

**GENETIC COMPONENTS AND HETEROSIS ANALYSIS OF F₂ AND BC₁F₁
POPULATIONS IN *Brassica juncea* L.**

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CERTIFICATE

*This is to certify that thesis entitled, “GENETIC COMPONENTS AND HETEROSIS ANALYSIS OF F₂ AND BC₁F₁ POPULATIONS IN *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 **Fatema Tuj Johora**, Registration No.: **15-06457** 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 duly acknowledged.

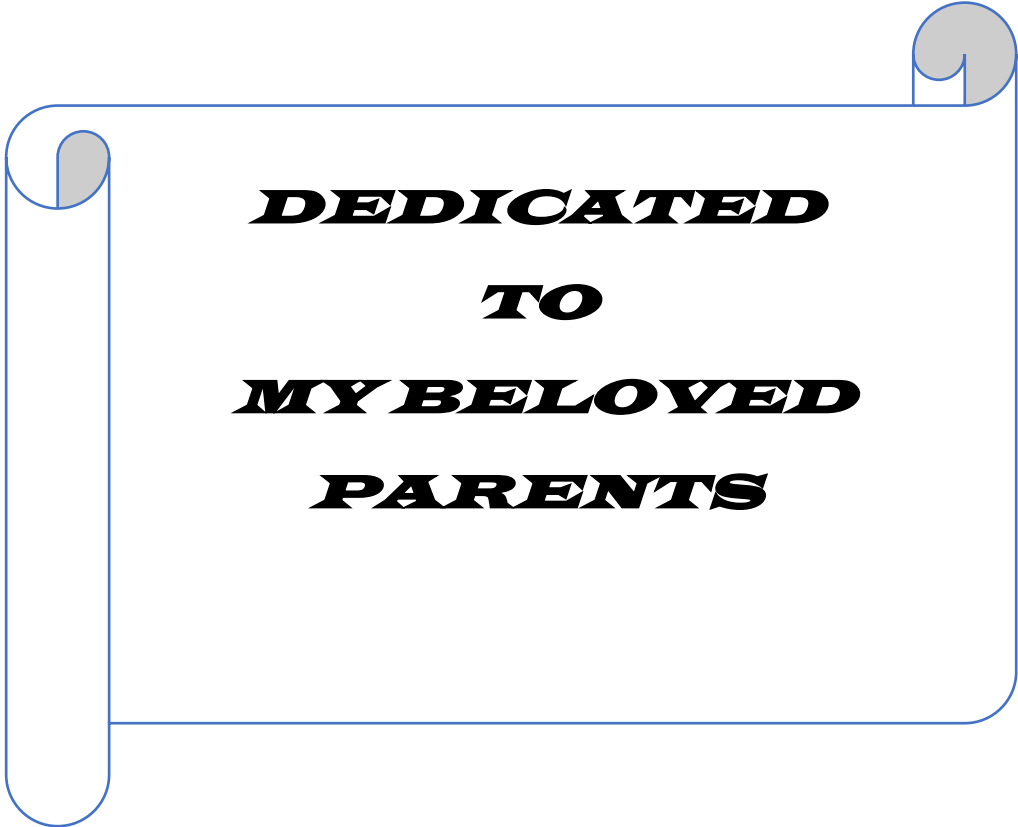
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DEDICATED
TO
MY BELOVED
PARENTS

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By

FATEMA TUJ JOHORA

ABSTRACT

The investigation was conducted to estimate the phenotypic performance, and to assess the genetic components, variability, heterosis and inbreeding depression among the twenty-one F₂ and six BC₁F₁ populations of Indian mustard (*Brassica juncea*). The research was conducted at Sher-e-Bangla Agricultural University during rabi seasons of 2021-22 in a randomized complete block design with three replications. All the twelve traits studied here showed significance variation among the F₂ populations. The phenotypic performance of the F₂ populations viz., G9, G12, G13, G16 and G4, G20, G17 showed comparatively better mean performance in terms of early maturity, and yield, respectively than the rest of populations. The populations G1 had the lowest days for acquiring 80% maturity (104.33 days), while G12 had the shortest plant height (126 cm) among the 21 F₂ populations, while G17 produced the highest yield (15.6gm) per plant among the twenty-one F₂ populations. All of the twelve traits displayed high heritability (h²_b) in the broad sense e.g., heritability for days to siliqua maturity (73.70%), for plant height (90.90%), for days to first flowering (82.50%), and for seeds per siliqua (82.27%), indicating that high genotypic effects accounted for the majority of total variation. The correlations study showed that yield per plant had positively and significantly correlation with number of primary branches, number of secondary branches, siliqua length, siliqua per plant. The F₂ populations G4, G14, G21 showed highest significant negative heterosis for day to maturity, while F₂ populations G8, G13, G17, G19, G20 showed highest significant positive heterosis for yield indicated that these populations might be considered for selection for earliness and yield improvement. G1, G13, G18, G20 (as these populations show highest positive inbreeding depression in case of earliness and plant height) are the considered potential lines for earliness, short stature) while G2, G8, G13, G17 had minimal inbreeding depression in terms of siliqua per plant, siliqua length and yield per plant, hence these are the genotype desired for higher yield. Among the backcrossed population, the combinations (P5×P6) × P5 showed the best result for yield contributing trait, early maturity and short stature. Altogether, the F₂ populations viz., G4, G5, G8, G13, G17, G19, and G20 might be chosen as potential populations for selection of early-maturing, and high-yielding lines in future.

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SOME COMMONLY USED ABBREVIATIONS

At the rate	@	Genetic advance	GA
Agro ecological zone	AEZ	Genotypic coefficient of variation	GCV
Agriculture	Agric	Heritability in broad sense	h^2_b
Agronomy	Agron.	Heritability in narrow sense	h^2_n
America	Am	Horticulture	Horti.
Analysis of variance	ANOVA	International	Int.
And others	<i>et al.</i>	Industrial	Ind.
Applied	Appl.	Journal	J.
Achieves	Arch.	Kilogram	Kg
Australia	Aus.	Meter	M
Bangladesh Agricultural Research Institute	BARI	Mean sum of square	MS
Bangladesh Bureau of Statistics	BBS	Muriate of potash	MOP
Bangladesh	BD	Ministry of agriculture	MOA
Bangladesh Institute of Nuclear Agriculture	BINA	Number	No.
By the way of	Via	Namely	Viz.
Biology	Biol.	Phenotypic coefficient of variation	PCV
Botany	Bot.	Percent	%
Breeding	Breed.	Phenotypic variance	σ^2_p
Cellular	Cell.	Percentage of coefficient of variation	CV%
Cultivars	cv.	Properties	<i>Prop.</i>
Current	Curr.	Residual effect	R
Centimeters	Cm	Research	<i>Res.</i>
Chemistry	Chem.	Randomized Complete Block Design	RCBD
Degree Celsius	°C	Science	<i>Sci.</i>
Degree of freedom	Df	Serial	Sl.
Days to first flowering	DFP	Standard error	SE
Days to 50% flowering	D50%F	Silique length	SL
Days after sowing	DAS	Seeds per silique	SPS
Days to maturity	DM	Seed yield per plant	SYP
Ecology	Eco.	Square meter	m ²
Electronic	Electron.	Sher-e-Bangla Agricultural University	SAU
Etcetera	etc.	Genetic advance	GA
Environment	Environ.	Genotypic coefficient of variation	GCV
Environmental variance	σ^2_e	Heritability in broad sense	H^2_b
Food and Agricultural Organization	FAO	Phenotypic coefficient of variation	PCV

CHAPTER I

INTRODUCTION

The genus *Brassica* has been marked as the most cautiously valued member in the population of Brassiceae, which is a member of family Brassicaceae. This family and genus consist of a multipurpose bunch of species that embraces major agricultural products used as oil source and vegetable source. Rapeseed-mustard (*Brassica napus*, *B. campestris* and *B. juncea* L) are grown all over the world as an important source of edible oil as described by the Triangle of U theory (Abideen *et al.*, 2013). *Brassica* oil crops are the most important group of species that supply major edible oil in Bangladesh (BBS, 2011a). Mustard and rapeseed seeds contain 40%-45% oil, 25% protein (BBS, 2011b). *B. juncea*, having its place to the Brassicaceae family, is a hybrid and also amphidiploid (AABB genome, $2n=36$) consequentially originated from the fusion of *B. rapa* (AA genome, $2n=20$) and *Brassica nigra* (BB genome, $2n=16$). Origin of *B. juncea* L. was thought in Asiatic region and its prime center of diversity found in China from where it migrated to India and other sub continental countries. Oil content in *B. juncea* L. generally varies from 30 to 48 % (Gupta *et al.*, 2013) and protein content varies in 28 to 36 % (Das *et al.*, 2009).

Mustard oil is the third largest edible oil produced in the world after soybean oil and palm oil (Devi and Sharma., 2018). Based on a comparison of 14 countries in 2021, Nepal ranked the highest in mustard seed production with 220,250 tons followed by Russia and Canada (FAOSTAT, 2022). On the other end of the scale was Iran with 3.26 tons, Kyrgyzstan with 14.1 tones and Bhutan with 331 tons. Total mustard seed production was recorded 532,769 tons in 2021 in the World (FAOSTAT, 2022). This is 1.45 % less than in the previous year. The top ranked country, Nepal, accounted for 41.3% of mustard seed production in the world. The best top 3 countries hold a 79.8% share while the ten largest countries have some 99.9% in 2021 (Jagonews24).

Mustard oil is produced by crushing mustard seeds, combining the crushed seeds with water, then distilling the mixture. Because of its potent flavor, overpowering scent, and high smoke point, mustard oil is frequently used as a cooking oil for sautéing and stir-frying vegetables. The market is observing a shift toward culinary culture that supports strongly flavored cuisines using mustard oil, and consumers in Bangladesh are observing a change in dietary habits. Rising health consciousness has an impact on

eating patterns as well. To meet different needs, a variety of mustard oils are available. Additionally, cooking was the only use for mustard oil. However, it is now used for a variety of pharmacological purposes, aromatherapy, etc., and serves a variety of purposes, such as stimulant, appetizer, anti-fungal, anti-bacterial, hair vitalizer, etc., offering a variety of advantages to the body and skin. Therefore, demand for mustard oil in Bangladesh is likely to be supported by the growing use of mustard oil in cosmetics and personal care products.

When it comes to providing high energy dietary components for human nutrition, edible oil is essential. One of the two required fatty acids is absent from many dietary oils; however, mustard gives humans the two essential fatty acids linoleic and linolenic acid. (Khan *et al.*, 2009).

According to USDA, the result of analyzing the total edible oil market in Bangladesh comes out as 65.81% is occupied by mustard/ rapeseed followed by peanut (13.77%), Soybean (11.13%), sunflower (2.08%) and others (7.21%). In the fiscal year of 2021-2022, 8,17,235.05 acres was cultivated by mustard which was calculated to be 8,14,288.54 acres in the immediate fiscal year 2020-2021. The yield for 2021-2022 stood for 501.27 kg/acre (BBS 2022) which was 487.04 kg/acre in the year 2020-2021 (BBS 2021). The production was 409659.06 MT and 396594.28 MT in the year of 2021-2022 and 2020-2021 respectively (BBS 2022).

There is a minimum 2.5 million MT demand for edible oil in Bangladesh, of which 0.5 million MT met from mustard oil. Consequently, approximately 2 million tons of edible oils must be imported each year. (Chowhan, 2022).

Compared to *B. napus*, *B. juncea* L. is better adapted to the arid conditions of Bangladesh (Niazi *et al.*, 2017) There are currently about ten different *B. juncea* L. varieties available in Bangladesh. All publicly available *B. juncea* L. varieties have brown-black seeds with a high erucic acid content (between 40 and 48%). None of them are canola grade (less than 2% erucic acid) and none have yellow seeds coats. Nevertheless, *B. juncea* L. cannot occupy the primary position to be cultivated as oil crop due to its long duration and tall stature (it makes the management operations difficult). The current study effort was carried out with a long-term goal to improve the *B. juncea* L. to breed new variety having traits such as short duration (<100 days maturity) and high yielding, and lower erucic acid content and yellow seed coat.

This study was conducted on F₂ populations derived from 7×7 half diallel, 6 BC₁F₁ cross to find out individual plant with early maturity, short plant stature and also desirable yield comparing to our local check variety of *B. juncea*. L. Given the aforementioned facts, the following goals of the current inquiry were pursued:

1. To estimate and compare the phenotypic performances of F₂ and BC₁F₁ populations;
2. To calculate the genetic components and variability in the F₂ and BC₁F₁ populations; and
3. To estimate heterosis and inbreeding depression in the F₂ populations.

CHAPTER II

REVIEW OF LITERATURE

Numerous researchers have focused on improving the *B. juncea* species in different areas of production and use, taking into account its adaptability to impending environmental changes. One of the most important sources of oil-producing crops worldwide, including in Bangladesh, is the *Brassicaceae* family. Numerous research projects on the genetic diversity, heritability, relationships, combining potential of *B. juncea* have been conducted around the globe. The following headings are used to describe the literature analysis on the studies:

- 2.1 Genotypic and phenotypic variability
- 2.2 Heritability and genetic advance
- 2.3 Correlation analysis among variables
- 2.4 Heterosis analysis
- 2.5 Inbreeding depression analysis
- 2.6 Gene interaction and genetic component analysis

2.1 Genotypic and phenotypic variability

Prasad *et al.* (2021) studied genetic variability, heritability and genetic advance for quantitative traits in 10 different genotypes of Indian mustard in both F₁ and F₂ generation and founded that F₂'s exhibited significance differences for all character except No. of Primary branches per plant, no. of seed per siliqua, Seed index and oil Content. Similar finding was reported by Verma *et al.*, (2021).

In another experiment, Shrimali *et al.*, (2016) worked with 10 parents and 45 crossing lines of F₁ and found that the phenotypic coefficient of variance was found to be higher than their genotypic coefficient of variance but the difference was quite meager. Number of secondary branches per plant, number of Siliqua per plant, seed weight, harvest index and erucic acid showed moderate GCV and moderate PCV (10- 20%) estimates in both generations. Total glucosinolate showed high estimates of GCV and PCV (>20%) in both generations.

Sikarwar *et al.* (2021) experienced high PCV and GCV for number of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and number of siliquae on main raceme. Number of seeds per siliqua showed

high PCV with moderate GCV. Higher magnitude of genetic variability indicated better scope of phenotypic selection through traits for improvement in yellow sarson.

Fayyaz and Ullah (2014), showed that environmental variance for Siliqua length (0.07) was smaller than genotypic variance (1.08). Genotypic (GCV) and phenotypic coefficients of variability (PCV) values for the said trait were 17.49 and 18.05%. Estimated for Siliqua length was high (0.94), which shows that selection for this trait shall be effective.

Saroj *et al.*, (2021) explored two hundred and eighty-nine diverse accessions of Indian mustard belonging to four continents that were analyzed for yield and yield-related traits (20 traits) over two seasons (2017–2018 and 2018–2019) using an alpha lattice design. The genetic variance was found to be significant ($P \leq 0.01$) for the individual and under pooled analysis for all of the evaluated traits, demonstrating the presence of significant genetic variability in the diversity panel, which bids greater opportunities for utilizing these traits in future breeding programs. High heritability combined with high genetic advance as percent of mean and genotypic coefficient of variation was observed for flowering traits, plant height traits, seed size, and seed yield/plant; hence, a better genetic gain is expected upon the selection of these traits over subsequent generations.

By Tiwari *et al.*, (2021) the estimates of heritability were observed as high for days to flower, days to maturity, number of primary branches, number of secondary branches, number of Siliqua per plant, number of seeds per siliqua, harvest index, 1000-seed weight, oil content and seed yield per plant. Moderate heritability estimates were observed for plant height and biological yield. The estimates of genetic advance in percent over mean of the characters ranged from 2.37 (oil content) to 36.41 (number of primary branches).

High genetic advance was recorded for number of primary branches, number of secondary branches, number of Siliqua per plant, number of seeds per siliquae, harvest index, 1000-seed weight and seed yield per plant. Moderate genetic advance was recorded for days to flower, days to maturity. Low genetic advance was exhibited for three attributes viz; plant height, biological yield and oil content. The results obtained are similar to the results obtained by Arifullah *et al.*, (2018) and Cai *et al.*, (2014).

The dominance hypothesis supposes that deleterious recessive alleles of one of the parents are complemented in the F₁ hybrid by the dominant alleles of the other parent. Results from several quantitative genetic experiments in crops like rice and maize favor the dominance hypothesis as manifested by Xiao *et al.*, (1995); Cockerham and Zeng, 1996; Swanson-Wagner *et al.*, (2009).

Niemann *et al.*, (2018) used five parental genotypes and twenty-two interspecific cross-derived *Brassica* lines were evaluated in a randomized complete block design with three replications in the Greater Poland region during 2009, 2010 and 2011. Generally, the variation among genotypes was evident for most of the tested fatty acids mean values, but the differences between genotypes were not always statistically significant when based on individual fatty acids (FAs). However, the highest number of significant heterosis effects was observed for behenic and lignoceric acids and for *Brassica* hybrid line H₁

Singh *et al.*, (2013) conducted an experiment consisted of six genetic population and they inbreeding depression estimated from F₂ over F₁, was positive and significant for plant height (cross V and VII), primary branches per plant (cross VIII), secondary branches per plant (cross IV, V and VI), number of siliquae on main raceme (cross II, IV, V and VII), length of main raceme (cross I and VIII), seeds per siliqua (cross I VII and VIII), 1000-seed weight (cross I and VII), seed yield per plant (cross II, VI, and VIII) and oil content (cross VIII) whereas, negative and significant inbreeding depression was noticed for days to 50% flowering in cross I, III and V and days to maturity in cross VI.

In another experiment, Singh *et al.*, (2016) noticed that in most of the cross the inbreeding depression was associated with heterobeltiosis this indicated that most of the characters showed higher magnitude of dominance gene action. The cross- showing absence of inbreeding depression may be used for further selection programs because in such crosses the additive and additive x additive gene interactions are present. Negative inbreeding depression was observed for days to 50 % flowering in cross-II and cross-IV, for days to maturity and 1000-seed weight significant inbreeding depression was not observed in any cross.

Laboni *et al.*, (2015) executed present investigation thus providing information about the nature and magnitude of genetic variation, segregation pattern and inbreeding

depression for yield and its components in okra so as to formulate suitable breeding strategy and isolate potential parents and promising crosses for further breeding program.

According to Kuki *et al.*, (2017) and Bernini *et al.*, (2013), inbreeding depression for any character is lower than the other character, when the dominance effects are less important in these traits.

2.2. Heritability and genetic advance

Narayan *et al.*, (2022) conducted a study was undertaken to collect information on genetic parameters for yield and its components from a ten parents line x tester mating design in Indian mustard at Agriculture research Farm, Bhagwant University, Sikar Road, Ajmer (Rajasthan) during Rabi season 2018-2019 with 51 treatments of mustard to assess the nature of variability. All genotypes were evaluated in a Complete Randomized Block Design with three replications.

The data were recorded by Narayan *et al.*, (2022) on twelve characters days to 50% flowering, days to maturity, length of main raceme, number of primary branches per plant, number of secondary branches per plant, number of siliquae on main raceme, number of seeds per siliqua, biological yield per plant, harvest index, 1000 seeds weight, oil content and seed yield per plant of 51 treatment of mustard. Highly significant changes between the treatments for each character were revealed by the analysis of variance. For seed yield per plant, high genotypic and phenotypic coefficients of variation (24.366 and 24.365) were observed. For seed yield per plant (g), the number of siliquae on the main raceme, and biological yield per plant, strong heritability along with high genetic advance were noted.

Khulbe *et al.*, (2000) estimated variability, heritability and genetic advance for yield and its components obtained using an 8×8 diallel in Indian mustard revealed maximum variability for seed yield. All the characters except oil content exhibited high heritability with high or moderate genetic advance. Environmental variance for Siliqua length (0.07) was smaller than genotypic variance (1.08). Genotypic (GCV) and phenotypic coefficients of variability (PCV) values for the said trait were 17.49 and 18.05%. Estimated heritability for Siliqua length was high (0.94) which shows that selection for this trait shall be effective.

Bind *et al.*, (2015) confessed basing on thirteen characters the genotypes Moderate magnitude of broad sense heritability coupled with genetic advance, phenotypic and genotypic coefficients in respect of number of branches, main shoot length, main shoot height, length of siliqua, number of seeds per siliqua and yield per plant indicates the scope for selection of superior genotypes due to preponderance of additive gene action.

Singh *et al.*, (2016) studied seven mustard genotypes to measure the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters. High heritability estimates with genetic advance were observed for 1000 seeds weight followed by yield per plant, no of siliqua per plant, and plant height that could be improved by simple selection.

Gadi *et al.*, (2020) worked on thirty-six diverse genotypes of Indian mustard (*Brassica juncea* L. Czern and Coss.) were evaluated for ten quantiles. The high heritability denotes a high proportion of genetic effects in the determination of these characters and can be adopted for improving seed yield. Whereas the low heritability was observed for the characters total number of Siliqua per plant (48.7%), Plant height (43.8%), Number of seed per siliqua (39.8%), number of siliquae on main shoot (22.3%) biological Weight (17.9%) and Harvest Index (7.1%). Genetic advance as percentage of mean was observed high for the character is highest in days to 50% flowering (20.995%), days to maturity (21.320%), total no of siliqua per plant (20.066%) and test weight (35.936%). The value of genetic advance for plant height, no. of siliqua on main shoot, No. of seed per siliqua, biological weight, harvest index and seed yield are low.

