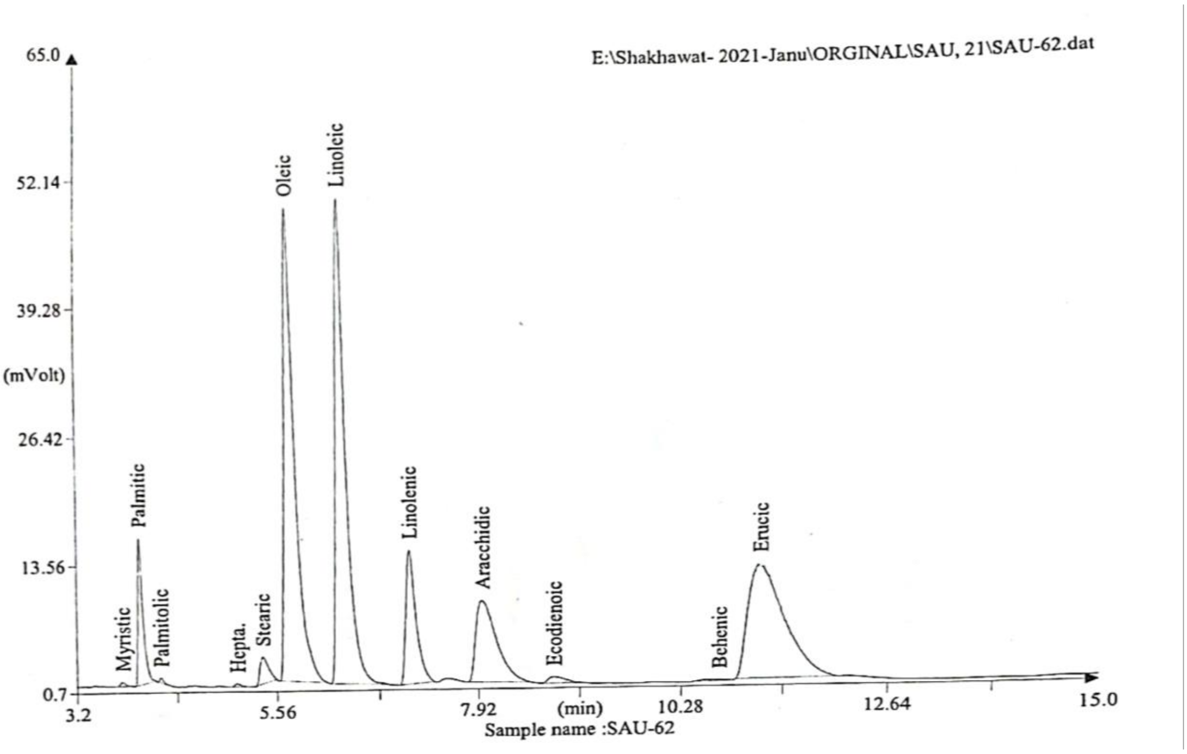
Appendix 4f: Fatty acid compositions in BARI16×BJ00 (Sample 2).