Twenty-five genotypes of Indian mustard were undertaken by Yadav and Yadav (2020), to determine relationship among yield and its components using direct selection parameters like variability, heritability and genetic advance for 13 yield and its contributing characters. Analysis of variance for the design of the experiment indicated highly significant differences for all the characters. Higher phenotypic coefficient of variation (PCV) was recorded for number of secondary branches per plant followed by seed yield per plant, 1000-seed weight, length of main raceme, number of primary branches per plant, number of seeds per siliqua.

High Heritability estimates were observed by Yadav and Yadav (2020) who ran an experiment on 25 genotypes of Indian mustard, for days to 50% flowering (77.59%), length of main raceme (77.39%), 1000-seed weight (76.44%), plant height (75.67%), days to maturity (75.23%), number of secondary branches per plant (73.63%), number of Siliqua per plant (71.64%), harvest index (70.63%), oil content (70.02%), biological yield per plant (69.09%), seed yield per plant (69.01%), number of primary branches per plant (68.98%), number of seeds per siliqua (67.60%).

Conducting the previously mentioned study on 25 genotypes of Indian mustard, Yadav and Yadav (2020), also said that the expected genetic advance as percent of mean was high for seed yield plant per plant, 1000-seed weight, number of Siliqua per plant, number of secondary branches plant, plant height. The high heritability coupled with high genetic advance for seed yield plant per plant, 1000-seed weight, number of Siliqua per plant, number of secondary branches plant, plant height would be helpful for indirect selection in improvement of seed yield.

Bind *et al.*, (2014) worked on genetic variability, interrelationship and genetic divergence on fourteen different quantitative characters of thirty indigenous collections of Indian mustard was studied in order to identify desirable genotypes on per se performance and to select promising donors to be used in breeding programs Significant differences were observed for all the traits among the genotypes. Genetic variability was found maximum for biological yield per plant and minimum for days to maturity as reflected by genotypic coefficient of variation. Heritability estimates in broad sense were high for 1000 seeds weight, day to maturity, day to flowering, plant height and main shoot length. Genetic advance as percent over mean was high for biological yield per plant, 1000 seeds weight, yield per plant, number of secondary branches and main shoot length.

Twenty-four released varieties of Indian Mustard were evaluated by Mandal *et al.*, (2022) to study character association for seed yield and its component trait. Significant differences were noticed for all the traits among the genotypes. The genotypic and phenotypic variation is higher for seed yield/plant, 1000 seeds weight, secondary branches/plant and total siliquae/plant. Heritability estimates were very high for 1000 seeds weight, siliqua length, plant height, seeds/siliqua, total siliquae/plant and days to maturity. Genetic advance as percent of mean were high for seed yield/plant, 1000 seeds weight, secondary branches/plant and total siliquae/plant.

Patel *et al.*, (2021) examined Forty-five genotypes of Indian mustard [*B. juncea* L. Czern and Coss] were evaluated for seed yield and quality traits in Randomized Block. The analysis of variance revealed that there is low difference between genotypic and phenotypic variances revealed that the contribution of genotypic variance to total variance was more for all the traits except days to maturity and plant height. The high values of genotypic and phenotypic coefficient of variation for the number of branches per plant, seed yield per plant which indicated the potential variability available for these traits.

Gupta *et al.*, (2013) took ninety-five diverse genotypes of Indian mustard [*B. juncea* L(L.) Czern and Coss] that were evaluated for yield and other quantitative traits during the rabi season of 2009–10. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied. The high heritability coupled with high genetic advance for 1000-seed weight and siliquae plant-1 would be helpful for indirect selection for improvement in seed yield.

An experiment was conducted by Sikarwar *et al.*, (2021) to evaluate variability among 188 Indian mustard genotypes based on diverse biochemical parameters viz., palmitic, oleic, linoleic, linolenic and erucic acids along with oil content. Analysis of variance indicated the existence of substantial magnitude of variability among studied Indian mustard genotypes, which suggest better possibilities for their improvement. Genotypic and phenotypic coefficient of variation was found to be higher for seed yield/plant, 1000 seeds weight, secondary branches/plant and total siliquae/plant had maximum heritability and genetic advance.

Sharma *et al.*, (2022) found out the existence of genetic variability for the selection of improved genotypes is a crucial necessity for crop improvement programs in Indian mustard (*Brassica juncea* L.) which is important to understand the relationship between attributes for effective indirect selection of traits. Five diverse parents were crossed in half diallel mating design and made 10 F1 hybrids during winter 2019- 2020.

Chowardhara *et al.*, (2020) showed that Genotypic source of variations was significant for all characters in 168 genotypes including 7 checks of Indian mustard at

5% level of significance. Highest GCV and PCV were recorded for seed yield per plant which indicates for improvement through selection among these genotypes. High heritability along with high genetic advance as percentage of mean has been noticed for seed yield per plant and harvest index indicating less influence of environment and also the presence of additive, dominance and interaction among genes in the expressions of these characters. Low genetic advance along with low heritability estimate were observed for number of primary branches per plant and number of seeds per siliqua. This indicates the involvement of additive and non-additive gene actions in their inheritance.

Rashmi *et al.*, (2019) made the estimates of σ^2S were found to be higher than the σ^2g for all characters except days to initial flowering, length of main raceme and 1000-seed weight indicating greater importance of specific combining ability in the inheritance of characters. Reference to the estimates of σ^2A and σ^2D for various characters revealed that the additive gene action was predominant for the expression of seven characters viz., days to initial flowering, days to maturity, plant height, length of main raceme, siliqua density, siliqua length and 1000-seed weight exhibiting greater importance of additive gene action for these traits whereas, non-additive gene action was preponderant for the expression of 8 characters viz., number of siliquae on main raceme, number of primary branches/plant, number of secondary branches/plant, number of seeds/siliqua, seed yield/plant.

Gowthami *et al.*, (2015) conducted an experiment to study the combining ability in Indian mustard was done using ten diverse landraces crossed in half diallel fashion to secure forty-five F1s. Data were recorded on these forty-five crosses along with their respective parents and two checks for days to first flower, days to maturity, plant height (cm), number of primary branches per plant, number of Siliqua per plant, 1000 seeds weight, seed yield per plant and oil content (%). Among all the 45 crosses ACNM-5 ACNM-15, ACNM-3 ACNM-5, ACNM-2 ACNM-11, ACNM-2 ACNM-3 showed predominance non-additive gene action and so reciprocal recurrent selection is suggested.

At phenotypic level seed yield per plant showed highly significant and positive association with harvest index, biological yield per plant, number of seeds per siliqua, number of primary branches per plant. The maximum coefficient of phenotypic

variation was observed for the number of secondary branches per plant by Yadava and Yadava (2020) conducting experiment on 25 genotypes of Indian mustard.

Variability analysis was performed by Kumar *et al.*, (2021) in a 10× 10 half diallel cross in Indian mustard genotypes for yield and quality traits. In this study, 45 F₁ hybrid and their parents were evaluated for 14 quantitative and qualitative traits. The results coming out from the analysis indicated that both additive and non-additive gene effect were responsible for expression of all the 14 characters. 8 Parental genotypes showed high additive gene effect for seed yield per plant and most of the important characters except days to 50% flowering and days to maturity.

Kaur *et al.*, (2022) marched forward with the aim to study the genetic variability and correlation between traits among these genotypes and their hybrids were evaluated. Study observed high PCV and GCV by siliquae/ plant. High heritability along with high genetic advance (GA) was observed for siliquae/ plant, biological yield/ plant and test weight (TW). At genotypic levels, it was revealed that harvest index (HI) had significant positive correlation with seed yield/ plant.

2.3 Correlation analysis among variables

Bind *et al.*, (2015) confessed all the characters showed positive correlation with seed yield per plant both at phenotypic and genotypic levels except days to 50% flowering and days to maturity. The path coefficient analysis at genotypic level revealed that biological yield per plant had the highest direct positive effect on seed yield per plant followed by harvest index, 1000 seeds weight, no of seeds per siliqua and no. of primary branches. Highest negative direct effect on seed yield per plant was observed for plant height at phenotypic level.

Mandal *et al.*, (2022) demonstrated the correlation of seed yield/plant shows significant positive association with days to maturity, primary branches/plant, secondary branches/plant, total siliquae/plant, siliqua length, seeds/siliqua, 1000 seeds weight and length of main shoot. From correlation coefficients and path analysis it appeared that length of main shoot, 1000 seeds weight, number of secondary branches/plant and days to maturity were most important yield components having highly positive direct and indirect effects.

Sikarwar *et al.*, (2021) found negative and high significant correlation occurred between the seed of a silique and oleic acid and linolenic acid proportion. Non-significant negative correlation was occupied by seed of a silique and height of plant, silique of a plant and weight of 1000 seeds. Seeds of a silique possessed positive and non-significant relation with primary branches. A discussion of positive correlation of seeds of a silique and yield of a plant presented by Ivanovska *et al.*, (2007), and Lodhi *et al.*, (2014).

A study was undergone by Gupta *et al.*, (2013) where seed yield per plant was positively correlated with plant height, number of primary branches plant-1, number of secondary branches plant-1, siliquae plant-1, seeds siliqua-1 and 1000-seed weight. The maximum direct effect for seed yield plant-1 was observed by 1000-seed weight, followed by seeds siliqua-1, siliquae plant-1, days to 50% flowering, number of secondary branches plant-1 and days to maturity

Rajpoot *et al.*, (2020) experimented among the yield attributing character days to 50% flowering and showed significant phenotypic correlation coefficient with number of primary branches per plant, number of secondary branches per plant and number of Siliqua per plant. Seed yield per plant was also found highly significantly correlated with harvest index. These traits are highly influenced by each other and if seed yield per plant is high, harvest index will also increase. Similarly, if days to 50% flowering is more, it will positively affect primary branches per plant, number of secondary branches per plant and number of Siliqua per plant. Earlier Ray *et al.*, (2014) and Dawar *et al.*, (2018) showed positive correlations for association of primary branches with plant height.

Patel *et al.*, (2021) did association analysis between seed yield per plant and other seventeen characters revealed significantly positive correlation of seed yield per plant with the number of Siliqua per plant, seeds per siliqua, length of siliqua, myristic acid and erucic acid. Correlation analysis revealed positive effects of the number of Siliqua per plant and seeds per siliqua towards seed yield per plant while the number of branches per plant also had a positive significant effect on seed yield per plant via the number of Siliqua per plant suggesting that the selection for such traits would be more effective for improving seed yield in Indian mustard.

In order to study correlation for seventeen quantitative and qualitative traits, Saiyad *et al.*, (2020) conducted an experiment with 60 different genotypes of Indian mustard (*B. juncea*). They discovered that seed yield per plant was significantly and positively correlated with plant height, number of branches per plant, number of Siliqua per plant, seeds per siliqua, length of siliqua, 1000-seed weight. These yield-contributing characteristics also showed a strong and favorable correlation among themselves.

With fifty mustard genotypes, Lavanya *et al.*, (2022) looked at the association and correlation analysis of twelve yield-contributing characters. Following the number of secondary branches per plant and the number of Siliqua per plant at the genotypic level, correlation analysis showed that the seed yield per plant is positively and substantially correlated with the harvest index. Conversely, both at the genotypic and phenotypic levels, the number of main branches per plant, the number of days until 50% flowering, and the number of seeds per siliqua all directly decreased the number of seeds produced per plant.

Seed yield and primary branches were also positively correlated with primary branches in the work of Khan *et al.*, (2002) and Khan *et al.*, (2013). There was a positive and highly significant relationship among secondary branches and oleic acid and linolenic acid proportion. Positive significant relations existed between secondary branches and the silique of a plant. Non-significant negative correlation was occupied by secondary branches and weight of 1000 seeds. Secondary branches possessed positive and non-significant relations with primary branches, oil proportion, protein proportion and erucic acid proportion. While negative and highly significant association occurred among secondary branches and primary branches and seeds of a silique.

Sadat *et al.*, (2010) also proved the same results on the yield aspects and highlighted the positive correlation between secondary branches and yield of seed and noted the high and positive significance between secondary branches and seeds in a silique.

Awal *et al.*, (2015) showed there was a positive and highly significant relationship among silique of a plant and plant height. While negative and high significant correlation occurred between silique of plant and weight of 1000 seeds. Positive significant relation existed between the silique of the plant and secondary branches. Non-significant negative correlation was occupied by the silique of plant and seeds of

a silique. Silique of a plant possessed positive and non-significant relation with primary branches and yield of seed.

Khan *et al.*, (2002) also notified the significant positive relationship among silique of a plant with seed yield. They concluded that selection of this parameter of yield could be fruitful for improvement of yield. There was a positive and highly significant relationship among the seed of a silique and primary branches, yield of seed and secondary branches. Non-significant negative correlation was occupied by seed of a silique and height of plant, silique of a plant and weight of 1000.

A discussion of positive correlation of seeds of a silique and yield of a plant presented by Rameeh *et al.*, (2015). There was a positive and highly significant relationship among the weight of 1000 seeds height of plant. On the other hand, negative and high significant correlation occurred between the weight of 1000 seeds and the silique of a plant. Non-significant negative correlation was occupied by weight of 1000 seeds and seeds of a silique, primary and secondary branches and yield of seeds.

Meena *et al.*, (2017) elaborated the positive significant correlation between weight of seeds and height of plant. Sabaghnia *et al.*, (2010) elaborated the significant and positive correlation with seed yield. There was a positive and highly significant relationship among height of plant and secondary branches, silique of plant. While the height of the plant had a high significant and negative correlation with the weight of 1000 seeds. Height of plant was positively correlated with protein and possessed positive and non-significant relation with primary branches, yield of seed. Negative and non-significant effects occurred between height of plant and seeds of a silique.

Ara *et al.*, (2013) reported the same results that plant height possessed highly positive and significant correlation impacts on yield of seed, weight of 1000 seeds, seeds of a silique and primary and secondary branches. There was a positive and highly significant relationship among Seed of a silique and the yield of seed and secondary branches.

Among the yield attributing character days to 50% flowering showed significant phenotypic correlation coefficient with number of primary branches per plant, number of secondary branches per plant and number of Siliqua per plant. Seed yield per plant was also found highly significantly correlated with harvest index. All these characters showed high significance at both the probability level (5% and 1%). These traits

highly influenced by each other and if seed yield per plant is high, harvest index will also increase. Similarly, if days to 50% flowering is more, it will affect primary branches per plant, number of secondary branches per plant and number of Siliqua per plant positively. Earlier Ray *et al.*, (2014) showed positive correlations for association of primary branches with plant height. Dawar *et al.*, (2018) reported the same.

2.4. Heterosis

Rameeh *et al.*, (2019) did half diallel crosses of eight spring genotypes of oilseed rapeseed (*Brassica napus L.*) were considered to evaluate heterobeltiosis effects of plant height, yield component characters, seed yield and harvest index.

Meena *et al.*, (2014) found the estimates of better parent heterosis for seed yield are presented in. Out of 36 hybrids, 13 hybrids exhibited highly significant and positive better parent heterosis and from them 11 hybrids showed > 15% better parent heterosis and seven hybrids possessed >15% better parent heterosis.

Heterosis for seed yield to the extent of 24.36 to 80.97% was also reported by Verma *et al.*, (2011) in 15 crosses and moderate level of heterosis for seed yield/plant, number of siliquae/plants, and number of secondary branches/plants.

To detect types of gene action especially epistasis for studied traits, Abdelsatar *et al.*, (2021) took six populations and they were evaluated in a field trial during 2019/2020 season Significant negative heterosis and heterobeltiosis were found for days to first flower, plant height and first siliqua height, whereas significant positive were found for seed weight per plant and its components in the corresponding crosses at both locations.

Chen *et al.*, (2009) showed that for heterosis analyses, TN, LN, LB and LW of Chinese vegetable mustard showed positive HPM and negative HPB. The other traits showed positive HPM and HPB. Heterosis arising from GE interaction was found to varying degrees for different environments.

It was shown that three main hypotheses exist to explain the genetic basis of heterosis—dominance, overdominance, and epistasis (Crow, 1999; Goodnight, 1999; Lippman and Zamir, 2007) in Chinese vegetable mustard.

Ramchiary *et al.*, (2007) and Yadava *et al.*, 2012 studied heterosis in mustard 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 for important yield components. Similar result was obtained for maize (Frascaroli *et al.*, 2007), wheat (Peng *et al.*, 2003). Studies on various crop species have consistently postulated that the genetic mechanism of heterosis is complex without any single explanation for its expression (Radoev *et al.*, 2008; Liang *et al.*, 2015; Shang *et al.*, 2016; Li *et al.*, 2018; Ma *et al.*, 2019; Liu *et al.*, 2020).

To assess heterosis over mid parent (MP) and superior parent (SP) or heterobeltiosis in Indian mustard, Aakanksha *et al.*, (2021) analyzed 10 parents diallel consisting of 10 strains and their 45 F₁ hybrids. The crosses Kranti × BEC-144 and RH-30×BEC- 286, respectively, yielded the highest heterosis for seed yield above mid parent, measuring 47.36% and 40.85%, respectively. The cross combination Kranti x BEC- 144 achieved the highest heterosis for seed yield above superior parent at 57.0%, followed by the cross-combination Pusa Bold × BEC-144 at 50.89%.

Akabari and Sasidharan (2016), showed Number of crosses exhibiting significant positive heterosis, heterobeltiosis, and economic heterosis for seed yield per plant were 9, 4 and 3, respectively. Three crosses depicted significant positive heterotic effects for seed yield per plant, viz., GM-2 x PYM-7, GM-3 x PAB-9511 and GM-3 x NUDH-45-1. Among these crosses, GM-2 x PYM-7, and GM-3 x PAB-9511 also exhibited significant and desirable heterotic effects for numbers of Siliqua per plant, primary branches per plant and secondary branches per plant.

Gupta *et al.*, (2018) Most of the crosses exhibiting high heterosis in desired direction involved at least one good general combiner for most of the characters but not necessarily high per se performance of the parents. In most of the crosses high heterosis did not involve parents with high mean this indicates the genetic diversity among the parents. In F₁ hybrids, maximum heterosis was recorded for Siliqua per plant followed by numbers of secondary branches and seed yield per plant. Considerable inbreeding depression was observed in the F₂ population which was highest for seed yield per plant followed by numbers of primary branches.

Lal *et al.*, (2018) underwent an experiment with 10 parents and their-45F₁'s and 45 F₂'s generated through Diallel system of mating Heterosis has important implications for both in F₁ and for obtaining transgressive segregants in F₂ generation. In succeeding selfing generation, homozygosity increases, vigor and productiveness reduce by 50% due to inbreeding depression. If F₂ hybrids still express a sufficient amount of heterosis over parents, the high cost due to low quantity of seed in F₁ will be paid off by more seed produced from F₂ hybrids. Improvement in both quantitative and qualitative traits can only be established when the nature of genetic effects such as additive or non-additive is thoroughly studied.

Ranjana *et al.*, (2018) used 10 × 10 diallel, diverse lines of *B. juncea L.* to estimate 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. To ascertain the heterotic performances of crosses for seed yield and significant yield components.

With 5 diverse genotypes in a 55 complete diallel crosses including the reciprocals, Gul *et al.*, (2019) calculated the standard heterosis potentiality for seed yield, its component traits of turnip rape (*Brassica rapa*). The greatest value of standard heterosis identified in terms of yield components was 41.43% for harvest index and the maximum values of standard heterosis recorded were 47.87% for seed yield per plant. He also found that it was possible to achieve mid-parent and better parent heterosis values for significant yield components.

2.5 Inbreeding Depression

Chauhan *et al.*, (2011) found high heterosis and inbreeding depression, the remaining crosses, had high heterosis and moderate inbreeding depression for primary branches per plant for all crosses except one. Very high heterosis was associated with relatively high inbreeding depression for secondary branch per plant and seed yield per plant. The promising crosses BPR 517 and BPR 520 showing high standard heterosis and heterobeltiosis but high inbreeding depression, might be exploited for heterosis breeding. Similar findings were reported by earlier workers Srivastava *et al.*, (2009); Singh *et al.*, (2009); Kumar *et al.*, (2008).

By Hirve and Tiwari (1991), several crosses have shown moderate to low inbreeding depression for seed yield and siliques/plant, silique length, and days to maturity, while many of the crosses exhibited negative heterosis for number of secondary branches. The crosses showing high estimates of heterosis for seed yield also had significant heterotic effects for some of the yield components.

Aghao *et al.*, (2010) and Ali *et al.*, (2015) stated the relationship between heterotic response and inbreeding depression indicated that the crosses TM 7 x Varona and RLM 198 x Varuna for seed yield, RLM 198 x Varuna, TM 7 x Sita, and RLM 198 x Prakash for number of siliques, showing high BP heterosis in F₁, also showed high inbreeding depression in F₂. This indicates the importance of nonadditive gene action in the Indian mustard. These could be successfully used for improving particular character for which improvement was desired. These parents /lines might be utilized for producing the inter-mating population in order to get desirable recombinants in Indian mustard.

Gupta *et al.*, (2018) studied inbreeding depression on 45 hybrids developed through 10 × 10 diallel set of Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. The inbreeding depression for seed yield ranged from - 35.2 to 12.8 per cent. The highest significant positive heterobeltiosis and standard heterosis and high inbreeding depression was recorded in hybrids Rohini × Varuna followed by RK 9870 × Vardan and Rohini × Vardan for seed yield. These crosses may be utilized for developing hybrids.

Tomar *et al.*, (2018) found that, homozygosity increases vigor and productiveness reduce by 50% due to inbreeding depression in succeeding selfing generation. If F₂ hybrids still express sufficient amount of heterosis over parents, the high cost due to low quantity of seed in F₁ will be paid off by more seed produced from F₂ hybrids. Improvement in both quantitative and qualitative traits can only be established when the nature of genetic effects such as additive or non-additive is thoroughly studied. heterosis has important implications for both in F₁ and for obtaining transgressive segregants in F₂ generation.

The present investigation was undertaken by Abhinaya *et al.*, (2021) with a view to generate information on heterosis and inbreeding depression for seed yield and its component traits in six hybrids of Indian mustard (*B. juncea* L. Czern and Coss). Out

of the six hybrids, two showed maximum relative heterosis while the cross GM-2 × EC766434 exhibited the highest heterobeltiosis. It also showed significant and positive estimates for both RH and HB for siliqua length, number of Siliqua per plant, yield per plant and oil content. Yield attributing characters like seeds per siliqua, siliqua length and number of siliquae are positive and significant for some crosses.

By Patel *et al.*, (2016) inbreeding depression were studied in 45 hybrids developed through 10×10 diallel set of Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Heterobilities varied from - 21.4 to 19.6 per cent and standard heterosis from - 23.6 to 29.6 per cent for seed yield. Significant desirable heterosis over best parent (Rohini) was observed for all the characters studied. Maximum significant standard heterosis was observed for main shoot length (56.6%) followed by secondary branches (35.8%), seed yield (29.6%), siliquae on main shoot (28.6%), seeds per siliqua (23.4%) and primary branches (22.4%) while heterobeltiosis for main shoot length (68.7%), secondary branches (49.8%), siliquae on main shoot (41.6%), seeds per siliqua (39.1%), primary branches (33.4%) and seed yield (19.6%). The inbreeding depression for seed yield ranged from - 35.2 to 12.8 percent.

Depression by inbreeding can be defined as the reduction of the mean phenotypic value shown by traits associated with the reproductive capacity or physiological efficiency of the plant. Inbreeding depression may limit the number of promising lines in a germplasm and indicate the potential of populations for genetic breeding (Hallauer *et al.*, 2010)

Pourdad and Sachan (2003), observed low inbreeding depression for oil content (2.2%), days to maturity (2.8%), 1000-seeds weight (6.7%), plant height (7.3%), siliqua length (12.3%), days to 50% flowering (13.4%) and number of seeds per siliqua (19.4%). High inbreeding depression was observed for number of secondary branches (53.9%), seed yield/plant (45.6%), number of primary branches (40.1%), harvest index (24.7%), length of main shoot (22.3%) and number of siliquae on main shoot (20.12%).

Yun and Agarwal (2014), found inbreeding depression is positively correlated with the stressfulness of the environment in which it is measured. However, it remains unclear why stress, per se, should increase δ . To our knowledge, only “competitive stress” has a logical connection to δ . Through competition for resources, better quality

(outbred) individuals make the environment worse for lower quality (inbred) individuals, accentuating the differences between them. For this reason, we expect inbreeding depression to be stronger in environments where the fitness of individuals is more sensitive to the presence of conspecifics (i.e., where fitness is more density dependent). Indeed, some studies suggest a role for competition within environments, but this idea has not been tested in the context of understanding variation in δ across environments. Using *Drosophila melanogaster*, we estimated δ for viability in 22 different environments. These environments were simultaneously characterized for (1) stressfulness and (2) density dependence. Although stress and density dependence are moderately correlated with each other, inbreeding depression is much more strongly correlated with density dependence. These results suggest that mean selection across the genome is stronger in environments where competition is intense, rather than in environments that are stressful for other reasons.

Stojanova *et al.*, (2021) founded among all the crosses, the cross GDM-4 \times EC766590 had significant estimates of inbreeding depression in desired direction for seeds per siliqua and siliqua length indicating the possibility for desired transgressive segregants for the characters under consideration.

2.6. Genetic component analysis

Philanim *et al.*, (2019) tested 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. 6 generations of two crosses. Presence of interaction effects and duplicate epistasis suggested the possibilities of obtaining transgressive segregants in later generations. The role of fixable and non-fixable gene action in controlling different yield and component traits was also apparent.

Abdelsatar *et al.*, (2021) conducted an experiment on six populations of mustard and observed high to moderate values of narrow sense-heritability coupled with high (more than (20%) values of expected response from selection (as % of mean) were detected for days to the first flower in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, first siliqua height in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish and seeds weight per plant in the 1st cross at both locations. The major role of dominance

gene effects as the ratio $((H/D)0.5 > 1)$ along with the duplicate epistasis was detected in the inheritance of most studied traits in the corresponding crosses at both locations

By Chowdhury *et al.*, (2021) it was found that genetic components D, H₁, H₂, and h² were all significant, and dominance genetic variance was larger than additive genetic variance across locations. Significance of both D and H components suggests that DTA is controlled by both additive and dominant effects in *Brassica rapa*.

Manjunath *et al.*, (2017) found the influence of additive component (D) was significantly different for all the observed characters. The influence of additives to the characters of the yield per plant, siliqua length, siliqua weight respectively was 29807, 531, 6501, 10813. The influence of the dominant component (H₁) was also significantly different for all the observed characters

Singh *et al.*, (2007) conducted an experiment on ten diverse parents of Indian mustard of 10 × 10 diallel design excluding reciprocals for genetic component analysis and the data on seed yield and its ten component characters suggested that dominant genes were more frequent than recessive ones for all the characters studied except days to flower in both the generations. Symmetrical proportions of positive and negative genes were observed for days to flower, plant height and seed yield per plant, while asymmetrical proportions of positive and negative genes were observed for the remaining characters. More than one major gene group were involved in the inheritance of most of the characters. Predominance of non-additive gene action was observed for seed yield and its components characters

Singh *et al.*, (2014) underwent generation mean analysis using two crosses (Maya x BPR 543-2) and (BPR-543-2 x BPR-2) to study the genetic components gene effects on seed yield and physiological characters in Indian mustard. were studied for eight physiological traits. The dominance (h) and dominance x dominance (l) non-allelic interactions were found to be the most important in BPR 543-2 x BPR-2 cross. In Maya x BPR-543-2, negative significant values of h and l were observed.

Ranjit *et al.*, (2016) figured out the proportion of positive genes would be seen from the value of H₁ against H₂. If H₁ > H₂ then the genes were more positive genes, on the other hand, if H₁ < H₂ then the genes were more negative genes. Genes involved more heavily in determining the character of the yield per plant, fruit length, fruit weight and fruit diameter were positive genes reflected in the value of H₁ > H₂ (Kant and

Gulati, 2001). To combat these complex interactions, we need to have a multipronged strategy by combining agronomical and breeding approaches. Hence, the major objective of the mustard improvement program is to develop varieties with high yield potential through the introgression of various yield component traits from the lines with high trait values.

Sabaghnia *et al.*, (2010) took a set of 36 diallel F₁ hybrids, their parents and four additional cultivars were evaluated in the breeding nurseries during 2008 and 2009. Plant height (PH), number of lateral branches per Siliqua (NBP), main stem length, number of grains per Siliqua, days to start flowering (DSF), 1000 grain weight (GW), harvest index (HI) were measured. Diallel analysis was carried out considering the additive dominance genetic model to estimate variance and covariance components. The additive genetic variance component was significant for NBP and DSF, the dominance genetic variance for PH and the additive by year interaction for PH and OC. GW. However, dominance component was significant for all characters under investigation and played a major role in the inheritance of these traits.

Wang *et al.*, (2010) High oil content is one of the most important characteristics of rapeseed (*Brassica napus* L.) breeding. In order to understand the genetic basis component, they found that the amount of dominance effects can be seen from the value $(H_1/D)^{1/2}$. The value $(H_1/D)^{1/2}$ of the yield per plant, fruit length and fruit diameter were less than one indicating a partial recessive, while the value of $(H_1/D)^{1/2}$ on the character of the fruit weight was more than one indicating over-dominance

Sabaghnia *et al.*, (2010) experimented with a set of 36 diallel F₁ hybrids, their parents and four additional cultivars were evaluated showed that shows that the character of the yield per plant, fruit weight and diameter of the fruit has a value of $K_d/K_r > 1$ (respectively 1203, 1674, and 2451), showing that the genes were more dominant in the parents. Meanwhile, the length of the siliqua character has a value $K_d/K_r < 1$ (0870), showing that the recessive genes were more in the parent.

Rashmi *et al.*, (2019) found that proportion of dominant genes to recessive genes is shown by F component and K_d/K_r ratio. The positive value of F component reflects a greater number of dominant genes than recessive genes in the parent. A ratio of K_d/K_r greater than one indicates more dominant genes in the parent; conversely, the ratio of K_d/K_r smaller than one indicated more recessive genes in the parent.

The value $(H_1/D)^{1/2}$ of length and shape of rice is less than 1 (0.31 and 0.38, respectively), which indicated the existence of partial dominance in these traits. Rice length controlled by a partial dominance gene was also reported by Kato (2023).

Manjunath *et al.*, (2017) conducted an experiment was conducted during winter seasons of 2005–06 and 2006–07 to study the nature and magnitude of gene effects involved in the genetic control of seed yield and yield attributing traits in Indian mustard [*B. juncea* L(L.) Czern and Coss.]. Both additive and non-additive gene effects were found to be significant for main raceme length, number of siliquae on main raceme, seed yield per plant and 1000-seed weight. Thus, on the basis of the above study it is advocated that the breeding methods which exploit both the components of genetic variation may be useful for further genetic amelioration. For the improvement of seed yield and its component characters; reciprocal recurrent selection or diallel selective mating would be helpful.

Barfa *et al.*, (2017) experiment was laid out in randomized block design with eight lines, five testers and their 40 hybrids of Indian mustard. They showed that both additive and non-additive components of variances were significant but magnitude of non-additive components were higher as compared to additive components for all characters investigated except number (s) of primary branches per plant, indicating pre-dominance of non-additive gene action for the almost parameters.

CHAPTER III

MATERIALS AND METHODS

This part explains the materials and statistical methods to describe all the experiment of the study. The mean performance, genetic variability, correlation, heterosis analysis, inbreeding depression, backcross analysis and analysis for genetic components had been performed on the 7 parental lines, 21 F₂ populations and 6 backcross lines. The detailed manifestation of material and methods and the experimental procedure implemented during the course of research are described below.

3.1 Experimental site

The research experiment was conducted at the research farm of Sher-e-Bangla Agricultural University, Dhaka during the period from mid November 2021 to March 2022. It is positioned at 23°46' N latitude and 90°22' E longitude at an altitude of 8.7 meters of elevation. The experimental field belongs to the Agro-ecological zone of the Madhupur Tract", AEZ-28. Photograph illustrates the experiment field (Appendix I).

3.2 Soil characteristics

The existing soil of the experimental field can be categorized as general soil type, shallow red brown terrace soils under Tejgaon Series. Soil classification matched with medium high land with pH varies from 5.6 to 5.8. Contrasted and plane surface made the experimental field suitable for easily impeded irrigation and drainage. Appendix III shows up with the Physicochemical properties of the soil later.

3.3 Climate

The experimental site was detected to be classified into the sub-tropical climate zone. Climatic feature of the area was covered by the hot or dry summer season, rainy season and dry winter season were prevailing into the experimental field as its climatic feature. 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, the recorded mean of air, temperature, humidity and rainfall data at the time of experiment conducting period were mentioned in Appendix III.

3.4 Design and layout

Randomized Complete Block Design (RCBD) was chosen for conducting this experiment with three replications. An area of 300 m² (25×12 m²) was used for the experiment. Span of each replication was 2.5 m² with 25 m² in length. For drainage and irrigation facilities 0.5 m² channel was set aside between two rows. The distance between line to line was 30 cm and plant to plant distance was 8cm for evaluating the morphological characters as well as performing the experiment program.

3.5 Land preparation

The land preparation activities were taken into account before 15 days of seed sowing on 2 November, 2021. 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.

3.6 Planting materials

In this experiment, seven genotypes of *B. juncea* L. (where one of them is canola grade) was used as parental lines, presented in Table 1 and Plate 1. 21 F₂ populations of *B. juncea*, L were also used as plant materials shown in Table 2 and Plate 2. The 6 F₁ combinations were used for backcross and the derived 6 backcrossed populations were mentioned in Table 2 and Plate 3.

Table 1. List of the selected seven *B. juncea* L. genotypes used as parent materials

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

Table 2. List of F₂ populations and selected F₁(hybrid) used for backcross breeding to generate BC₁F₁ lines

Combination *	F ₂ Populations*	F ₁ cross combinations used for backcross*	BC ₁ F ₁ lines
G1=P1×P2	BINA7×Rye5	G5=P1×P6	(P1×P6) × P1
G2=P1×P3	BINA7×Daulat	G10=P2×P6	(P2×P6) × P2
G3=P1×P4	BINA7×BS10	G14=P3×P6	(P3×P6) × P3
G4=P1×P5	BINA7×BS16	G17=P4×P6	(P4×P6) × P4
G5=P1×P6	BINA7×BJ00	G19=P5×P6	(P5×P6) × P5
G6=P1×P7	BINA7×BS11	G21=P7×P6	(P7×P6) × P7
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=P7×P6	BS11×BJ00		

*Department of Genetics and Plant Breeding, SAU, Dhaka

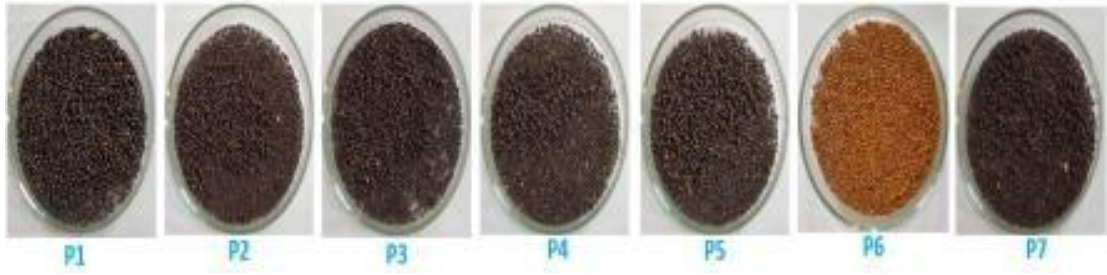


Plate 1. Photographs of 7 *B. juncea* L. parental lines

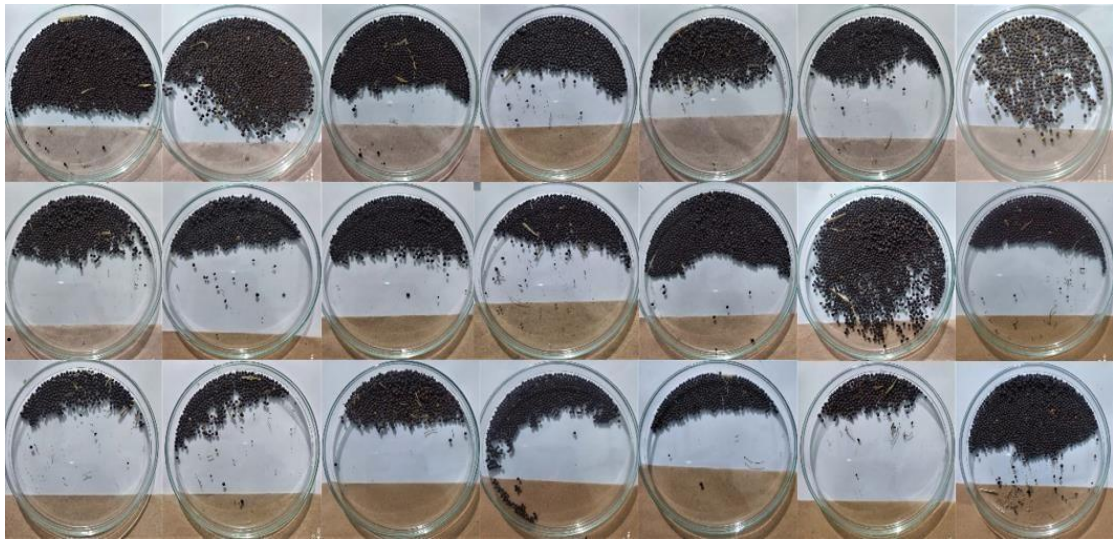


Plate 2. Photographs of 21 F_2 population of *B. juncea* L. genotypes derived from 7×7 crossing program



(P1 × P6) × P1 (P2 × P6) × P2 (P3 × P6) × P3 (P4 × P6) × P4 (P5 × P6) × P5 (P7 × P6) × P7

Plate 3. Photos of seeds obtained from BC_1F_1 of *Brassica juncea* L.

3.7 Fertilizer application

All the essential organic and inorganic fertilizers including viz. Cow dung, urea, TSP, MOP, gypsum, zinc oxide and boric acid were applied in the field conferring to the dose obligatory for 300 m² area of land. All fertilizers were nicely merged into the soil with a light irrigation after that. The suggested dose of fertilizer was stated in Table 3 for cultivating the mustard varieties in the field.

Table 3. List of fertilizers with dose and application procedure

Sl. No.	Fertilizer name	Fertilizer dose	Application procedure
1.	Cow dung	225 kg	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 g	Basal dose

3.8 Seed sowing

For growing F₂ population the seeds were sown on 17 November, 2021. To ensure optimum moisture in the experimental field, a light irrigation was facilitated for proper germination before seed sowing. Seeds were positioned 1.5 cm deep in the soil. After sowing, less cold soil covering was ensured on the soil surface to protect the seeds.

3.9 Intercultural operations

After a light irrigation before seed sowing, another light irrigation was served after the emergence of seedlings with same good drainage system, 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. The 2nd thinning program was performed



Plate 4. Weeding and thinning was carried out to eliminate undesired plants from the plot



Plate 5. Tagging

just after 7 days later to confirm plant to plant distance at 10 cm. Before the application of the rest of urea, 2nd weeding was done, hence plants would have got their nutrients 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.

3.10 Backcross procedure for developing of BC₁

Among the 21 F₁ cross combinations, six cross combinations that were combined with P6 (BJ00) in F₁ generation were selected as female parents. Later on, these six female parents were mated with their respective Bangladeshi cultivars to obtain the backcrossed population. Backcross was done with an objective of making the P6 genotype of short-duration, higher yielding and short stature.

3.10.1 Plant selection

During the flowering stage, 20 plant sample were selected for crossing program for each cross combination. Plants are selected on the basis of stem thickness, stem color, leaf hairiness, leaf apex shape and size.

3.10.2. Emasculation

About to open floral buds were carefully chosen for emasculation. Removal of petal, sepal and pollen were done at morning usually 6:30 am to 9:00 am. The stigma was strictly kept unaffected during emasculation practice.

3.10.3. Hand pollination

Crossing was made by hand pollination (demonstrated in Plate 6) to get the desired cross combinations. Pollen was collected from the selected plant at the time sloughing off. Desired pollens were dusted on each of the stigma of the emasculated bud.

3.10.4. Crossing technique

To create the intended combinations, hand pollination was used on the desirable plants. Hand pollination was done using the bagging technique. Every dawn, emasculation was carried out. The ready-to-open floral buds of each of the parents and of the chosen F₁ were emasculated, and the leftover buds were removed. A yellow paper bag was placed over the emasculated buds. The buds were properly tagged.



Plate 6. Pollens were dusted on the emasculated buds



Plate 7. Pictorial view of the whole plot



Plate 8. Siliquae achieved by backcross



Plate 9. Harvesting

After 7-8 days, these bags were taken out to enable the siliqua to develop normally.

The BC₁F₁ combinations were mentioned in Table 2.

3.10.5 Bagging

After hand pollination, bagging with transparent bag (so that enough sunlight to eliminate fungal infestation) was done to protect the crossings from unwanted pollination. The bag was removed after a week ensuring optimum growth of siliqua.

3.10.6 Seed collection

The matured siliqua was meticulously collected afterward. The seeds were then removed from the siliques, counted, bagged individually, and stored with the appropriate tag for analysis during the following generation.

3.11 Crop harvesting

Plants that showed 80% symptoms of maturity like straw color of siliquae, leaves, stems and desirable seed color were harvested. At maturity, 5 plants were selected for morphological analysis from each of the line. The sample plants were harvested by uprooting carefully and tagging was kept for analyzing morphological and biochemical traits.

3.12 Threshing and storage

Harvesting was done maintaining individual line and seeds of F₂ populations 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 5 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 first 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.



Department of Genetics and Plant Breeding
SAU, RAIPUR
TITLE: ESTIMATION OF HETEROGENEITY AND COMBINING ABILITY OF F2'S DULCEL OF F2
POPULATION OF MUSTARD (BRASSICA SINENSIS L.)

Crop : Mustard	Design: Randomized Complete Block Design (RCBD).
Plot no : 27	Location: SAU Farm
No of parents : 07	
No of population : 43	
No of replication : 03	

Supervisor: Dr. Anwar Rehan Professor Department of Genetics and Plant Breeding	Researcher: Farzana Taj Johora Reg No : 18-00457 M.S. in Genetics and Plant Breeding
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Plate 10. Research field visited by the honorable supervisor

3.13.3 Days to 80% siliquae maturity

The data were recorded from the date of sowing to siliquae maturity of 80% plants of 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 risen from main stem was considered to measure this trait.

3.13.6 Number of secondary branches per plant

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

3.13.7 Number of Siliqua per plant

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

3.13.8 Siliquae length(cm)

Siliquae length was measured into centimeter (cm), from the base to the tip (with beak) of the siliquae.

3.13.9 Number of seeds per siliquae

Siliqua that was occupied with well filled seeds were counted and it was considered as the number of seeds per siliquae.

3.13.10 Thousand seeds weight (g)

Five randomly selected thousand seeds of each entry were weighed in grams which was recorded as thousand seed weight.

3.13.11 Yield per plant (g)

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

3.13.12 Harvest index (%)

Harvest index (expressed in percentage) 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 fifteen randomly selected plants (5 plant samples from each replication) were used for recording the data. The observed data were totaled for each of the twelve traits for each genotype in each replication and were subjected 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, coefficient of variation was estimated using Statistix 10 software. Diallel analysis was performed by using AGD-R (version 5.0) while, genetic variability of parental lines, correlation coefficient between selected variables, combining ability test and genetic components were performed by using R 4.2.1. software. Heterosis and inbreeding depression were calculated through Microsoft Excel.