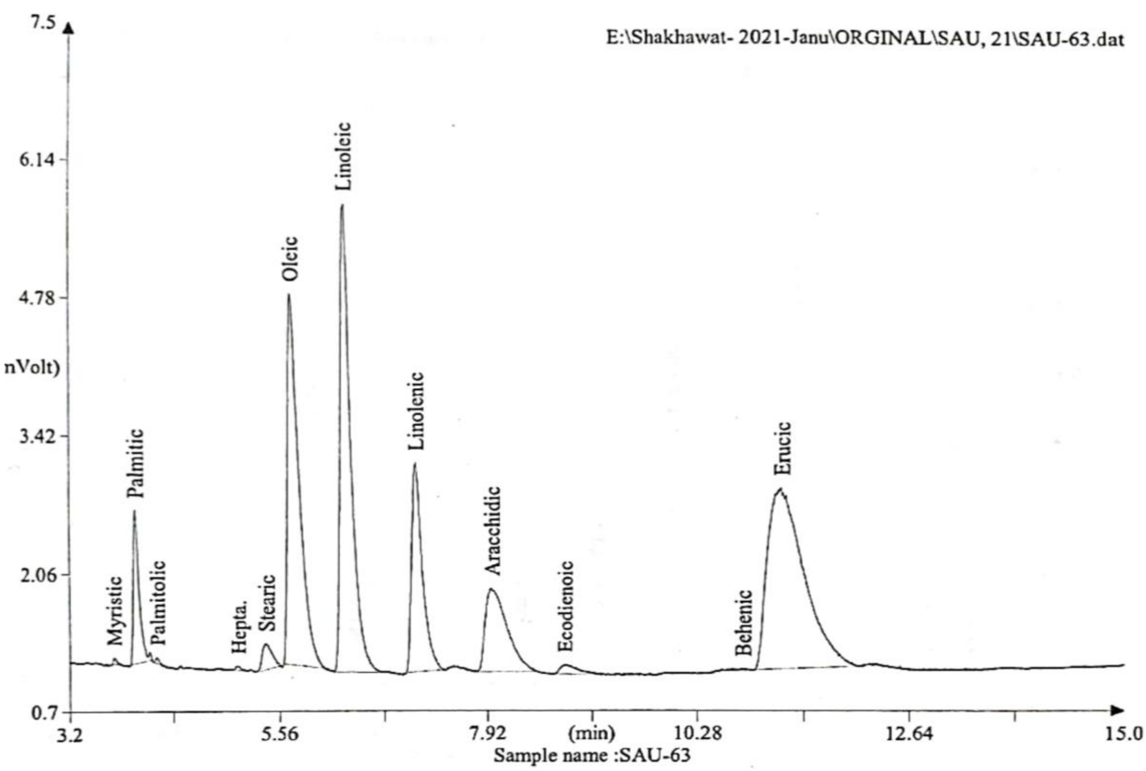
Appendix 4g: Fatty acid compositions in BJ00× BARI16 (Sample 1).



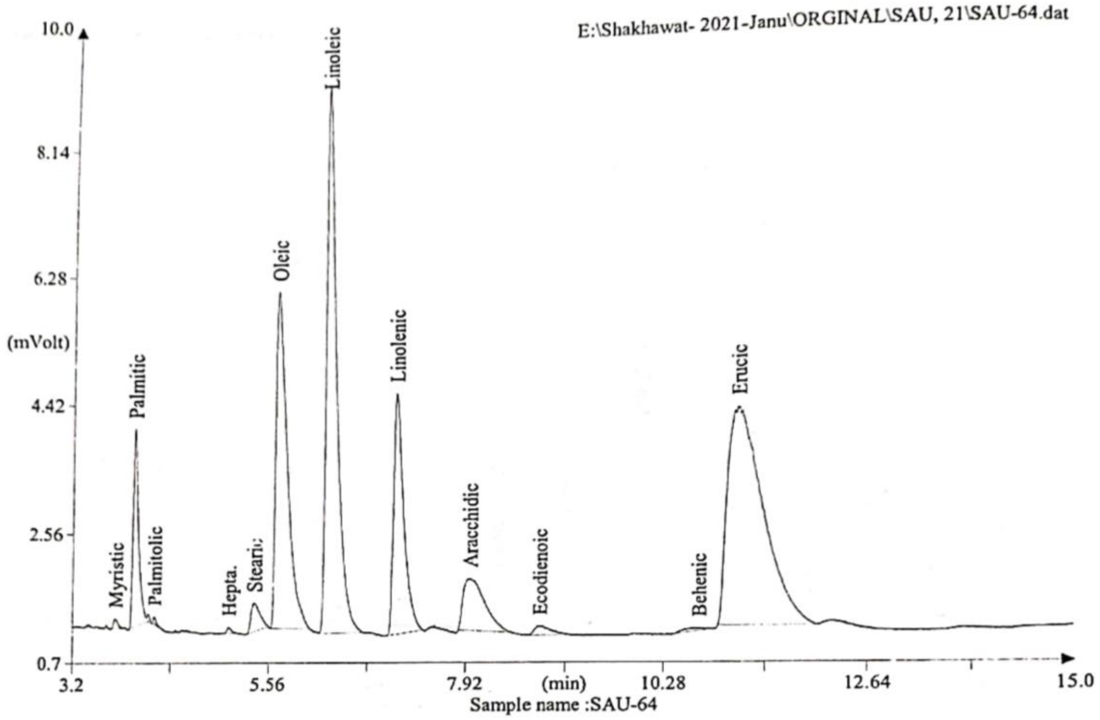
Appendix 4h: Fatty acid compositions in BJ00× BARI16 (Sample 2).