3.14.1 Analysis of variance

The statistical analysis to determine the existing difference between two or three means used is called “Analysis of variance (ANOVA)”. Cochran and Cox (1957) set the goal of ANOVA 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 F-test.

Table 4. Analysis of variance (ANOVA)

Source of variation	Degree of freedom (df)	Mean sum of squares (MSS)	Expected MSS
Replication	(r-1)	Mr	$g\sigma^2_r + \sigma^2_e$
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^2_r = 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,

$$S.E = \sqrt{2Ee/r(1+ru/q+1)}$$

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 (σ^2g) = $GMS-EMS/r$

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares

r = Number of replications

σ^2g = Genotypic variance

σ^2e = Error variance

3.14.3 Genotypic (GCV) and phenotypic coefficient (PCV) of variation

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

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

Where,

σ^2g = Genotypic variance

\bar{x} = Population mean

Similarly, the phenotypic coefficient of variation was calculated from the following formula,

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

Where,

σ^2_p = Phenotypic variance

\bar{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).

$$\text{Heritability in broad sense, } H^2 = \sigma^2g / \sigma^2p \times 100$$

Where,

H^2 = Heritability in broad sense

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

$$\text{Genetic advance, GA in percentage of mean} = (\text{Genetic advance} / \bar{x}) \times 100$$

3.14.5 Heterosis

The improved or increased function of any biological trait in a hybrid offspring is known as heterosis, hybrid vigor, or outbreeding enhancement. It is typically assessed in two ways. Mid-parent heterosis or relative heterosis refers to the success of a hybrid when compared to the average performance of its parents. Heterobeltiosis is another word for heterosis and alludes to comparing a hybrid's performance to that of the cross's superior parent. Standard or economic heterosis is a different term that is commonly used to describe heterosis in terms of the performance of a hybrid variety relative to a check variety. Heterosis, also known as hybrid vigor, is a result of genetic and phenotypic variation and refers to a hybrid's superior performance in comparison to its progenitors. It is also known as economic superiority over checks because the first filial generation outperforms the standard commercial check type (Sharief *et al.*, 2005). The performance of a hybrid in contrast to the best commercial variety of the relevant crop species will largely determine its economic viability. Because it is preferable to estimate heterosis in relation to the best commercial variety, only hybrids were evaluated here against a variety of widely cultivated hybrid varieties. The amount of heterosis was estimated as the percentage of F_1 's hybrid from better parent value.

Heterosis over better parent (heterobeltiosis %) = $(F_2 - BP) / BP$

Where,

$\overline{F_2}$ = Mean of F_2 population

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

Heterosis over check variety was calculate by the same was,

Heterosis over check variety (Standard heterosis in %) = $\frac{\overline{F_2} - \overline{CV}}{\overline{CV}} \times 100$

Where,

$\overline{F_2}$ = Mean of F_2 population

\overline{CV} = Mean of better parent

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

Critical differences (CD) = $t \times \sqrt{2EMS/r}$

Here,

EMS = Error mean sum of squares

r = Number of replications

t = Tabulated t value at error df

CD values were compared with the values obtained from (F_2 -B.P) and (F_2 -C.V) to test the significance of respective heterotic effects.

3.14.6 Inbreeding Depression

Inbreeding depression (ID) was estimated by using formula of Oupadissakoon *and* Wersman (1977).

ID (%) = $[(F_1 - F_2) / F_1] \times 100$.

3.14.7 Hayman's ANOVA and Morley Jones modification

Hayman (1954a) provided a variance analysis for the entire diallel table, building on Yates' work in one way. However, this is frequently not the case, and only one of each set of reciprocal crosses is raised. For such a circumstance, Morley Jones (1965) modified Hayman's strategy in some ways. The determination of the sums of squares corresponding to additive effects (a) and on the assumption of no epistasis to mean dominance (b_1), to additional dominance effects that can be influenced by genes having one allele present in only one-line (b_2) (the remaining (n-1) lines being assumed to

carry the same alternative allele), is done in this modification using the same model as Hayman.) and to residual dominance effects (b_3), is in essence a straightforward application of fitting constants by least squares. HAYMAN (1954b) defined five components of genetic variation in a diallel system exhibiting additive and dominance, but no epistatic variation.

Table 5. Hayman's ANOVA of diallel following Morley Jones modification

Item	df	Sum of squares	Mean squares
a	n-1	$(1/N+2) \text{dev}^2_{ur}$	Ma
b ₁	1	$[1/ \{n (n^2 -1)\}] [2X... - (n+1) X.]^2$	Mb ₁
b ₂	n-1	$\{1/(n^2-4)\} \text{dev}^2_{tr}$	Mb ₂
b ₃	n(n-3)/2	Total SS – (a ss + b ₁ ss + b ₂ ss) 1	Mb ₃
b	n(n-1)/2	b ₁ ss + b ₂ ss + b ₃ ss $[2X... - (n+1) X.]^2$	Mb
Error	(r-1) (t-1)	ESS	Me

Where,

a = Additive effects

b = Dominance effects

b₁ = Mean dominance

b₂ = Dominance deviation due to arrays

b₃ = Residual dominance effect

Genetic component

F₂ and backcross generations, these were calculated according to Jinks (1956) and Mather and Jinks (1971). The various components estimated were as follows:

Table 6. Component in F₁, F₂ and backcross population

Component	F ₁	F ₂ and backcross population
D	VOLO – E	VOLO – E
F	$2 \text{VOLO} - 4 \text{WOLO} - 2 (n-2) E/n$	$4 \text{VOLO} - 8 \text{WOLO} - 4(n-2) E/n$
H ₁	$\text{VOLO} - 4 \text{WOLO} + 4 \text{V1L1} - (3n-2) E/n$	$4 \text{VOLO} - 16 \text{WOLO} + 16 \text{V1L1} - 4(5n-4) E/n$
H ₂	$4 \text{V1L1} - 4 \text{VOL1} - 2E$	$16 \text{V1L1} - 16 \text{VOL1} - 16 (n-1) E/n$
h ²	$4 (M L1 - MLO)^2 - 4 (n-1) E/n^2$	$16 (M L1 - MLO)^2 - 16 (n-1) E/n$
E	{(Error SS + Rep. SS) / df} / No. of Replication	VE/r = Me of F ₂

Where,

D = Variation due to additive gene effect

H₁ = Variation due to dominance gene effect

H₂ = H₁ [1 - (u - v)²] = Proportion of dominance variation that is due to positive and negative effects of gene. Here, u = proportion of positive genes and v = proportion of negative genes in the parents

h² = Dominance effect (as algebraic sum over all loci in heterozygous phase in all crosses

F = The mean of Fr over all arrays, where Fr is the covariance of additive and dominant effects in a single array

E = Expected environmental component of variance or error variance

VOLO = Variance of parents

V1L1 = Mean variance of the arrays

WOLO1 = Mean covariance between parents and the arrays

VOL1 = Variance of the means of arrays

(ML1-MLO)² = Dominance relationship i.e. the difference between the mean of the parents and the mean of the n² progenies.

In order to test the significance of each component viz. D, F, H₁, H₂, h² and E, the standard error (SE) is calculated for each of them by the formula:

$$SE = \{C (s^2 / n^5)\}^{1/2}$$

Where, s² = 1/2 [Var (Wr - Vr)] and

C = a multiplier specific to each component as calculated as bellows:

Table 7. Multiplier specific describer to each component

Component	F ₁	F ₂
D	(n ⁵ + n ⁴)/n ⁵	(n ⁵ + n ⁴)/n ⁵
F	(4 n ⁵ + 20 n ⁴ - 16n ³ + 16n ²)/ n ⁵	(16 n ⁵ + 80 n ⁴ - 64 n ³ + 16 n ²) / n ⁵
H ₁	(n ⁵ + 41 n ⁴ - 12 n ³ + 4 n ²) / n ⁵	(16 n ⁵ + 656 n ⁴ - 192 n ³ - 64 n ²) / n ⁵
H ₂	36 n ⁴ / n ⁵	576 n ⁴ / n ⁵
h ²	(16 n ⁴ + 16n ² - 32n + 16)/ n ⁵	(256 n ⁴ + 256n ² - 51n + 256)/n ⁵
E	n ⁴ /n ⁵	n ⁴ /n ⁵

The allied genetic parameters were as follows: $(H_1/D)^{1/2}$ = Mean degree of dominance.

If the ratio $(H_1/D)^{1/2} = 0$, there is no dominance, if the ratio $(H_1/D)^{1/2} < 1$, it indicates partial dominance, if the ratio $(H_1/D)^{1/2} = 1$, there is complete dominance and if the ratio $(H_1/D)^{1/2} > 1$, it indicates over-dominance. In F_2 , mean degree of dominance = $[1/4 (H_1/D)^{1/2}]^{1/2}$

$H_2/4H_1$ = Proportion of dominant genes with positive and negative effects in the parents. If the positive and negative alleles are symmetrically distributed this ratio is 0.25.

$KD/ KR = [(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ = Proportion of dominant and recessive genes in the parents. If it is less than 1, it indicates an excess of recessive genes but if it is greater than 1, it indicates an excess of dominant genes. In F_2 , $KD/KR = [1/4(4DH_1)^{1/2} + F]/[1/4(4DH_1)^{1/2} - 1/2F]$

$r_{xy} = \text{Cov} (Y_r, W_r + V_r) / \{ \text{VOL} \times \text{Var} (W_r + V_r) \}^{1/2}$ = Correlation between parental measurement (Y_r) and parental order of dominance ($W_r + V_r$)

CHAPTER IV

RESULTS AND DISCUSSIONS

In this experiment, data was assembled on twelve yield attributing characters from seven parental lines, 21 F₂ populations obtained from half diallel crosses, six BC₁F₁ populations of *B. juncea* L. The following sections simplify with the data that underwent different biometrical analysis and the obtained outcomes:

4.1 Mean performance and genetic variability analysis of F₂ population

Analysis of variance showed highly significance for all the examined parameter which indicated the presence of considerable genetic variations among the genotypes for all the traits (Table 8). The mean sum square value of days to first flowering, days to 50% flowering, days to 80% maturity, plant height, number of primary branches, number of secondary branches, siliqua length, siliqua per plant, seed per siliqua, 1000 seeds weight, yield per plant and harvest index is 26.78, 34.85, 19.15, 421.90, 2.06, 13.56, 0.62, 3065.84, 6.99, 0.91, 17.66, 38.13, respectively. So, this variation will affect all the growth promoting traits (number of primary branches, number of secondary branches and plant height), traits for earliness (days to first flowering, days to 50% flowering, days to 80% maturity), reproductive traits (siliqua per plant, siliqua length, number of seeds per siliqua) and economic traits (1000 seeds weight, yield per plant and harvest index). With the exception of seed per siliquae, highly significant variances were estimated for all the examined parameters. A detailed discussion is given below of the twelve parameters' variability.

Table 8. Analysis of variance (ANOVA) for twelve yield attributing traits of 21 F₂ hybrids with their parents

Source	DF	DFE	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
Replication	2	1.51	1.71	3.89	20.00	0.23	0.23	0.02	17.23	0.16	0.09	0.04	0.15
Genotype	27	26.78**	34.85**	19.15**	421.90**	2.06**	13.56**	0.62**	3065.84*	6.99**	0.91**	17.66**	38.13**
Error	54	2.18	2.26	3.77	8.72	0.08	0.16	0.01	15.55	0.22	0.0024	0.04	0.17

Note:

DFE=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g) and HI=Harvest index

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

To figure out the difference of performance among the populations, morphological characterization of 21 F₂ hybrids along with their parents, was done. The 12 quantitative yield contributing parameters were used to choose the finest lines possible. According to the chosen parameters, the results of mean performance and genetic variability analysis of 21 F₂ populations are shown in Tables 9 and 10.

4.1.1.1 Days to first flowering

First flowering's duration varied from 32.33 DAS to 43 DAS, with an average of 36.83 DAS. When crossing, the minimal value was noted. In the parental line P1 (32.33 DAS), the minimal duration for flower initiation was seen in hybrid G12, G13 (33 DAS), and a nearly same value was also seen in G7, G16, and G20 (34). (Table 9). On the other hand, G8 (43) had the longest duration, followed by G2 (42), G18 while P6 (40.67DAS) had the greatest first flowering rate among parents (Table 9). The outcome was nearly identical to that reported by Patel *et al.* (2019), who found that the time between seeding and the first flowering varied between 35.33 and 49days for different lines and varieties of *B. juncea* L.

In case of days of first flowering, the phenotypic variance was (10.37) slightly higher than the genotypic variance (8.20). The less difference between genotypic and phenotypic variance shows that environmental influence was negligible on the genes controlling this trait. Genotypic and phenotypic coefficient of variations was 7.77 and 8.75, respectively. This little difference between phenotypic and genotypic coefficient of variation implied that, the present variation was mainly contributed by the genes and minimally contributed by the environment. The value of GCV and PCV indicated considerable variation was present among the genotypes for the traits. Days to first flowering showing the high heritability (79.01%) with moderate genetic advance as percentage of mean (14.24%) indicated, inheritance of days to first flowering might be controlled by the additive gene effects and selection for genetic improvement in terms of this trait would be effective (Table 10). High genotypic and phenotypic coefficient of variation was recorded by Lekh *et al.*, (1998).

Table 9. Mean performance of yield and yield related characters of 21 F₂ populations and their 7 parents of *B. juncea* L.

	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP	HI
P1	32.33 g	37 h-l	102.67 l	141.89klm	4.67 i-l	8.67 jk	4.03 pq	249.45 d	12.39 h-j	3.63 c	8.67 kl	29.64 e
P2	34.67 e-g	39 e-i	103.67 kl	151 f-h	4.55jkl	7.67 lm	3.92 qr	206.78 kl	11.443 kl	3.02 fg	5.57 r	26.23 ij
P3	34 fg	39.33 e-h	104 j-l	141.33 k-n	5.22 d-h	8.777 j	4.25 m-o	220.78 h	14.61 cd	2.81 i	6.2 q	27.15 gh
P4	35.67 d-f	42.67 b-d	105.33 h-l	158.22 b-d	5.11 e-i	9.223 ij	4.29 l-o	234.78 e	14.11 de	2.97 gh	8.13 m	28.67 f
P5	37.67 cd	43.33 bc	108.67 b-g	169.56 a	5.56 c-e	8.13 kl	4.55 g-j	234.89 e	11.88i-k	2.96 gh	7.57 o	24.37 k
P6	40.67 ab	46.67 a	111.33 ab	149.89 g-i	3.22 n	5.57 o	3.05 s	207.33 j-l	12.446 h-j	2.67 j	6.01 q	27.19 g
P7	36 d-f	40.67 d-g	107 e-j	154.44 dg	5.67 cd	9 j	4.43 i-l	214.11 i	12.56 hi	3.05 f	8.66 kl	28.02 f
G1	34 fg	39 e-i	104.33 i-l	137.83 mo	4.22 lm	8.67 jk	4.22 no	213.67 ij	14.11 de	2.11 q	9.47 hi	31.39 c
G2	42 a	44 b	109.67 b-e	143.33 jkl	4.67 k-m	7.33 m	5.33 a	189 m	15 bc	3.82 b	9.97 g	26.70 g-i
G3	37 c-e	41.33 c-e	108 c-h	159.33 bc	6 bc	11 de	4.66 e-g	227.78 fg	14.09 de	2.38 n	9.47 hi	23.50 lm
G4	38 cd	42.67 b-d	106 g-k	158 bcd	5.33 d-g	12 c	4.46h-l	287.5 b	14 de	2.56 kl	13.87 b	28.33 f
G5	37.67 cd	41.33 c-e	109 b-g	155.56 c-f	4.67 i-l	8.67 jk	3.77 r	226 gh	11.89 i-k	3.16 e	7.63 no	23.30lm
G6	38 cd	41 c-f	110.67 a-c	145.33 i-k	4.33 k-m	9.00j	4.13 op	233.33 ef	10.89 lm	2.24 op	7.13 p	20.36 o
G7	34 fg	36.33 j-l	105.33 h-l	136.22 op	4.33 k-m	6.33 n	4.27 no	195.11 m	12.44 h-j	2.31 no	8.47 l	20.07 o
G8	43 a	46ab	106.33 f-k	172 a	7 a	13.34 b	4.40 j-m	274.33 c	10.92 lm	2.19 p	8.57 l	24.12 kl
G9	34 fg	38 h-l	107.67 c-h	136.67 n-p	4.67 i-l	10 gh	4.79 de	211.5 i-k	12.89 f-h	2.89 h	10.47 f	33.56 b
G10	37 c-e	41.33 c-e	109.33 b-f	168.33 a	4.78 h-k	8.11 kl	4.56 g-i	204 L	14.45 cd	2.63 jk	8.57 l	25.94 j
G11	37.67 cd	42 b-d	106.33 f-k	144.67 j-l	6 bc	13.77 ab	4.13 op	272 c	13.45 ef	3.37 d	12.73 c	30.2 de
G12	33 g	38.67 f-j	105.33 h-l	126 r	5 f-j	10.33 fg	4.8 de	272 c	15.67 b	2.31 no	9.13 ij	28.67 f
G13	33 g	36 kl	104.33 i-l	151.89 e-h	6.22 b	10 gh	4.13 op	224.11 gh	17 a	3.35 d	12.53 cd	35.27 a
G14	37 c-e	41.33 c-e	107.67 c-h	132.89 pq	3.89 m	8.89 j	5.13 b	189.33 m	12.63 gh	2.56 kl	7.97 mn	27.17 g
G15	39 bc	43.33bc	105.33 h-l	128.78 qr	5 f-j	10.78 df	4.87 cd	233.17 ef	14 de	2.47 m	8.97 jk	27.05gh
G16	34 fg	44 b	108 c-h	151.17 f-h	5 f-j	9.67 hi	4.46 h-k	271.67 c	12.557 hi	2.10 q	9.63 gh	26.48 h-j
G17	37 c-e	38.33 g-k	107.33 d-i	147.22 h-j	6 bc	14.33 a	4.75 d-f	297.78 a	12.223 h-j	2.3 no	15.6 a	22.3 n
G18	39 bc	43.33bc	106g-k	143.56 j-l	6.44b	11.34 d	4.60 f-h	271.33 c	14.333 cd	2.54 lm	11.63 e	30.43 d
G19	39 bc	48 a	110.33 a-d	140.33 l-o	4.33 k-m	10.67 ef	4.73 d-f	239.44 e	11.77 jk	3.8 b	12.3 d	28.48 f
G20	34 fg	35.67 l	107 e-j	156.5 b-e	5.44 d-f	12.33 c	4.32 k-n	285.89 b	10.44 m	3.98 a	12.47 cd	23.36 m
G21	39 bc	44 b	113.33 a	160.67 b	4.88 g-j	11.33 d	4.97 bc	268.33 c	13.47 eg	2.31 no	9.97 g	28.41 f
MAX	43	48	113.33	172	7	14.33	5.33	297.78	17	3.99	15.6	35.27
MIN	32.33	35.63	102.67	126	3.22	5.57	3.05	189	10.44	2.10	5.56	20.10
MEAN	36.83	39.33	107.14	148.66	5.08	9.82	4.43	237.69	13.13	2.8	9.54	27.01
CV	4.01	3.73	1.81	1.99	5.49	4.06	2.25	1.66	3.56	1.73	2.2	1.53
LSD	2.41	2.46	3.17	4.83	0.46	0.65	0.17	6.46	0.77	0.1	0.33	0.67

Note: DFF= Days to first flowering, D50%F= Days to 50% flowering, DSM= Days to 80% maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NS= Number of secondary branches per plant, SL= Siliqua length (cm), SPP= Siliquae per plant, SPS= Seeds per siliqua, TSW= 1000 seeds weight (g), YPP= Yield per plant (g) and HI= Harvest index (%).

Table 10. Different genetic parameters for twelve yield and yield contributing characters of F₂ populations of *B. juncea* L

Traits	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	h^2_b (%)	GA	GA (mean) (%)
DFF	10.37	8.20	2.17	8.75	7.77	79.01	5.24	14.24
D50F	13.12	10.86	2.26	8.98	8.17	82.80	6.17	15.32
DSM	8.90	5.13	3.77	2.78	2.11	57.62	3.54	3.30
PH	146.45	137.73	8.72	8.14	7.89	94.05	23.44	15.77
NPB	0.74	0.66	0.08	16.93	16.01	89.47	1.58	31.20
NSB	4.62	4.46	0.16	21.91	21.53	96.57	4.28	43.59
SL	0.21	0.20	0.01	10.40	10.15	95.32	0.90	20.41
SPP	1032.31	1016.76	15.55	13.52	13.41	98.49	65.19	27.43
SPS	2.47	2.25	0.22	12.00	11.45	91.20	2.96	22.52
TSW	0.34	0.32	0.02	19.69	19.61	99.21	1.13	40.24
YPP	5.91	5.87	0.04	25.48	25.38	99.25	4.97	52.10
HI	12.82	12.65	0.17	13.26	13.17	98.67	7.28	26.95

Note: σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, σ^2_e = 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, DFF= Days to first flowering, D50%F= Days to 50% flowering, DSM= Days to 80% siliquae maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, SL= Siliquae length (cm), SPP= Siliquae per plant, SPS= Seeds per siliqua, TSW= 1000 seeds weight (g), YPP= Yield per plant (g) and HI= Harvest index (%).

4.1.1.2 Days to 50% flowering

A mean value of 39.33 DAS was used to estimate the variation, which ranged from 35.67 to 48. Days to 50% flowering were reported by Mishra and Nath in 2022 in *B. juncea* L. species from 47 to 57.33 days. According to the present study, G19 (48) followed by G8 (46) and G2 (44), G16(44) as well as P1 (37 DAS) in the parental lines, in crossings needed the most time to reach 50% flowering. On the other hand, for attaining 50% flowering in the field, P6 (46.67), P5 (43.33) among the parental line, and in F₂ populations G20 (35.67), G7 (36.33) had taken the shortest period of time. (Table 9). While working with 60 advanced lines of Indian mustard with three checks, Hyder *et al.*, (2021) discovered that plants need 48 to 69 days after sowing to reach 50% flowering coverage.

The phenotypic variance was (13.12) slightly higher than the genotypic variance (10.86) for this trait. The margin of difference between genotypic and phenotypic variance being seemingly low indicates unremarkable environmental influence on the genes controlling this trait. Genotypic and phenotypic coefficient of variations was 8.17 and 8.98, respectively. This minute difference between phenotypic and genotypic coefficient of variation decides that, the present variation was mainly caused by the genes and the variation caused by the environment is minimum. The value of GCV and PCV indicated considerable variation was present among the genotypes for the traits. Trait with the high heritability (82.80%) and moderate genetic advance as percentage of mean (15.32%) indicates inheritance of days to 50% flowering is under control of additive gene and this trait would be proven effective if chosen for genetic development. (Table 10). The highest magnitude was obtained days to 50% flowering (77.59%) by Tripathi *et al* (2019). For days up to 50% blooming, Akoju *et el.* (2020) discovered a moderate PCV (10.51) and lowest GCV (8.54). High heritability coupled with moderate genetic advance as a percentage of the mean for this feature were observed by Jahan *et al.* (2014) and Hussain (2014). The study also showed that the genotypes' blooming attributes were moderately sensitive and affected by changes in the ambient temperature, and that the expression of the features was regulated by additive gene activity.



G1 G2 G3



G4 G5 G6



G7 G8 G9



G10 G11 G12



G13 G14 G15



G16 G17 G18



G19 G20 G21

Plate 11. Flowering stage of 21 F₂ population derived from 7×7 half diallel crosses

4.1.1.3 Days to 80% maturity

Days to 80% maturity ranged from 102.67 DAS to 113.33 DAS among the genotypes, with an average of 107.14 (Table 9). In terms of parents, P1 was determined to have the lowest value (102.67), followed by P2 (103.67). However, cross combinations G13 (104.33) which statistically resembled to F₂ population's G1 (104.33) and G12 (105.33), revealed the lowest duration. According to Shekhawat *et al.* (2014), 80% of plants in a line reached maturity between 121 to 141 days following seeding. While it was discovered that *B. juncea* L. species needed 196 to 228.00 for days to maturity by Hyder *et al.* (2021). However, among the F₂ populations G21 (113.33), and among the parents, P6 (111.33), followed by P5 (108.67) required the longest time to reach 80% siliqua maturity.

Like the previous two traits, the phenotypic and genotypic variance went almost neck to neck numerically for days to 80 Siliqua maturity. The genotypic and phenotypic variance was 5.13 and 8.90 respectively while the genotypic and phenotypic coefficient variation was 2.11 and 2.78 respectively. The difference between genotypic and phenotypic variance, phenotypic and genotypic coefficient of variation not high in amount indicates that there was ordinary environmental influence on the trait controlling genes. The value of GCV and PCV indicated considerable variation was present among the genotypes for the traits. The trait held moderate heritability (57.62%) and low genetic advance (3.54) and low genetic advance as percentage of mean (3.30%) indicated inheritance of days to 80% siliqua maturity was under control of non-additive gene and this trait would be proven ineffective if chosen in terms of genetic development (Table 10). Jahan *et al.*, (2014) observed high heritability with low genetic advance in percent of mean for days to maturity. Ara (2010) found high heritability with low genetic advance and genetic advance in percentage of mean.

4.1.1.4 Plant height (cm)

Plant height estimations ranged from 126 cm to 172 cm, with a mean of 148.66 cm. (Table 9). Among the parental lines, P5 (169.56 cm) had the tallest plant, followed by P4 (158.22 cm) and P7 (154.44 cm). Among the F₂ population's G8 (172.00 cm), G21 (160.67 cm) and G10 (168.33 cm) were all virtually equal with the highest value. In an experiment with 38 genotypes of Indian mustard, Akoju *et al.*, (2020)

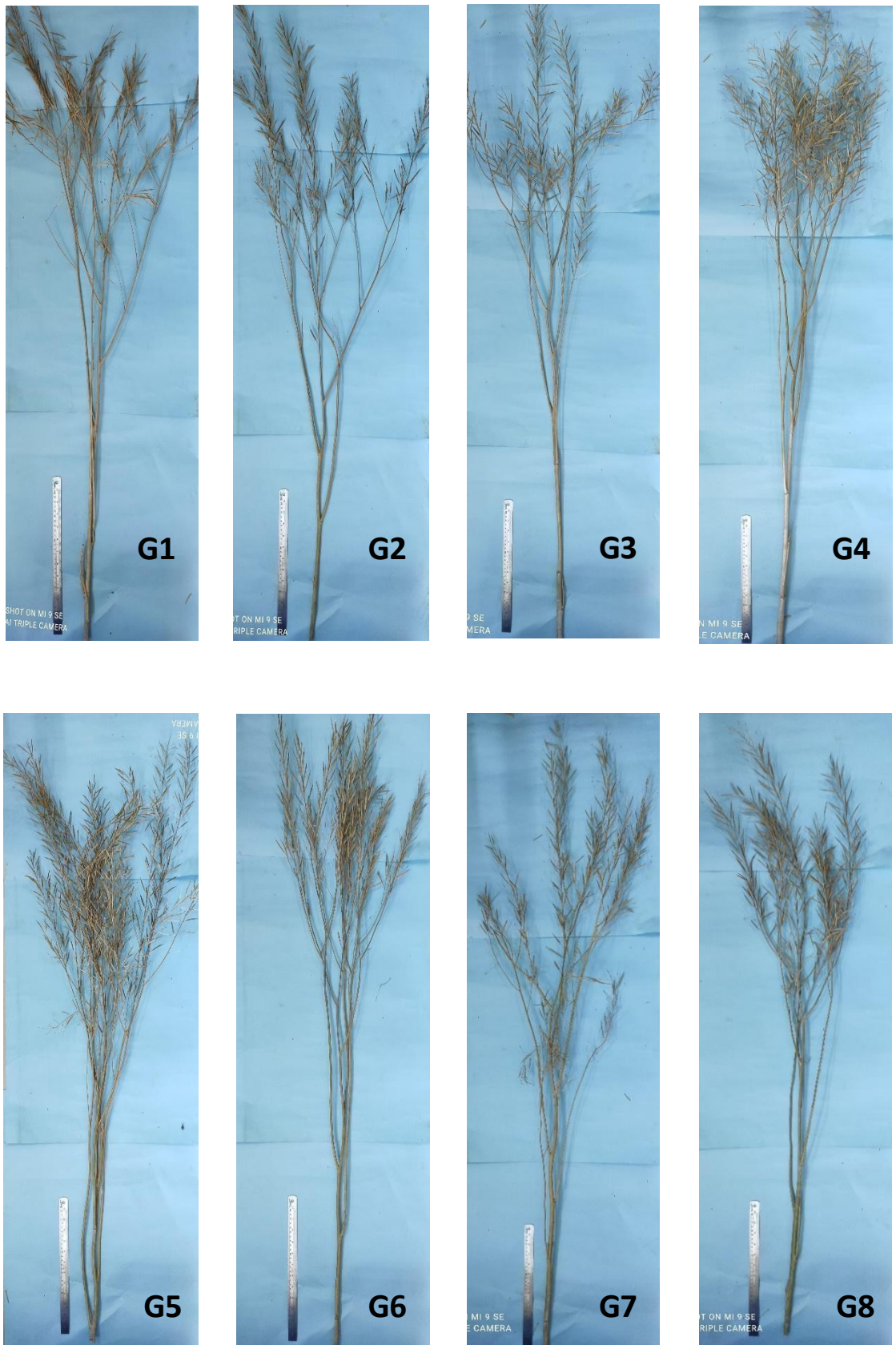


Plate 12a. Height of selected plant of (G1-G8) genotypes of F₂ populations of *B. juncea* L.

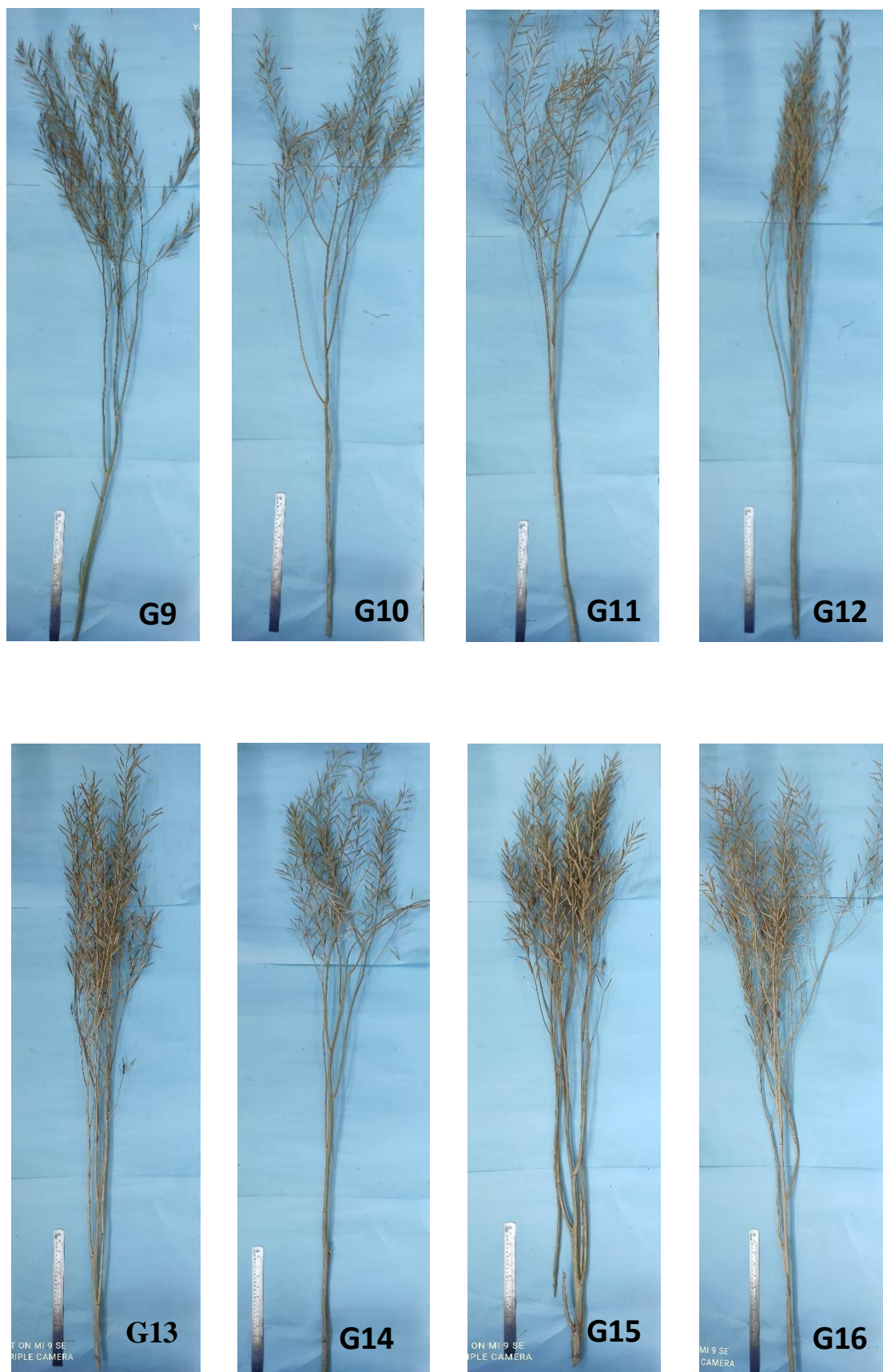


Plate 12b. Height of selected Plant of (G9-G16) genotypes of F₂ populations of *B. juncea* L.



Plate 12c. Height of selected plant of (G17-G21) genotypes of F2 populations of *B. juncea* L

Plate12. Height of selected plant of (G1-G21) genotypes of F2 populations of *B. juncea* L

discovered that plant height varied from 108.00 to 168.00 cm. The lowest value, however, was calculated for parents P3 (141.33 cm) and was estimated for G12 (126 cm). The genotypic variance and the phenotypic variance for plant height was 137.73 and 146.45, respectively with moderate level of environmental variance (8.72) which means the gene controlling this trait was influenced by the environment was noticeable. 8.14 and 7.89 are the phenotypic and genotypic coefficient variance respectively with minor difference between them. The trait went with high heritability (94.05%) paired with high genetic advance (23.44) and moderate genetic advance as percentage of mean (15.77). 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 change to this trait into desirable height (Table 10). According to Jahan *et al.*, (2014), plant height has a high heritability and a modest genetic advancement. However, Fayyaz *et al.*, (2014) and Ara *et al.*, (2010) discovered that plant height had the highest heritability and highest genetic advance.

4.1.1.5 Number of primary branches per plant

An average of 5.08 primary branches per plant, with a range of 3.22 to 7.00 was found among all the population. The F₂ population's G8 (7) held the most primary branches per plant, followed by G18 (6.44) and G13 (6.22), while parental line P7 (5.67) produced the highest primary branch (Table 9). Mishra and Nath (2022) observed 5.78 to 10.67 primary branches on average for several *B. juncea* L. lines and their parents. P6 had the lowest value (3.22), which was comparable to P2. (4.55). G14 (3.89), followed by G1 (4.22) and G6, G7 (4.33) had the smallest number of primary branches per plant of all the crossings. Identical range of primary branches was also observed in Gangapur *et al.*, (2009) findings.

Number of primary branches unveiled its genotypic variance and the phenotypic variance as 0.66 and 0.74, respectively. The difference between phenotypic and genotypic variance was almost ignorable which implies that the gene controlling this trait was minimally influenced by the environment. Showing a moderate assortment of phenotypic coefficient variance (16.93) and the genotypic coefficient variance (16.01) by this trait indicated the existence of inherent variability among the genotypes. This trait combining with high heritability (89.47%), low genetic advance (1.58) and a higher genetic advance as percentage of mean (31.20) indicates legacy of number of

primary branches was under control of additive gene and this trait would be proven productive if chosen in genetic development purpose (Table 10). High heritability and high genetic advance were estimated as percentages of the mean for this character by Singh *et al.* (2010) and Rout *et al.* (2019). For the chosen characters, Alamerew and Woyessa (2017) discovered low heritability (34.20%) and strong genetic progress as a percentage of mean (30.10%). Relatively high PCV and GCV was shown in terms of number of primary branches by Mekonnen *et al.* (2014) Sikarwar *et al.*, (2017) and Gupta *et al.*, (2019). Low heritability with low genetic advance and low genetic gain 9.50% that showed non additive gene action and so ineffective of the selection. This decision was given by Mekonnen *et al.* (2014) but reverse decision was confessed by Alam (2010) and Rout *et al.* (2018).

4.1.1.6 Number of secondary branches per plant

The range of the projected value was 5.56 to 14.33, with an average of 9.82. F₂ population's G17 (14.33) had the highest secondary branches at crossings. Additionally, it was demonstrated that the paternal line P4 (9.22) and F₂ population's G11 (13.77) and G9 (13.34) had greater values for the quantity of secondary branches per plant. (Table 9). The secondary branches count per plant varied from 11.95 to 17.73, according to Yadava *et al.*, (2012). P6 (5.57) had the lowest values in parents, while G8 (6.33), G2 (7.33) had the lowest values in cross combinations. According to Akoju *et al.*, (2020), each *B. juncea* L. genotype plant produced between 6.00 and 17.00 secondary branches.

The number of secondary branches showed that the genotypic and phenotypic variances were 4.46 and 4.62, respectively. The gap between phenotypic and genotypic variance was essentially preventable, which suggested that the environment had a minimal influence on the gene governing this feature. The presence of inherent variability across the types was shown by screening a moderate array of phenotypic coefficient variance (21.91) and genotypic coefficient variance (21.53) by this trait. Combined with low genetic advance and a higher genetic advance as a proportion of mean, this variable has a high heritability (96.57%). Walle *et al.*, (2014), Alam *et al.*, (2010) and Khan *et al.*, (2013) described heritability as high along with low genetic gain.

4.1.1.7. Siliqua length

Different F2 populations were varied from 3.05 cm (parent) to 5.33 cm, with a mean value of 4.43 cm for this trait. F2 population's G2 (5.33 cm) had the longest siliquae, followed by the parents P5 (4.55 cm) and P7 (4.43 cm) and F2 population's G14 (5.13 cm) and G21 (4.97 cm). The estimated length of siliquae for various F2 lines reported by Patel et al. (2021) was increased from 3.68 to 5.46 cm. As for siliquae length, G5 had the lowest value among parents (3.77 cm), followed by G6 (4.13 cm) P6 (3.05 cm), and P1 (4.03 cm) (Table 9). As for siliquae length, G5 had the lowest value among parents (3.77 cm), followed by G6 (4.13 cm), G13 (4.13 cm), G7 (4.22), P6 (3.05 cm), and P2 (3.92 cm). (Table 9). Both Gangapur et al., (2009) and Dawar et al., (2018) reported that the siliquae's length ranges from 3 to 6 cm. In Plate 13, the siliquae length of several individuals is displayed.

Almost similar value of genotypic variance and the phenotypic variance was observed for this trait which is 0.20 and 0.21 respectively while the difference between two variance is nearly zero. Screening a moderate array of phenotypic coefficient variance (10.40) and the genotypic coefficient variance (10.15) by this trait indicated the existence of inherent variability among the varieties. The least deviation in both cases shows the scarce influence of environment on trait controlling genes while genotypes take the lead. This trait held with high heritability (95.32%) and low genetic advance with a higher genetic advance as percentage of mean (20.41) which indicated the control of additive gene effect on this trait. Additive gene effect ensured large siliqua to be formed if chosen for this trait in breeding program (Table 10). Length of siliquae had (77.39%) heritability which was high. High heritability with high genetic gain allowed to speculate the presence of additive gene effects on the trait proposed by Mahmud *et al.*, (2019) and Uzair *et al.*, (2016).

4.1.1.7 Siliquae per plant

The average siliquae number was 237.69, although the range was 189.00 to 297.78. The F2 population's G17 (297.78) had the highest siliqua per plant, whereas G4 (287.5) and G8 also showed values. (274.33). The highest siliquae yielding per plant in parents was P1 (249.45), followed by P5 (234.89) and P4 (234.78), which

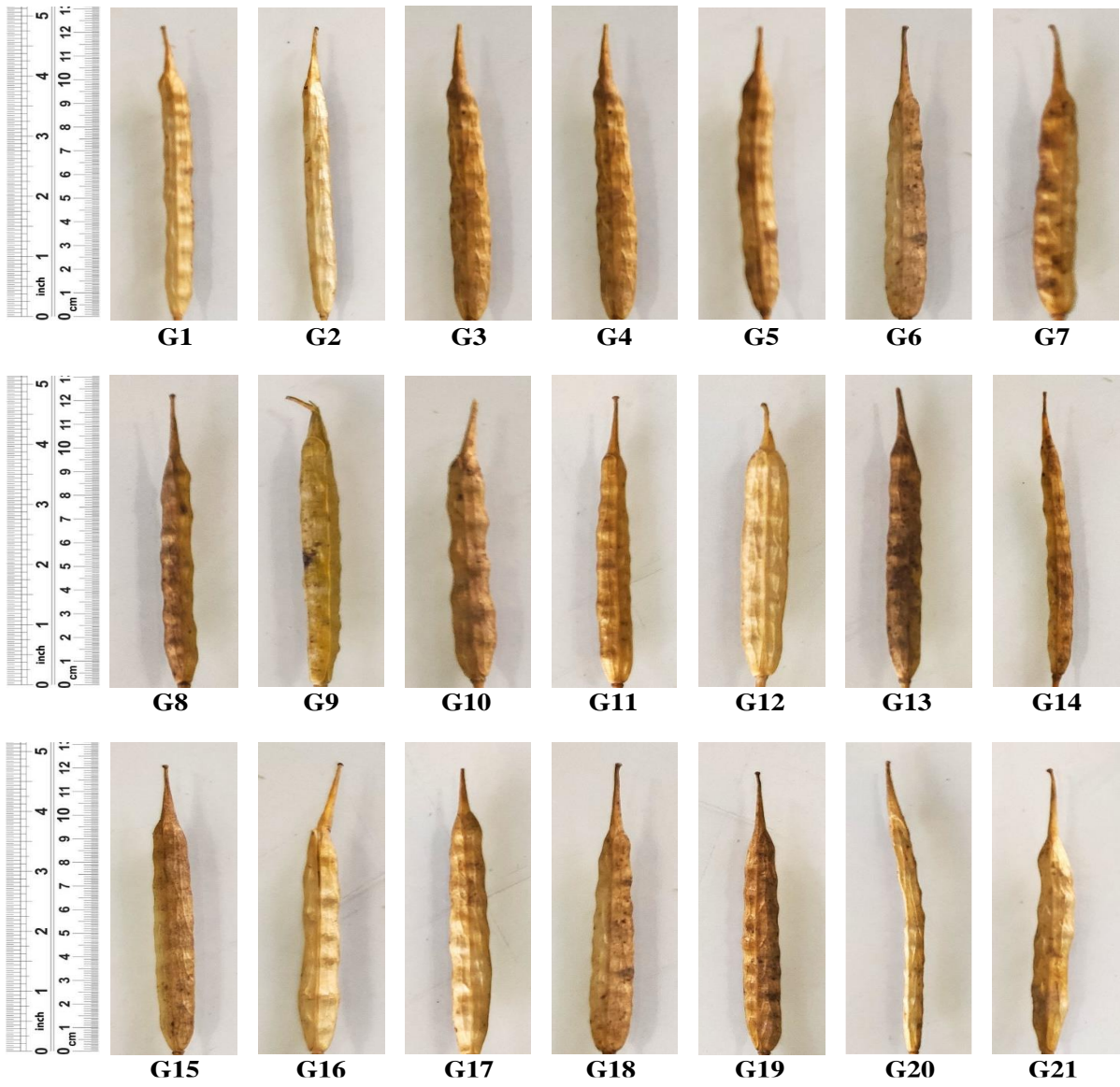


Plate 13. Siliquae length variation among the 21 F₂ populations (G1-G21)

showed a good capability for yielding from a plant. Yadava *et al.*, (2011) published their research findings and found that each plant produced between 223.23 and 482.60 siliqua per plant. Among the parents, P2(206.78) was assessed to have the lowest number, followed by P6 (207.33) and P7 (214.11). In addition, F₂ population's G2 (189), G14(189.33), and G7(195.11) also displayed the lowest number content in the production of siliquae. (Table 9). In *B. juncea* L species and the generated F₂ lines, the number of siliquae varied from 297.78 to 189, with Yadava *et al.*, (2011) estimating 237.69. The highest siliquae yielding per plant was P5 (234.89), which showed that a plant had a good yielding capability.