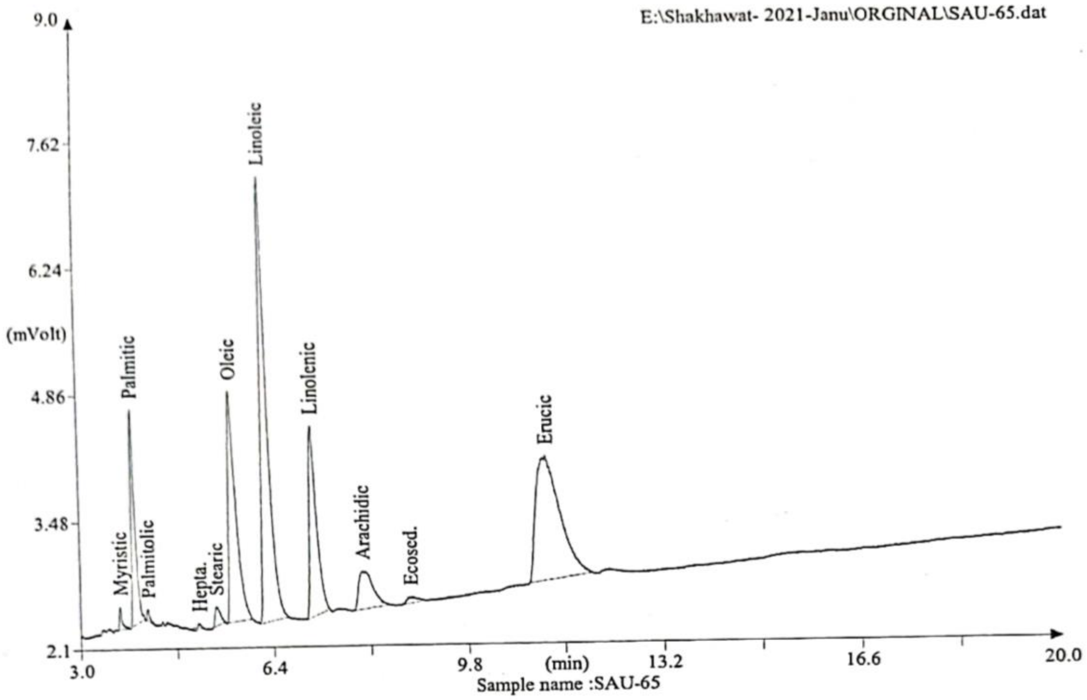
Appendix 4i: Fatty acid compositions in BINA7×BJ00 (Sample 1).



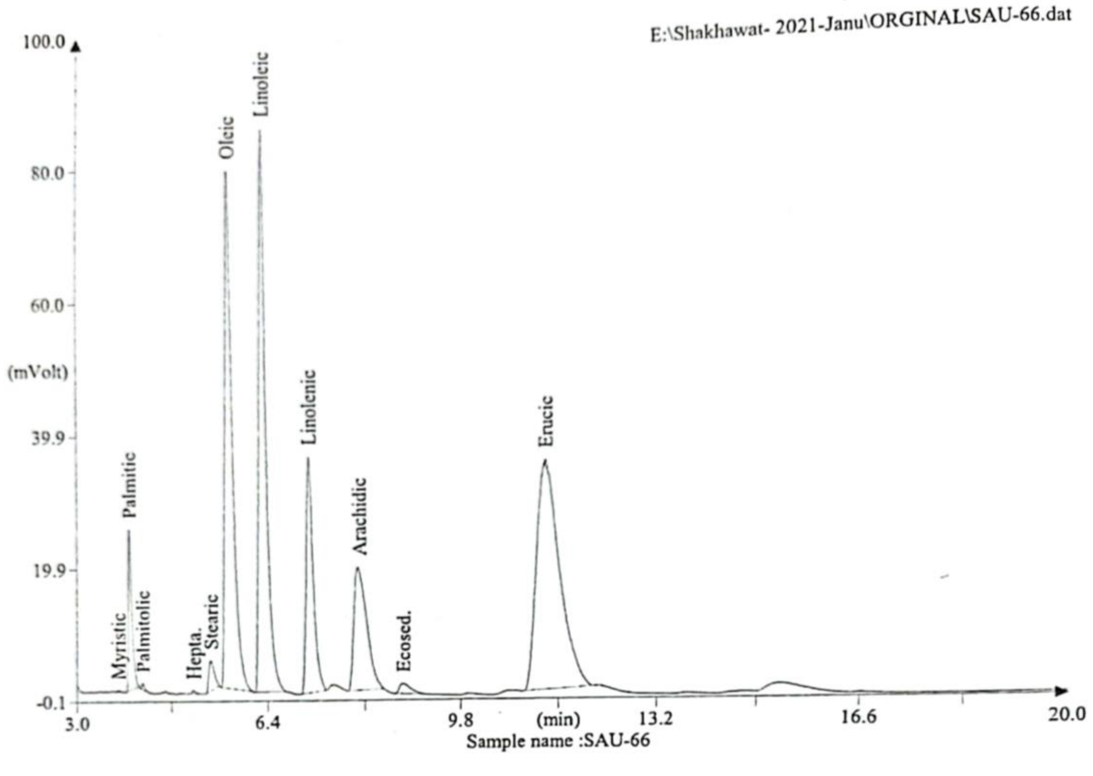
Appendix 4j: Fatty acid compositions in BINA7×BJ00 (Sample 2).