High genotypic variance (1016.76) and the phenotypic variance (1032.31) were detected with considerably high environmental variance (15.55) for the trait number of siliqua per plant which defined the prominent environmental influence on the trait controlling gene rather than genotypic influence. Screening a less gap of phenotypic coefficient variance (13.52) and the genotypic coefficient variance (13.41) by this trait indicated the existence of inherent variability among the genotypes. This trait grasps with high heritability (98.49%) and high genetic advance with a high genetic advance as percentage of mean (27.43) which indicated the control of additive gene effect on this trait. Additive gene effect ensures higher number of siliquae to be formed if selected for this trait in breeding program (Table 10). Joya *et al.*, (2016), Afrin *et al.*, (2017), Aktar *et al.*, (2019) got the result matched with this result.

4.1.1.8 Seeds per siliqua

The range of seeds per siliquae was 10.44 to 17, with a mean value of 13.13. (Table 9). In the genotypes and their descended lines of the *B. juncea* species, Czern (2020), reported that the seeds per siliqua ranged from 11.90 to 14.05. The F₂ population's cross G13 (17) had the highest number of seeds per siliqua, which statistically corresponded to the parent P3(14.61) and G2 (15) population. (14.61). For seeds per siliqua, however, F₂ population's G20 (10.44) and parent P2 (11.44) were shown to have the lowest values. (Table 9). The trait's mean sum square was 6.99. (Table 8). In addition, according to Ali *et al.*, (2015) and Tripathi *et al.* (2019), the number of seeds per siliquae varied between 11.6 and 16.2 in *B. juncea* L. species.

Lower value of genotypic and the phenotypic variance were observed for this trait which were 2.25 and 2.47, respectively while the difference between two variation was nearly unimportant to be worth consideration. Showing a low difference of

phenotypic coefficient variance (12.00) and the genotypic coefficient variance (11.45) by this trait indicated the existence of inherent variability among the genotypes. The least deviation in both cases shows the scarce influence of environment on trait controlling genes while genotypes take the lead. This trait embraced with high heritability (91.20%) and low genetic advance with a high genetic advance as percentage of mean (22.52) which indicates the regulation of additive gene effect on this trait. Additive gene effect ensures desired count of seed per siliquae to be formed if chosen for this trait to increase yield in breeding program (Table 10). On the other hand, Gupta *et al.*, (2019) demonstrated high heritability with high genetic advance while Rout *et al.*, (2019) found the result matched with the results of the present investigation.

4.1.1.9 Thousand seeds weight (g)

The populations' seed weights ranged from 2.10 g to 3.99 gm, with an average of 2.8 g per 1000 seeds (Table 9). In terms of F₂ hybrids, G20 (3.99 g) had the highest estimated thousand seed weight, followed by G2 (3.82 g), had the lowest value. According to Patel *et al.* (2019), 1000 seeds weigh between 4.13 g and 5.97 g each plant, while (Czern., 2020) reported that 1000 seeds weigh between 1.25 and 6.25 g per plant. The two parental lines with the highest values for 1000 seeds weight were P1 (3.63 g) and P7 (3.05 g). (Table 9). Similar findings were published by Patel *et al.*, (2021) who found that the weight of 1000 seeds per plant ranged from 3.59 to 6.14 gm.

The genotypic variance of thousand seed weight was 0.32, while the phenotypic variances were 0.34. The divergence indicates that genotypic influence was the main promoter here and that the gene determining the characteristic had the least environmental influence. The variation of the genotypic and phenotypic coefficient were 19.69 and 19.61, respectively. This trait exhibited high heritability (99.21%), low genetic advance, and a high genetic advance as a percentage of the mean (40.24%), which suggests that additive gene influence was regulated on this trait. If required for this characteristic to boost yield in the breeding program, additive gene effect ensured that the desired weight of 1000 seeds would be generated (Table 10) Yared and Misteru (2016) along with Parveen *et al.*, (2015) demonstrated the same combination of results for this parameter.

4.1.1.10 Yield per plant (gm)

The mean yield per plant was 9.54 g, with a range of 5.56 to 15.6 g. F₂ population G17 (15.6 g) had the largest yield, followed by G4 (13.87 g) and P1 (8.67 g) in the parents. (Table 9). Mandal *et al.*, (2022) estimate of the seed output per plant, which ranged from 6.58 to 14.48 g, provided support for this report. In parental lines, P2 (5.57 g) had the lowest value, followed by P6 (6.01 g), and P3 (6.2 g), while in F₂ population's G6 (7.13 g) and G5 (7.63 g) (Table 9). also displayed the lowest yield per plant. Shekhawat *et al.* (2014) reported that the seed yield of each plant of several varieties of *B. juncea* L. and their derivatives ranged from 14.56 g to 19.74 g, and similar results were obtained statistically.

Yield per plant exhibited the lowest value for genotypic (5.87) and phenotypic variance (5.91) whereas, the environmental variance was negligible. The negligible environmental variance showed the negligible influence of environment on the trait controlling gene and genotypic influence was highly prominent. Genotypic and phenotypic coefficient of variations was 25.38 and 25.48 respectively which was moderate. The value of GCV and PCV indicated considerable variation was present among the genotypes for the traits. Salam *et al.*, (2017) also found moderate level of GCV and PCV amount for yield per plant. Yield per plant showing the high heritability (99.25%) with low genetic advance with high genetic advance as percentage of mean (52.10%) indicated, inheritance of yield per plant might be controlled by the additive gene effects and selection for genetic improvement in terms of this trait would be effective (Table 10). Ahmad *et al.*, (2013), Ali *et al.*, (2015) founded high heritability also with high genetic advance.

4.1.1.11 Harvest index (%)

The range of the data variation was from 20.10 to 35.27, with an average of 27.01. G13 (35.27) had the highest harvest index among the crossing lines, followed by F₂ population G9 (33.56) and G10 (33.56). P1 (29.64) had the highest harvest index among the parents. F₂ population G6 (20.36) and G7 (20.07) both showed the lowest values, while P4 (24.35) and P6 (26.23) displayed the lowest harvest index in terms of percentage value. (Table 9). These results were corroborated by Mishra and Nath (2022), who discovered that distinct F₂ populations of *B. juncea* L. had harvest indices ranging from 24.55 to 34.16.

Genotypic variance (12.65) and phenotypic variance (12.82) were estimated with low environmental variance (0.17). Genotypic and phenotypic coefficient of variations were 13.17 and 13.26, respectively. This minute difference between phenotypic and genotypic coefficient of variation decided that, the present variation was mainly caused by the genes and the variation caused by the environment was minimum. The value of GCV and PCV indicated considerable variation was present among the genotypes for the traits. Trait with the high heritability (98.67%) and high genetic advance as percentage of mean (26.95%) indicated inheritance of harvest index was under control of additive gene and this trait would be proven effective if chosen for genetic development (Table 10). Ahmad *et al.* (2013) and Sikarwar *et al.*, (2017) found high heritability with moderate genetic advance for this trait.

4.2. Correlation coefficient analysis of 21 F₂ populations of *Brassica juncea* Indirect selection via other characters can be a pathway to improve specific trait in all the breeding program. For the approximation of correlation of yield with their related characters, a thoughtful perception of different characters with the target trait and among the different characters themselves is looked-for. For the pictorial valuation of population, an idea should be there among the breeders on correlation of yield with other traits. There is found two types of correlation viz., positive correlation which defines the change of two variables into same direction (like if the independent variable increases so does the dependent variable) and while, the negative correlation which means the increase in the first variable combined with a decrease in the second variable (or reverse). The phenotypic and genotypic correlation established the level of connotation among different characters; hence, it helps to base selection procedure to an obligatory balance in terms of selecting two opposite characters, influencing the main characters. 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. To evaluate the range and nature of relationship prevailing among yield and yield related

characters (as yield is a complex polygenic trait) the influence of each character on yield can be determined through correlation analysis. Therefore, the correlation coefficient values of twelve traits of F₂ populations of *B. juncea* L. were evaluated and estimated. The results revealed that genotypic correlations were greater than the phenotypic correlation coefficients. Research findings were illustrated in Table 11. Mahla *et al.*, (2003) showed the genotypic estimates were higher than the phenotypic ones, indicating an inherited association between the characters.

4.2.1 Days to first flowering

Day to first flowering had a substantial significance and a positive correlation with both genotypically and phenotypically determined days to 50% flowering (0.79, 0.71) and days to 80% Siliqua maturity (0.57, 0.38). Days to first flowering had a highly significant and positive correlation with days to 50% flowering, plant height, Siliquas per plant, and seed output, according to Jamali *et al.*, (2016) but they reported a negative correlation with secondary branches per plant. This characteristic had a negative non-significant correlation with 1000 seeds weight (-0.17, -0.15), yield per plant (-0.09, -0.07) and harvest index (-0.16, -0.15) at both the genotypic and phenotypic levels. Negative correlations between seeds per siliqua, siliquae length, 1000 seeds weight, and number of siliquae per plant were discovered by Sultana *et al.*, (2020) at both the genotypic and phenotypic levels for days before first flowering. Plant height (0.20,0.17), number of primary branches (0.08, 0.07), number of secondary branches (0.09, 0.06), siliqua length (0.12, 0.09), siliqua per plant (0.23,0.20) and seeds per siliqua (0.014, 0.012), these characteristics exhibited no significance at any genotypic or phenotypic level but have positive correlation at both levels (Table 11).

Table 11. Genotypic (r_g) and phenotypic (r_p) correlation coefficients among different pairs of yield and yield contributing characters of F2 populations of *B. juncea* L.

	R	DFE	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	YPP
D50%F	r_g	0.79**										
	R_p	0.71**										
DSM	r_g	0.57**	0.68**									
	R_p	0.38**	0.48**									
PH	r_g	0.20	0.18	0.33								
	R_p	0.17	0.19*	0.24*								
NPB	r_g	0.08	-0.14	-0.33	0.42*							
	R_p	0.07	-0.12	-0.22*	0.39**							
NSB	r_g	0.09	-0.08	-0.06	0.12	0.72**						
	r_p	0.06	-0.07	-0.05	0.14	0.68**						
SL	r_g	0.12	-0.03	0.16	-0.19	0.21	0.33					
	r_p	0.09	-0.02	0.14	-0.18	0.20*	0.31**					
SPP	r_g	0.23	0.06	-0.05	0.20	0.58**	0.82**	0.07				
	r_p	0.20	0.05	-0.03	0.19	0.55**	0.83**	0.06				
SPS	r_g	0.014	-0.14	-0.28	-0.25	0.16	-0.05	0.25	-0.14			
	r_p	0.012	-0.12	-0.22*	-0.22*	0.14	-0.04	0.26*	-0.13			
TSW	r_g	-0.17	0.05	-0.06	0.03	-0.02	-0.06	-0.06	-0.11	-0.06		
	r_p	-0.15	0.04	-0.05	-0.02	-0.01	-0.05	-0.05	-0.10	-0.05		
YPP	r_g	-0.09	-0.21	-0.02	-0.03	0.47**	0.74**	0.35	0.62**	0.18	0.17	
	r_p	-0.07	-0.19	-0.007	-0.02	0.44**	0.60**	0.34**	0.61**	0.15	0.16	
HI	r_g	-0.16	-0.11	-0.32	-0.24	0.07	0.07	0.07	-0.04	0.60**	0.23	0.24
	r_p	-0.15	-0.09	-0.23*	-0.23*	0.05	0.06	0.06	-0.03	0.57**	0.22*	0.23*

Note: DFE= Days to first flowering, D50%F= Days to 50% flowering, DSM= Days to 80% maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, SL= Siliquae length (cm), SPP= Siliqua per plant, SPS=Seeds per siliqua, TSW= 1000 seeds weight (g), YPP= Yield per plant (g) and HI= Harvest index (%).

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

4.2.2. Days to 80% siliqua maturity

Days to first flowering (0.57, 0.38), days to 50% flowering (0.68, 0.48) were all positively correlated with days to 80% Siliqua maturity, and these correlations were both genotypically and phenotypically highly significant while days to 80% Siliqua maturity showed positive significance to plant height (0.23, 0.24*) only in phenotypic level. and negative phenotypic significance to number of primary branch (-0.33, -0.22*), seed per siliqua (-0.28, -0.22*) and harvest index (-0.32, -0.23*) was found. Days to 80% Siliqua maturity revealed negative interaction with non- significance at both level in terms of number of secondary branch (-0.06, -0.05), siliqua per plant (-0.05, -0.03), 1000 seeds weight (-0.06, -0.05) and yield per plant (-0.02, -0.007) (Table 11). Siliqua length (0.16, 0.14) showed favorable correlation 80% siliquae maturity but at nonsignificant level. According to Mekonnen *et al.*, (2014), Naznin *et al.*, (2015), and Kumari *et al.*, (2018), days to siliquae maturity may have a favorable and insignificant association with seed production per plant. (Table 11)

4.2.3. Plant height (cm)

Plant height did not change significantly in the same direction both genotypically and phenotypically with the change of any other parameter except with number of primary branches (0.42*,0.39**). It had only phenotypical strong positive relationship with days to 50% flowering (0.18, 0.19*) and 80% Siliqua maturity (0.33, 0.24*) and every relationship was seemingly significant. In line with (Zhang *et al.*, 2014), Afrin *et al.*, (2011), Ali *et al.*, (2015) and Jamali *et al.*, (2016), plant height was substantially correlated with the number of days until flowering, the number of days until ripening, the number of Siliquas per plant, the number of yields per plant, and the harvest index. This trait was negatively correlated with 1000 seeds weight (-0.03, -0.02) at genotypic and phenotypic level. Plant height had positive non-significant association with days of first flowering (0.20,0.17), number of secondary branches (0.12, 0.14) and siliqua per plant (0.20, 0.19) at both genotypic and phenotypic level. This trait had negative association at both levels with seed per siliqua (-0.25, -0.22*), and harvest index (-0.24, -0.23*) but significant at phenotypic level only. Siliqua length (-0.19, -0.18) yield per plant (-0.03, -0.02) had showed non-significant negative correlation with plant height at both level (Table 11). According to Siddique *et al.*, (2017) and Kumar *et al.*, (2014), plant height was negatively correlated with the number of siliqua per plant, 1000 seeds weight, the number of primary and secondary branches, the number of seeds per

siliquae, the length of the siliqua and the harvest index at the genotypic level. They also discovered a negative correlation between these variables at the phenotypic level.

4.2.4. Number of primary branches per plant

Number of primary branches was positively related with plant height (0.42*, 0.39**), number of secondary branches (0.72**, 0.68**), siliqua per plant (0.58**, 0.55**) and yield per plant (0.47**, 0.44**) at both genotypic and phenotypic level and these associations were strongly significant. Days to first flowering (0.08, 0.07), seeds per siliqua (0.16, 0.14) and harvest index (0.07, 0.05) were the parameter those were positively correlated with number of primary branches at both index but non-significantly. Siliqua length (0.21, 0.20*) was positively correlated with number of primary branches but was significant only at phenotypic level. Days to 80% Siliqua maturity (-0.33, -0.22*) was strongly and negatively correlated with number of primary branches but non-significantly at genotypic level and significant at phenotypic level. Days to 50% flowering (-0.14, -0.12) and 1000 seeds weight (-0.02, -0.01) were negatively associated with this trait insignificantly at both levels (Table 11). According to Rashid *et al.*, (2007), there was a positive and substantial link between the number of primary branches and the yield per plant which supported our finding.

4.2.5 Number of secondary branches per plant

At together phenotypic and genotypic levels, number of secondary branches per plant was positively associated with siliqua per plant (0.82**, 0.83**), yield per plant (0.74**, 0.60**) and all of the associations were strongly positive in term of significance. Siliqua length (0.33, 0.31**), had shown a strongly positive and significant association with this trait phenotypically only. Afrin *et al.*, (2017) and Devi and Sharma (2018) observed that number of secondary branches had positive correlation with days to maturity, siliquae length and 1000 seeds weight. Strongly negative correlation for days to 50% flowering (-0.8, -0.07), days to 80% Siliqua maturity (-0.06, -0.05), seeds per siliqua (-0.05, -0.04) and 1000 seeds weight (-0.06, -0.05) was observed with number of secondary branches per plant at both genotypic and phenotypic levels. Days to first flowering (0.09, 0.06), plant height (0.12, 0.14) and harvest index (0.07, 0.06) were

strongly and positively correlated with number of primary branches but non-significantly (Table 11).

4.2.6. Siliqua length(cm)

Siliqua length was not significantly correlated with any of the traits studied in the present investigation except with number of secondary branches per plant at phenotypic level. Number of secondary branches per plant (0.33, 0.31*), seeds per siliqua (0.25, 0.26*) and yield per plant (0.35, 0.34*) had shown a positive correlation at both level but significant at phenotypic level only. Positive non-significant correlation at both genotypic and phenotypic level was found for days to first flowering (0.12, 0.09), days to 80% Siliqua maturity (0.27), number of primary branches per plant (0.96, 0.94) siliqua per plant (0.48, 0.41) and harvest index (0.07, 0.06) against the trait siliqua length. Nonsignificant and negative correlation at genotypic and phenotypic level was found for days to 50% flowering (-0.03, -0.02), plant height (-0.19, -0.18) and 1000 seeds weight (-0.06, -0.05). For the genotypic association with siliqua length was both negative and non-significant while the phenotypic association with siliqua length was both negative but significantly correlated (Table 11). Islam *et al.*, (2016) and Naznin *et al.*, (2015) discovered that number of Siliqua per plant had significant positive linkage with yield per plant. Ejaz *et al.*, (2014) observed that silique length had direct positive effect (0.241) on yield.

4.2.7 Siliqua per plant

Siliqua per plant was associated with number of primary branches per plant (0.58**, 0.55**), number of secondary branches per plant (0.82**, 0.83*) and yield per plant (0.62**, 0.61**) at both genotypic and phenotypic levels significantly which was seemingly strongly linked with this trait positively, significantly only at phenotypic index. Days to 80% Siliqua maturity (-0.05, -0.03), seeds per siliqua (-0.14, -0.13), 1000 seeds weight (-0.04, -0.03) and harvest index (-0.04, -0.03) was accompanied to Siliqua per plant negatively with non-significance at genotypic level and at phenotypic level. Positive non-significance was seen at both level in terms of days to first flowering (0.23, 0.20), days to 50% flowering (0.06, 0.05), plant height (0.20, 0.19) and siliqua length (0.07, 0.06) with Siliqua per plant (Table 11). Similarly, Ara

et al., (2010) found that both at the genotypic and phenotypic levels, seed yield exhibited a positive and highly significant correlation with the number of seeds per siliqua.

4.2.8 Seeds per siliquae

In case of number of seeds per siliquae, days to first flowering (0.014, 0.012), number of primary branches (0.16, 0.14) and yield per plant (0.18, 0.15) showed positivity at genotypic and phenotypic level but non-significantly. Days to 50% flowering (-0.03, -0.01), number of secondary branches (-0.05, -0.04), Siliqua per plant (-0.14, -0.13) and 1000 seeds weight (-0.06, -0.06) showed negative non-significant link at genotypic and phenotypic levels. Positive association was found with harvest index (0.60**, 0.57**) at both genotypic and phenotypic levels which was strongly significant whereas, siliquae length (0.25, 0.26*) is also associated to seeds per silique at both index but reveals significance only at phenotypic level. (Table 11). Jamali *et al.*, (2016) and Rauf and Rahim, (2018) similarly estimated positive and strong significance with yield per plant both at genotypic and phenotypic levels. Negative correlation was observed for days to Siliqua maturity (-0.28, -0.22*) and plant height (-0.25, -0.22*) at genotypic and phenotypic index for both traits but both traits were showing significant correlation in case of phenotypic index. Dawar *et al.*, (2018) reported negative association was present in case of seeds per siliquae with days to 50% flowering, plant height, siliquae length, number of siliquae and 1000 seeds weight.

4.2.9. 1000 seeds weight

1000 seeds weight was negatively correlated to days to first flowering (-0.17, -0.15), days to Siliqua maturity (-0.06, -0.05), number of primary branches (-0.02, -0.01), number of secondary branches (-0.06, -0.05), siliqua length (-0.06, -0.05), Siliqua per plant (-0.11, -0.10) and seed per siliquae (-0.06, -0.06) at both index levels (Table 11). Whereas days to 50% flowering (0.05, 0.04) and yield per plant (0.17, 0.16) show positive non-significant correlation at genotypic and phenotypic level with 1000 seeds weight. Interestingly, harvest index (0.23, 0.22*) showed positive correlation at both levels, but significant only at phenotypic index. In case of plant height (0.03, -0.02) the correlation result was non-significant at both genotypic and phenotypic levels, while the correlation was positive genotypically and negative phenotypically (Table

11). For this trait, Saifullah (2010) discovered a strong positive link at both levels, Alam (2010) found non-significant positive correlation between the characteristic and yield.

4.2.10. Yield per plant(gm)

Number of primary branches (0.47**, 0.44**), number of secondary branches (0.74**, 0.60**) and Siliqua per plant (0.62**, 0.61**) were positively correlated with yield per plant. Seeds per siliquae (0.18, 0.15) and 1000 seeds weight (0.17, 0.16) showed positive association at both genotypic and phenotypic levels, but non-significant at genotypic level and phenotypic index level. Siliqua length (0.35, 0.34**) and harvest index (0.23, 0.22*) had shown positive association with yield per plant at both levels, but showed significance at phenotypic level only. Siliqua length and harvest index was strong and moderate correlated with yield per plant, respectively. Days to first flowering (-0.09, -0.07), days to 50% flowering (-0.21, -0.19), days to 80% Siliqua maturity (-0.02, -0.007) and plant height (-0.03, -0.02) had shown a negative and non-significant association with this trait genotypically and phenotypically (Table 11). Halder *et al.*, (2016) testified that seed yield had significant negative correlation with days to flowering.

4.2.11. Harvest Index (%)

Harvest index was positively correlated seeds per siliquae (0.60**, 0.57**) at both genotypic and phenotypic levels. Yield per plant (0.23, 0.22*) and 1000 seeds weight (0.24, 0.23*) were positive correlated with the targeted parameter at both levels, but were significant at only phenotypic level. Every trait was positively correlated with harvest index which was significant either at both levels or at a single level except plant height (-0.24, -0.23*) and days to 80% Siliqua maturity (-0.32, -0.23*) showed significance in case of negative correlation at phenotypic levels. Days to first flowering (-0.16, -0.15), days to 50% flowering (-0.11, -0.09) and Siliqua per plant (-0.04, -0.03) and have shown a negative non-significant association with this trait at genotypic and phenotypic levels. Number of primary branches (0.07, 0.05), number of secondary branches (0.07, 0.06) and siliqua length (0.07, 0.06) were positively correlated. (Table 11).

4.3.1 Heterosis analysis of F₂ populations

When a new hybrid variety is released, the degree of heterosis is typically measured over a commercially grown popular variety or hybrid variety. BARI Sharisha-11 (P7) was used in this experiment as a check variety to compare the 12 yield-contributing traits of the 21 F₂ populations. Table 12 displays the percentage of heterosis for various F₂ population of 12 characters over the corresponding better and check varieties. From character to character or population to population, the percentage of heterosis was found fluctuating.

4.3.1.1 Days to first flowering

For earliness negative heterosis is desirable for days to flowering which helps to measure one of the reproductive parameters in terms of yield. For days to first flowering (Table 12), the highest significant positive heterosis over better parent represented by 23.53% (G2), while the range of significant positive heterosis over better parent was 23.53% (G2) to 3.54% (G16). On the other hand, the highest significant positive heterosis over check variety represented by 19.44% (G8), and the range of significant positive heterosis over check variety was 19.44% (G8) to 4.63% (G5) and (G11). The highest significant negative heterosis over better parent represented by -18.85% (G14), while the range of significant negative heterosis over better parent was -18.85% (G14) to -5.56% (G20). On the other hand, the highest significant negative heterosis over check variety was represented by -8.33% (G14), and the range of significant negative heterosis over check variety was -8.33% (G14) to -5.56% (G7), (G17), (G20). Out of 21 crosses, ten crosses showed positive heterosis and eleven crosses showed negative

Table 12. Heterosis (heterobeltiosis, HB) over better parent (BP) and standard heterosis (SH) over the check varieties (BARI Sharisha-11) in 21 F₂ populations in *Brassica juncea* L.

Genotype	DFF		D50%F		DSM		PH		NPB		NSB	
	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)
G1	-1.92	-5.56*	-7.69*	-11.48*	0.64	-2.80**	-8.70**	-10.75**	-9.46*	-25.47**	0.00	-3.70
G2	23.53**	16.67**	11.86*	8.20**	4.78*	2.17*	1.13	-7.08*	-10.68*	-17.65*	-16.46*	-18.52**
G3	3.74	2.78	-3.12	1.64	1.89*	0.62	0.70	3.17	17.39**	5.88*	19.28*	22.22**
G4	0.88	5.56*	-14.62**	-9.02	-3.34*	-1.24	-6.71*	2.41	-4.00	-5.88*	47.90**	33.33**
G5	-7.38*	4.63	-11.43*	1.64	-2.97*	1.55*	1.06	-1.47	0.05	-17.65*	0.00	-3.70
G6	5.56*	5.56*	0.82	0.82	3.11**	3.11**	-5.90*	-5.90*	-23.53**	-23.53**	0.00	0.00
G7	-1.92	-5.56*	-7.63	-10.66	0.64	-1.86	-9.71**	-11.72**	-17.06**	-23.53**	-27.85*	-29.63**
G8	20.56**	19.44**	0.78	5.74	0.31	-0.93	8.71**	11.37**	36.96**	23.53**	44.58**	48.15**
G9	-9.73*	-5.56*	-12.31*	-6.56	-1.82	0.31	-19.39**	-11.51**	-16.00*	-17.65**	23.25*	11.11**
G10	-9.02*	2.78	-18.57**	-6.56	-2.67	1.86	11.47**	9.00**	4.90*	-15.71*	8.70*	-7.41*
G11	4.63	4.63	3.28	3.28*	-3.11**	-0.93	-6.30*	-6.33	5.88*	5.88*	53.07**	53.07**
G12	20.56**	19.44**	1.56	6.56	-0.63	-1.86*	-20.26**	-18.31**	-4.30	-11.76	12.05*	14.81*
G13	-12.39*	-8.33*	-16.92**	-11.48	-4.86**	-2.80**	-10.46**	-1.69	12.02**	9.82**	13.92*	11.11*
G14	-18.85**	-8.33*	-20.71**	-9.02	-4.15	0.31	-13.98**	-16.15**	-25.54**	-31.35**	1.24	-1.26
G15	2.78	2.78	-4.92	-4.92	-1.86	-1.86	-16.58**	-16.58**	-11.76*	-11.76*	27.19**	27.19**
G16	3.54*	8.33*	1.54	8.20	-1.52*	0.62	-11.05**	-2.34	-10.00*	-11.76*	4.82	7.41*
G17	-16.39**	-5.56*	-18.57**	-6.56	-4.45**	0.00	-6.98*	-4.71	17.39**	5.88*	55.42**	59.26**
G18	2.78	2.78	-12.30*	-7.38	-1.24*	-1.24	-10.14**	-7.95*	13.71*	13.71*	22.89**	25.93**
G19	-4.10*	8.33*	2.86	18.03**	-1.78*	2.80	-17.13**	-9.03**	-22.00	-23.53	31.47**	18.52*
G20	-5.56*	-5.56*	-12.30*	-12.30	-0.31	-0.31	1.33	1.33	-3.94	-3.94	37.04**	37.04**
G21	-16.39**	-5.56*	-25**	-13.93	-6.53**	-2.17	-7.19*	-7.19*	-29.41**	-29.41**	-7.41*	-7.41*

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed, per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g), HB=Heterobeltiosis, and HI=Harvest index (%). Note: **: Significant at 1% level of probability *: Significant at 5% level of probability

Table 12. Heterosis (heterobeltiosis, HB) over better parent (BP) and standard heterosis (SH) over the check varieties (BARI Sharisha-11) in 21 F₂ populations in *Brassica juncea* L.

Genotype	SL		SPP		SPS		TSY		YPP		HI	
	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)	HB (%)	SH (%)
G1	4.55*	-4.82*	-14.34**	-1.28	13.68*	12.67*	-41.67**	-30.71**	9.23**	9.27**	4.43*	10.48**
G2	13.65**	20.20**	-24.23**	-12.68**	2.66	20.00**	5.34	25.14*	15.00**	15.04**	-9.90*	-4.68
G3	8.61**	5.15**	-8.66*	5.26*	-0.20	12.67**	-34.41**	-22.08**	9.23**	9.27**	-20.99**	-15.69**
G4	-2.38	0.26	12.81**	32.83**	14.35**	13.33*	-29.25**	-15.96**	60.00**	60.06**	-4.12	1.44
G5	-6.61*	-14.97**	-9.40*	4.41	-4.24	-4.67	-12.79*	3.61	-11.92	-11.89*	-21.42**	-16.87**
G6	-6.70	-6.70**	-6.46	7.80*	-12.67*	-12.67*	-38.27**	-26.67**	-17.69**	-17.66*	-31.39**	-27.42**
G7	-0.78	-4.82*	-11.60	-9.83**	-15.02*	-0.67	-23.43**	-24.26**	37.30**	-2.27*	-26.59**	-28.86**
G8	2.40	-0.87	16.85**	26.75**	-22.64**	-12.67	72.71**	-28.09**	49.55**	40.05**	-16.40**	-14.43**
G9	5.13**	7.98**	-9.96*	-2.28*	5.68**	3.33*	-4.09	-5.14*	38.51**	20.82**	27.85**	19.71**
G10	16.38	2.90	-1.61	-5.75*	15.85*	15.33*	-12.71*	-13.66*	62.97**	13.12**	-5.09*	-7.89*
G11	-6.70	-6.70**	25.67**	25.67**	7.33*	7.33*	10.38*	10.38*	46.98**	46.98**	7.99*	7.99**
G12	11.92**	8.35**	15.85**	25.67**	7.79*	26.00**	-22.11*	-24.15*	12.57**	5.43*	0.31	2.67
G13	-9.16*	-6.70*	-4.56*	3.57	16.35**	36.00**	13.30*	9.84*	65.86**	44.67**	29.17**	25.18**
G14	20.59**	15.69**	-14.24*	-12.53**	-13.31**	1.33	-9.02*	-16.17*	29.93**	-8.04	-0.70	-3.63
G15	10.05**	10.05**	5.61*	7.73*	-3.61*	12.67*	-18.80**	-18.80**	3.50	3.50	-3.49	-3.49
G16	8.79**	11.74**	15.66**	25.51**	-10.83**	0.67	-29.41**	-31.26**	18.73**	11.20**	-7.21	-5.02
G17	10.56**	7.04**	26.86**	37.60**	-13.19**	-2.00	-22.56**	-24.59**	91.45**	79.30**	-22.83**	-21.01**
G18	15.84**	3.84*	15.57**	25.36**	1.56	14.67**	-16.72*	-16.72*	34.28**	34.28**	4.27*	6.72**
G19	4.03*	6.85**	1.96	10.65**	-4.91	-5.33	28.52**	24.59**	62.77**	41.98**	5.61*	2.49*
G20	-2.41	-2.41*	29.47**	32.06**	-14.26**	-16.67**	30.71**	30.71**	43.90**	43.90**	-15.91**	-15.91
G21	4.97**	4.97**	-10.06**	-10.06**	13.33**	13.33**	-11.91*	-11.91*	-0.35	-0.35	1.96	1.96

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% 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 siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g), HB=Heterobeltiosis, and HI=Harvest index (%). Note: **: Significant at 1% level of probability *: Significant at 5% level of probability

heterosis for better parent. For the check variety thirteen crosses showed positive and rest eight crosses showed negative heterosis (Table12). Considering the plant height, combinations showing negative heterosis are the suitable variety for this trait to be added into development study. In a study by Wolko *et al.*, (2019) using 12 F₁ lines to assess heterosis, they found that 7 cross combinations showed significant and negative heterosis over mid parent.

4.3.1.2. Days to 50% flowering

For days to 50% flowering, the highest positive significant heterosis was observed in 11.86 % G2 over better parent, while the positive heterosis array was 11.86% G2 to 3.28% G11 and better parent highest negative significant was in -25% G21 followed by -20.71 % G14, -18.57 % G10 and G17 and -16.92 % G13. In case of check variety highest positive significant heterosis was observed in 18.03% G19 while the positive significant heterosis array was 18.03 % G19 to 3.28% G11 and highest negative significant heterosis was in -20.71 % (G14) followed by -18.57 % (G10, G17), -16.92 % (G13) respectively. Among the standard check three crosses showed positively significant and one cross showed negatively significant heterosis. Among the better parent heterosis fourteen crosses showed negatively significant and seven crosses showed positively significant heterosis (Table 12). Barupal *et al.*, (2017) Nassimi *et al.*, (2006), Gupta *et al.*, (2010) and Ferdous *et al.*, (2019) observed expected negative heterosis over mid parent and better parent for most of the genotypes for these traits whereas, Singh *et al.*, (2012) found positive heterosis over mid parent and better parent.

4.3.1.3. Days to 80% maturity

Days to 80% maturity is an important yield component of *Brassica juncea L.* Among the 21 F₂ hybrids only 6 crosses showed positive heterosis and rest 15 crosses showed negative heterosis for better parent, ten crosses showed positive and eleven crosses showed negative heterosis for check variety. Positively significant heterosis was ranged from 4.78% G2 to 1.89% G3 for better parent, positively significant heterosis is ranged from 3.11% G6 to 1.55%. G5 for check variety. Highest

positive significant heterosis was showed by 4.78% G2 for better parent heterosis and 3.11% G6 for check variety. Negatively significant heterosis was ranged from -6.53% G21 to -1.24% G18 for better parent, negative heterosis was ranged from -2.80% G13 to -0.31% G20 for check variety. Highest negative significant heterosis was showed by -6.53% G21 for better parent heterosis and -2.80% G13 for check variety. Barupal *et al.*, (2017) and Gupta *et al.*, (2010) showed positive heterosis over both parent for this trait.

4.3.1.4. Plant Height (cm)

Negative heterosis is generally desirable for plant height to develop short stature variety which helps to increase acceptability to the farmers. The positive highest significant heterosis over better parent was represented by 11.47% G10, while the positive highest significant value of check variety was represented by 11.37% G8 respectively. Out of twenty-one crosses, in the better parent only six crosses showed positive and rest fifteen crosses showed negative heterosis but in standard check five crosses showed positive heterosis and sixteen crosses showed negative heterosis (Table 12). Considering the plant height, significant positive heterosis range was observed between 11.47% G10 to 8.71 % G8 over better parent and 11.37% G8 to 9.00% G10 over check variety. On the other hand, the negative highest significant heterosis over better parent was represented by -20.26% G12 while the negative highest significant value of check variety was represented by -18.31% G12 and significant negative heterosis range was observed between -17.13% G19 to -5.90% G6 over better parent and -18.31% G12 to -5.90% G6 over check variety respectively (Table 12). Ferdous *et al.*, (2019) and Wolko *et al.*, (2019) testified significant heterosis and standard heterosis for plant height Huq (2007) and Turi *et al.*, (2006) founded the opposite result.

4.3.1.5. Number of primary branches per plant

Eight crosses out of twenty-one combinations showed positive heterosis and rest seventeen combinations showed negative heterosis for better parent. For better parents, highest positive significant value was observed in 36.96 % G8 and the highest negative significant value was -29.41 % G21. In case of range of positive significant value for better parent, heterosis was ranged from 36.96 % G8 to 4.90 % G10 and in case of range of negative significant value -29.41 % G21 to -9.46 % G1. For check variety, highest positive significant value was observed in 23.53 % G8 and highest negative significant value was -31.35 % G14. In case of range of positive significant value for

check variety, heterosis was ranged from 23.53 % G8 to 5.88 % G11 and G17 and in case of range of negative significant value -31.35 % G14 to -5.88 % G4. Six crosses out of twenty-one combinations showed positive heterosis and rest fifteen combinations showed negative heterosis for check variety. Meena *et al.*, (2014), Turi *et al.*, (2006) reported positive heterosis on primary branches per plant. Wolko *et al.*, (2019) found both positive and negative heterosis with significance.

4.3.1.6. Number of secondary branches per plant

Eighteen crosses out of twenty-one combinations showed positive heterosis and rest three combinations showed negative heterosis for better parent. For better parents, Highest positive significant value was observed in 55.42 % G17 and the highest negative significant value was -27.85 % G8. In case of range of positive significant value for better parent, heterosis was ranged from 55.42 % G17 to 12.05 % G12 and in case of range of negative significant value -27.85 % G8 to -7.41 % G2. Three combinations for better parent showed nil heterosis like G1, G5 and G6 For check variety, highest positive significant value was observed in 59.26 % G17 and highest negative significant value was -29.63 % G7. In case of range of positive significant value for check variety, heterosis was ranged from 59.26 % G17 to 7.41% G11 and G16 and in case of range of negative significant value -29.63 % G14 to -7.41 % G10, G21. Fourteen crosses out of twenty-one combinations showed positive heterosis and rest seven combinations showed negative heterosis for check variety (Table 12). Positive heterosis was noted on each plant's principal branches, according to Turi *et al.*, (2006) and Ferdous *et al.*, (2019). Both positive and negative heterosis were discovered with significance by Wolko *et al.*, in 2019.

4.3.1.7. Siliquae length (cm)

It is revealed that the heterosis over better parent for siliquae length varied from 20.59 % G14 and 4.03% G19 in terms of positive significant heterosis. Out of 21 crosses fourteen crosses showed positive heterosis and rest seven combinations showed negative heterosis for better parent. Significant negative heterosis was -9.16 % G13 and -6.61% G5 which indicated smaller the length size than their parents. In case of the better parent heterosis the highest positive significant heterosis was observed in 20.59 % G14 and the highest negative significant heterosis was observed in -9.16 % G13 (Table 12). In case of the check, the significant negatives heterosis was observed in -

14.97% G5 to -2.41 % G20 Meena *et al.* (2014), Satwinder *et al.*, (2000) and Jorgensen *et al.*, (1995) found similar results in their experiments. The rest of the crosses exhibited positive significant heterosis ranges from 20.20% G2 to 3.84% G18. However, the combinations presented significant and positive heterosis over both better parent and with the standard checks, might be useful for development of seed producing variety.

4.3.1.8. Siliquae per plant

Among the better parent hybrid combinations, the highest positive significant heterosis was observed in 29.47 % G20, while the significant positive heterosis range value varied from 29.47 % G20 to 5.61 % G15 and better parent highest negative significant was in -24.23 % G2, while the significant negative heterosis range value varied from -24.23 % G2 to -4.56 % G13. In case of number of seeds per siliquae, all of the crosses manifested positive significant heterosis except G19. In case of check variety, highest positive significant heterosis was observed in 37.60 % G17 and the highest negative significant heterosis was in -12.68 % G2 while the significant positive heterosis range value varied from 37.60 % G17 to 5.26 % G3 and the significant negative heterosis range value varies from -12.68 % G2 to -2.28 % G9. Among the standard check, fourteen crosses showed positive and seven crosses showed negative heterosis (Table 12). Yadav *et al.*, (1999 a and b) found positive heterosis over better parent and negative heterosis over check variety.

4.3.1.9. Seed per siliquae

Positive heterosis is also desirable for siliqua per plant which helps to increase yield. For siliqua per plant (Table 12), the highest significant positive heterosis over better parent was represented by 16.35% G13 while the range of significant positive heterosis over better parent was 16.35% G20 to 5.68% G9. On the other hand, the highest significant positive heterosis over check variety was represented by 36% G13 and the range of significant positive heterosis over check variety was 36% G13 to 3.33% G9. The highest significant negative heterosis over better parent was represented by -22.64% G8, while the range of significant negative heterosis over better parent was -22.64% G8 to -3.61% G15. On the other hand, the highest significant negative heterosis over check variety was represented by -16.67% G20 and the range of significant negative heterosis over check variety was -16.67% G20 to -2.00 % G17. Out of 21 crosses, ten crosses showed positive heterosis and eleven crosses showed negative

heterosis for better parent. For the check variety fourteen crosses showed positive and rest seven crosses showed negative heterosis (Table 12). Considering the plant height, combinations showing positive heterosis was the suitable variety for this trait to be added into development study. Gurajal *et al.*, (2011) found positive significant heterosis in most of the line.

4.3.1.10. 1000 seeds weight(gm)

Positive heterosis is desirable for 1000 seeds weight which helps to increase yield count. The positive highest significant heterosis over better parent is represented by 72.71% G8 while the positive highest significant value of check variety represented by 10.38% G11, respectively. Out of twenty-one crosses, in the better parent only six crosses showed positive and the rest fifteen crosses showed negative heterosis, but in standard check ratio of positive heterosis and negative heterosis was alike to better parent heterosis (Table 14). Considering 1000-seeds weight, significant positive heterosis range was observed between 72.71% G8 to 10.38% G11 over better parent and 30.71% G21 to 9.84% G13 over check variety. On the other hand, the negative highest significant heterosis over better parent represented by - 41.67% G1 while the negative highest significant value of check variety represented by -31.26% G16 and significant negative heterosis range was observed between -41.67% G1 to -9.02% G14 over better parent and - 31.26% G16 to -5.14% G9 over check variety respectively. In case of better parent, G2, G9 combination was the only non-significant one (Table 12). Gupta *et al.*, (2010) found significance over both better parent and check variety. Dar *et al.*, (2012) showed desirable significance over both better parent and check variety.

4.3.1.11. Yield per plant(gm)

Positive heterosis was targeted for yield per plant which helps to increase seed yield. The highest positive significant heterosis over better parent was represented by 91.45% G17. On the other hand, the highest positive significant heterosis for standard check was 79.30% G17 respectively. Out of 21 crosses 18 crosses showed positive heterosis and three crosses showed negative heterosis for better parent. For the standard check only sixteen crosses showed positive and rest five crosses showed negative heterosis (Table12). The positive significant heterosis range over better parent was represented by 91.45% G17 to 9.23% G1, G3 and over check variety was represented by 79.30% G17 to 5.43% G12. The highest negative significant heterosis over better parent was

represented by -17.69% G6 and over check variety was represented by -17.66% G6 to -2.27% G7 (Table 12). Meena *et al.*, (2014), Yadava *et al.*, (2012), Vaghela *et al.*, (2011), reported positive heterosis on yield per plant.