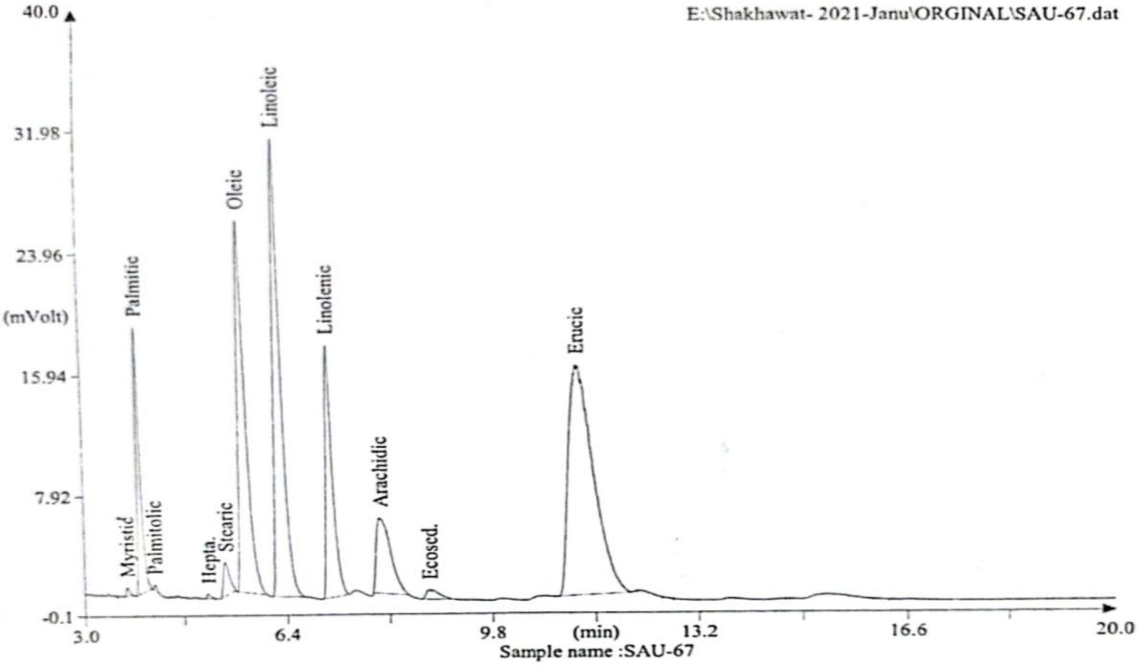
Appendix 4k: Fatty acid compositions in BARI10×BJ00 (Sample 1).



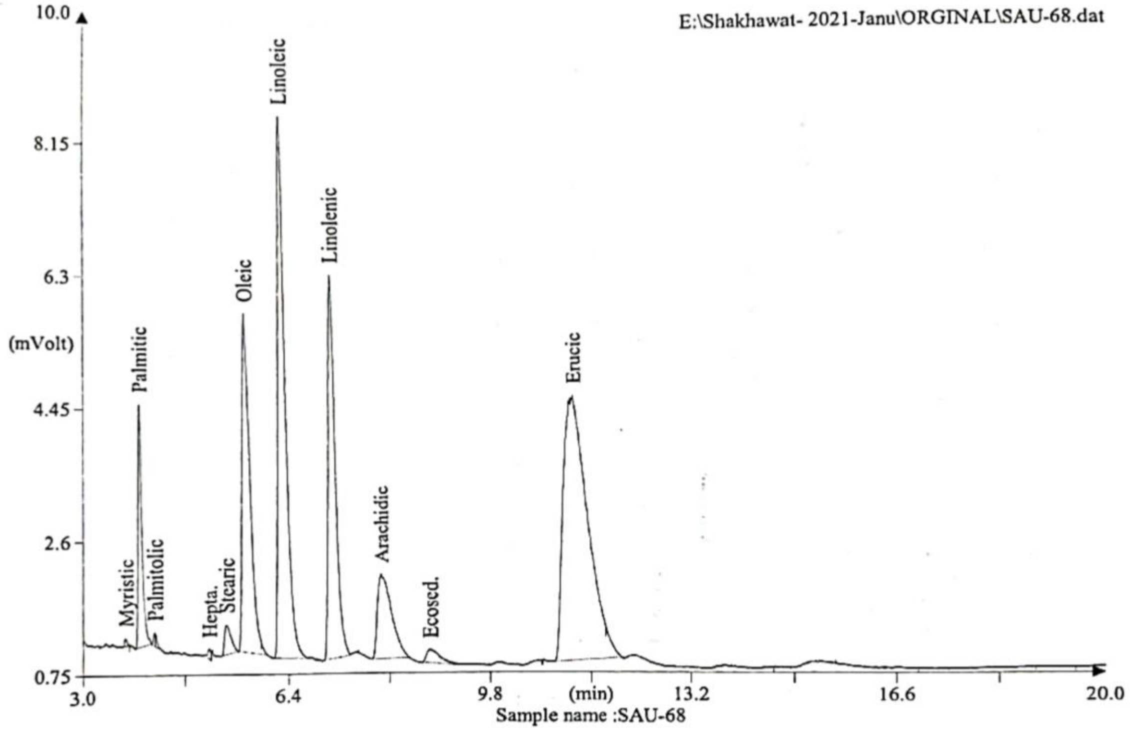
Appendix 4l: Fatty acid compositions in BARI10×BJ00 (Sample 2).



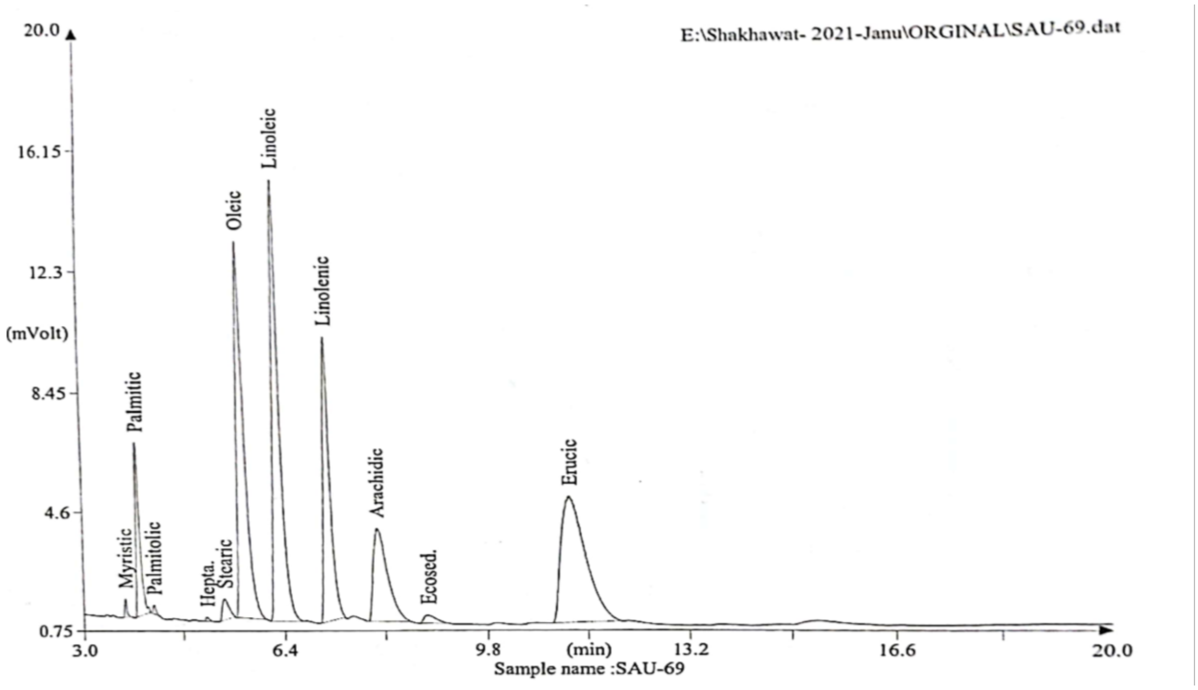
Appendix 4m: Fatty acid compositions in Rye5×BJ00 (Sample 1).



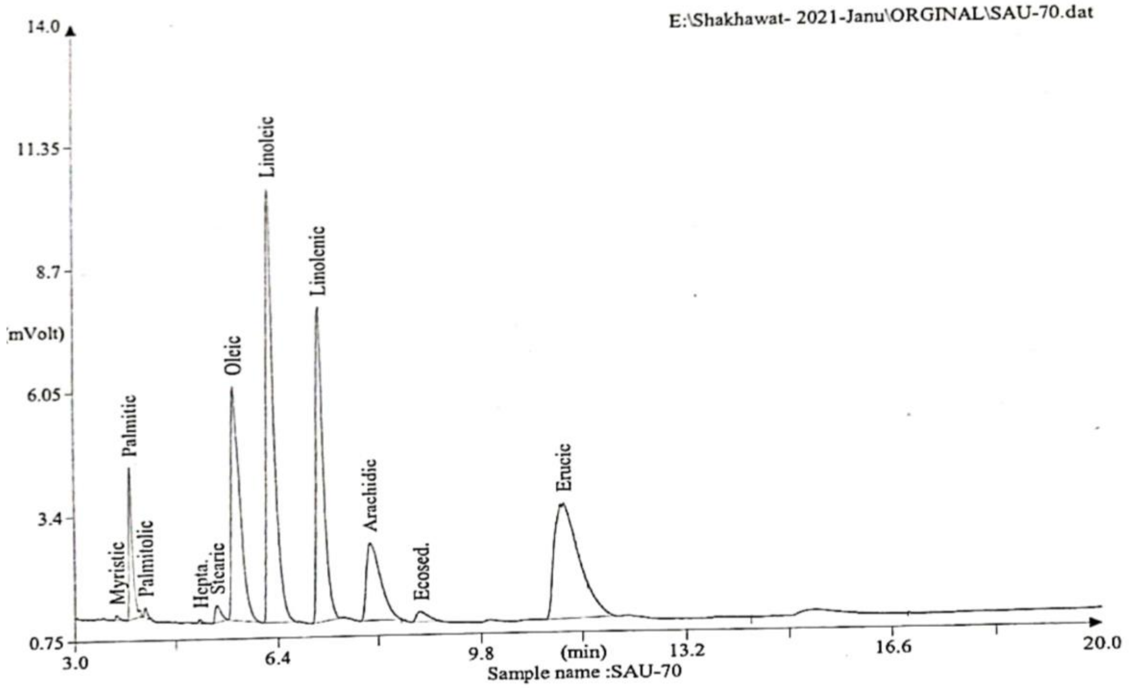
Appendix 4n: Fatty acid compositions in Rye5×BJ00 (Sample 2).



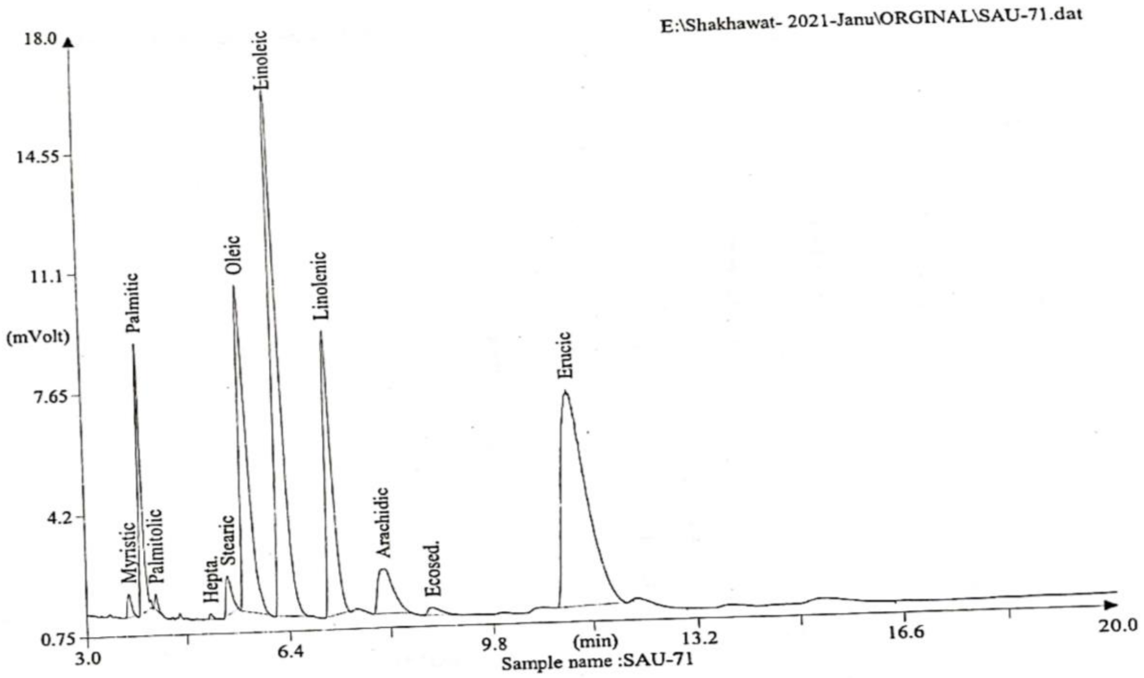
Appendix 4 o: Fatty acid compositions in BARI11×BJ00 (Sample 1).



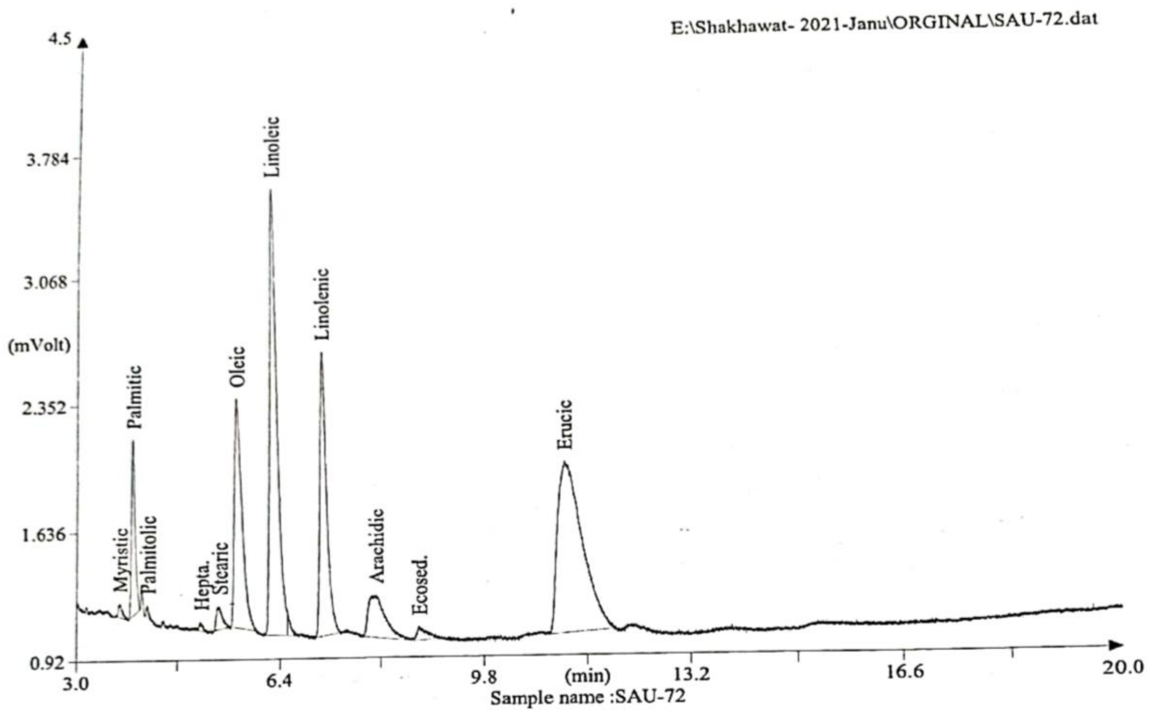
Appendix 4p: Fatty acid compositions in BARI11×BJ00 (Sample 2).



Appendix 4q: Fatty acid compositions in Daulat×BJ00 (Sample 1).



Appendix 4r: Fatty acid compositions in Daulat×BJ00 (Sample 2).



Appendix 5: Research field visited by the honorable personnel.