4.3.1.12 Harvest index (%)

For harvest index (%) trait, a large number of genotypes had favorable significant heterotic effects. The cross combination G13 (29.17%), which was preceded by G9 (27.85%), had the highest significant positive heterosis over the better parent. In contrast, G1 (4.43), which was followed by G18 (4.27) and had the lowest effect over the better parent. Cross combination G13 (25.18) had the highest significant positive heterosis over the check parent, followed by G9 (19.71). G12 (2.67), G19 (2.49), and G21 (1.96) were the hybrids that out-performed BARI sharisha-11 in a non-significant manner. Additionally, G6 (-31.39) showed the highest negative significant heterotic impact over both better parent and over check variety G13 (25.18) was the highest positive significant heterosis (Table 12). It was supported by Gupta *et al.*, (2010) who calculated heterosis for the harvest index. According to the results, 8 lines and 9 crosses revealed a positive heterotic effect over the better parent and a favorable heterotic effect over the check variety.

4.3.2. Inbreeding Depression

4.3.2. Inbreeding depression analysis of F₂ populations

Inbreeding is the mating of individual who are connected to one another by descent or ancestry. When individuals are closely related and mated of selfing among themselves, there is a significant level of inbreeding. Inbreeding increased homozygosity in the offspring. Increasing homozygosity is the main consequence of inbreeding. Positive and negative inbreeding depressions are two of its dimensions, and the expected dimension relies on the corresponding traits. Table 13 shows inbreeding depression analysis of 21 F₂ populations.

4.3.2.1. Days to first flowering

For this trait, positive inbreeding depression is generally desired so that the days required for first flowering will drop down. The range of inbreeding depression for the trait was from -19.44 to 22.14. Among 21 combinations, 12 combinations showed positive inbreeding depression and the rest 9 combinations showed the opposite direction. The 16 F₂ cross-combinations showed significant, among them 10 cross-

combinations were positive, and 6 cross-combinations were negative significance. The cross-combinations G20 showed the highest positive significant inbreeding depression (Table 13).

4.3.2.2 Days to 50% flowering

Positive inbreeding depression is desirable for days to 50% flowering, so that the days required for first flowering will get reduced also for this trait. The range of inbreeding depression for the trait was from -8.27 to 21.74. Among 21 cross-combinations, sixteen combinations showed positive inbreeding depression and the rest five combinations showed the negative one. Fourteen combinations were significant, among them thirteen were positive and one combination was negative. The cross-combination G13 showed the highest positive significant inbreeding depression, which may prove fruitful if used in breeding program for improvement of the trait (Table 13).

4.3.2.3 Days to 80% siliqua maturity

Like the two previous traits, days to 80% siliqua maturity is another important trait which is desirable in F₂ generation if that combination shows positive inbreeding depression. The range of inbreeding depression for the trait was from -1.54 to 6.29. Among the total combinations, sixteen combinations showed positive inbreeding depression and the rest five combinations showed the negative. Eleven combinations among the twenty-one, were significant, where nine combinations were positive and two combinations were negative. The cross-combination G1(6.29) showed the highest positive significant inbreeding depression followed by G21(2.78) and G11(2.74) (Table 13).

Table 13. Inbreeding depression in 21 F₂ populations in *Brassica juncea* L.

Genotype	DFE	D50F	DSM	PH	NPB	B	SL	SPP	SPS	YPP	TSY	HI
G1	4.67	14.29**	6.29**	3.99*	17.37*	14.29*	1.56	19.57**	-8.97*	35.57**	38.02**	-0.10
G2	-16.67**	-0.76	-1.54*	-4.49	4.57	29.03**	-18.26**	24.03**	-10.02*	-43.13**	32.97**	13.31**
G3	-11.00*	0.80	0.31	-5.99*	-5.86	-11.22*	7.33*	22.59**	-5.34	35.18**	32.15**	19.38**
G4	-2.70	16.54**	1.55	-13.52**	0.00	-12.50*	-12.35**	-9.55	-28.83**	6.22*	-13.49*	-1.44
G5	-4.63*	3.88	2.68**	-2.47	22.22**	27.78**	17.38**	24.97**	7.00*	1.25	38.01**	8.96*
G6	-10.68*	1.60	0.00	0.46	20.41*	10.98**	4.62*	13.01*	3.36	37.29**	39.69**	22.17**
G7	12.82**	17.42**	0.32	8.37**	33.90**	41.23**	7.12**	42.67**	6.10*	8.82*	49.88**	40.55**
G8	-21.70**	-1.57	-0.31	-15.35**	7.38	-62.14**	5.80**	-30.02**	25.94**	42.28**	9.68	15.76**
G9	9.73**	14.29**	0.92	10.80**	35.36**	13.45*	-7.10*	22.46*	1.49	-0.93	32.54**	-5.82*
G10	8.26**	10.24*	2.67**	-17.90**	30.66**	31.82**	4.00*	42.91**	-16.55*	9.20*	30.99**	13.64**
G11	6.61**	9.35*	2.74**	11.25**	10.45*	6.43*	8.46**	12.48*	-5.81	-3.06	21.95**	7.41**
G12	-19.44**	-1.56	-0.64	11.22**	2.17	-12.08*	-0.91	-3.86	-15.56*	22.89**	32.42**	-0.12
G13	8.33**	21.74**	1.57*	7.48**	1.74	23.74**	22.11**	32.68**	-34.99**	8.64*	9.90*	-17.84**
G14	13.16**	17.16**	-0.62	8.59**	33.96**	-6.64*	-12.23**	17.80*	8.06**	10.81*	43.13**	8.73**
G15	-3.74	13.43**	1.56*	11.29**	26.24**	-3.00	-20.83**	21.29*	-7.42	26.44**	37.87**	10.52**
G16	-3.54	-0.76	0.61	1.20	4.21	-6.11*	-4.77	9.21*	4.83	44.34**	23.18**	1.94
G17	5.56**	13.64**	2.72**	6.60**	3.54	5.14*	-21.42**	2.53	14.31**	24.18**	-29.23**	16.02**
G18	6.72*	16.91**	-1.60*	12.78**	3.38	-18.59**	9.26**	3.63	-8.38*	31.35**	22.99**	1.39
G19	3.31	-8.27*	0.30	10.00**	29.08**	-12.94**	5.77**	-16.39*	21.69**	-21.28**	17.06*	5.64*
G20	22.14**	18.32**	2.13*	-1.38	23.48**	-12.11**	5.33	-4.07	5.62*	-39.07**	2.59	16.03**
G21	11.30**	20.45**	2.78**	0.23	30.80**	26.47**	0.21	26.32**	-13.84*	30.52**	38.49**	5.92*

Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g) and HI=Harvest index (%). **: Significant at 1% level of probability *: Significant at 5% level of probability.

4.3.2.4. Plant height (cm)

Positive inbreeding depression is the key for the trait of any combination get to be selected in any breeding program as extra height sometimes causes difficulties for maintenance and management. The range of inbreeding depression for the plant height was from -17.90 to 12.78. Among the 21 cross-combinations, fourteen combinations showed positive inbreeding depression and the rest seven combinations showed the negative. Fourteen combinations were significant, among them eleven cross-combination was positive and three were negative. The cross-combination G18(12.78) showed the highest positive significant inbreeding depression followed by G15(11.29), G11(11.25), G12(11.22) (Table 13).

4.3.2.5. Number of primary branches per plant

Negative inbreeding depression is desirable in terms of this trait, because the higher the number of branches the higher the possibility of producing more siliqua. The range of the depression for this trait was to -5.86 from 35.36. Only a single combination showed negative inbreeding depression which is G3 (-5.86). The total number of significant cross-combinations was twelve, and as per mentioned every significant combination was positive except the cross-combination G3, among them G9 (35.36) was the highest (Table 13).

4.3.2.6. Number of secondary branches per plant

Negative inbreeding depression is desirable for this trait if yield is to be increased. Among all the combinations, ten cross-combinations were showing negative inbreeding depression, while the rest eleven cross-combinations were positive. All the combination showed significance except G15. The range of the inbreeding depression was from -62.14 to 41.23. The cross-combination G8 (-62.14) was the highest negative depression showing combination which was highly significant. It might look good for breeding program if used against this trait (Table 13).

4.3.2.7. Siliquae length (cm)

Siliqua length is directly involved with total count of seed per siliqua and so negative inbreeding depression is highly desirable for this trait. The range of the inbreeding depression was from -21.42 to 22.11. Among all the 21 cross-combinations, eight combinations showed negative inbreeding depression, and the rest of the cross-

combination showed positive inbreeding depression. Total number of significant combinations were fifteen and ten cross-combinations among of them were positive and five were negative. The highest negative inbreeding depression recorded in cross-combination G17(-21.42) followed by G15(-20.83), G2(-18.26) (Table 13).

4.3.2.8. Siliqua per plant

This trait is directly influencing the yield, the higher the siliqua number, the higher the seed count and that leads to higher yield. The array of inbreeding depression for siliqua per plant was from -30.02 to 42.91. Five cross-combination were negative and sixteen genotypes were positive heterosis. Significant positive inbreeding depression counted in fourteen cross-combination and significant negative inbreeding depression was counted in two cross-combination. The highest negative inbreeding depression recorded by the cross-combination G8(-30.02) followed by G19(-16.39) (Table 13).

4.3.2.9. Seeds per siliqua

Negative inbreeding depression is the key for the trait of any combination gets to be selected in any breeding program as it implies the yield. The range of inbreeding depression for the trait was from -34.99 to 25.94. Among the 21 cross-combinations, ten cross-combinations showed positive inbreeding depression, and the rest eleven combinations showed the negative. Sixteen cross-combinations were significant, among them six cross-combinations were positive and ten combinations were negative. The cross-combination G13(-34.99) showed the highest positive significant inbreeding depression followed by G4(-28.83), and G12(-15.56) (Table 13).

4.3.2.10. Yield per plant (gm)

This is the targeted trait what breeding program is all about. Negative depression is highly recommendable for this. Among all the combinations, five cross-combinations showed negative inbreeding depression, while the rest sixteen cross-combinations were positive. Eighteen cross-combinations showed significance among the total cross-combination. The range of the depression was from -43.13 to 44.34. The cross-combination G2(-43.13) was the highest negative depression followed by cross-combination G20 (-39.07). These might be the desirable cross-combinations for breeding program if used against this trait (Table 13).

4.3.2.11. 1000 seeds weight (gm)

Like the immediate previous traits, 1000 seeds weight is another trait which is desirable in F₂ generation if that combination shows negative inbreeding depression. The range of inbreeding depression for the trait is from -29.23 to 49.88. Among the total combinations, all combinations show positive inbreeding depression except G17(-29.23) and G4(-13.49). Seventeen combinations among the twenty-one, were showing positive significance where earlier mentioned two combinations showing negative significance can be the targeted combination for the settlement of breeding program (Table 13).

4.3.2.12. Harvest index (%)

Harvest index is the direct indicator of how the yield happens to be. Higher harvest index points out higher economic yield. So inbreeding depression is not welcomed at all when it comes to harvest index. The range of inbreeding depression for the trait was from -17.84 to 40.55. Among the 21 cross-combinations, sixteen cross-combinations showed positive inbreeding depression, and the rest five cross-combinations showed the negative. Sixteen cross-combinations were significant, among them the fourteen cross-combinations were positive and single cross-combination was negatively significant. The cross-combination, G13(-17.84) showed the highest negative significant inbreeding depression followed by combination G9(-5.82). These two cross-combinations would be under consideration (Table 13).

4.3.3. Mean performance and genetic variability analysis of BC₁F₁ populations

Backcross breeding lets breeders to introduce a desired trait into the preferred genetic background of recipient parent (generally called recurrent parent) from donor parent. To breed the canola grade *B. juncea*. in previous year, we had crossed with the Bangladeshi six varieties of *B. juncea*. with a canola grade *B. juncea*, (P6).

But, the duration of the canola grade mustard variety was very long (140 -165 days) as well as the F₁ hybrids produced from this combination required longer vegetative period. Hence, to produce the short stature canola grade mustard variety of Bangladesh the backcrossing program was undertaken (P6 parental line with 6 Bangladeshi *B. juncea* L. varieties (P1, P2, P3, P4, P5, and P7, please see the methodology section for the parental lines used in the experiment). Here we compared yield and yield contributing traits of six selected BC₁F₁ and six respective F₂ populations that were

obtained from combination involved with P6. The genetic variability of the six selected BC₁F₁ populations is presented in Table 14 and mean performance of the six selected BC₁F₁ and six corresponding F₂ populations is presented in Figure (1-6) and in Table 15.

4.3.3.1. Days to first flowering

The mean performance of backcrosses BC₁F₁ populations was analyzed for days to first flowering, in case of six backcrosses, (P1× P6) × P1= (34.10), (P2× P6) × P1= (35.15), (P7× P6) × P1= (34.56) showed comparative earliness than their F₂ population's respective combination such as (P1× P6=37.67), (P2× P6=37.00), (P7× P6=39.00). While the grand mean (36.06) of the six backcrosses also showed lesser value than the grand mean F₂ population's (36.83). The rest of backcrosses like (P3× P6) × P3 = (37.67), (P4× P6) × P4= (35.43), (P5× P6) × P5= (40.67) showed the requirement of higher days than their respective F₂ combinations needed. As, (P1× P6) × P1, (P2× P6) × P2, (P7× P6) × P7, these there BC₁F₁ populations showed lesser mean for days of first flowering, backcrossing was promising for this trait (Figure 1).

The phenotypic variance was (8.25) little greater than the genotypic variance for days of initial flowering. (6.81). The fact that genotypic and phenotypic variance differ so little indicated that little environmental effect existed on the genes governing this feature. The coefficients of variation for genotype and phenotype were 7.27 and 7.74, respectively. This slight difference between the phenotypic and genotypic coefficients of variation suggested that the environment only had a minor genetic influence on the current variance. The GCV (6.88) and PCV (7.81) values showed that the genotype for the characteristics showed significant variation as environmental variance is minor. Days to first flowering showed a high heritability (88.26%) with a moderate genetic advance as percentage of mean (14.07%), suggesting that the additive genetic factor may be responsible for controlling days to first flowering inheritance (Table 14).

Table 14. Genetic parameters for twelve yield and yield related characters of backcrossed BC₁F₁ populations of *B. juncea* L.

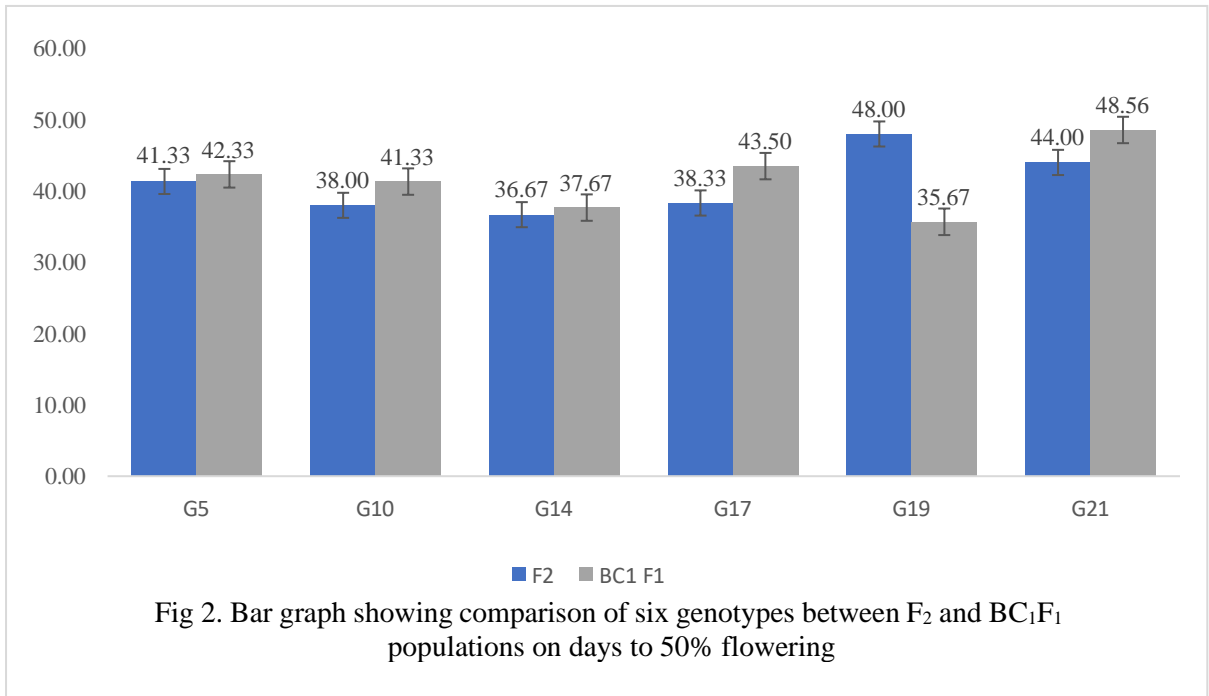
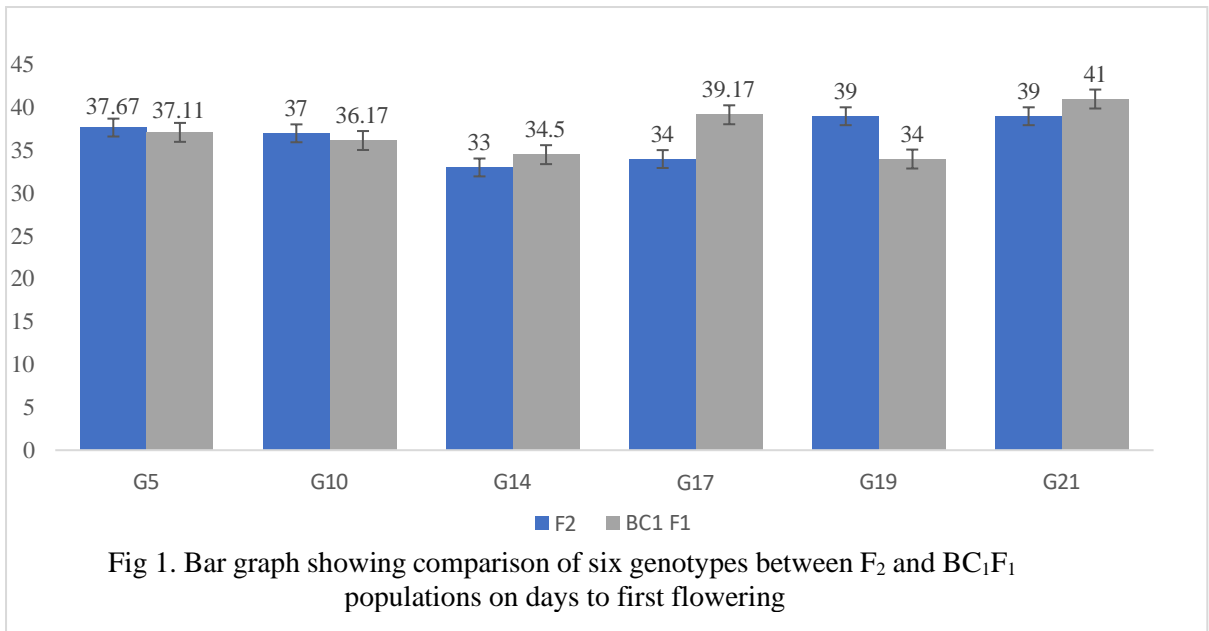
Traits	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	h ² (%)	GA	GA (mean) (%)
DFF	7.81	6.88	0.91	7.74	7.27	88.26	5.07	14.07
D50F	11.56	10.01	1.55	8.32	7.75	86.64	6.07	14.86
DSM	14.32	10.51	3.81	3.56	3.05	73.38	5.72	5.39
PH	113.73	104.31	9.42	7.07	6.77	91.72	20.15	13.73
NPB	0.46	0.28	0.18	12.21	9.54	61.1	0.86	15.37
NSB	3.58	2.91	0.66	18.73	16.89	81.36	3.17	31.39
SL	0.121	0.104	0.07	7.55	7.00	85.8	0.62	13.35
SPP	1181.52	1085.81	95.7	15.11	14.49	91.9	65.07	28.62
SPS	1.21	0.86	0.35	8.13	6.85	70.91	1.61	11.87
TSW	0.18	0.17	0.01	12.33	12.23	98.52	0.85	25.02
YPP	5.07	4.95	0.12	21.85	21.6	97.67	4.53	43.97
HI	4.45	4.05	0.36	7.73	7.41	91.93	4.00	14.65

Note: DFF= Days to first flowering, D50%F= Days to 50% flowering, DSM=Days to 80% 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= Seed per siliquae, TSW= 1000 seeds weight (g), YPP= Yield per plant (g) and HI= Harvest index (%), GA= Genetic advance, σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, σ^2_e = Environmental variance, PCV=Phenotypic coefficient variation, GCV= Genotypic coefficient variation, GA(mean)% =Genetic advance mean percentage

4.3.3.2. Days to 50 % flowering

In the case of six backcrosses BC₁F₁ populations, the mean performance for days to first flowering showed that (P1×P6) ×P1= (39.33), (P5×P6) ×P5= (46.33) and (P7×P6) ×P7= (38.67) showed comparative earliness to their respective F₂ populations combinations of (P1×P6=41.33), (P5×P6=48), and (P7×P6=44.00). While the overall average of the six backcrosses (40.32) was also lower than the overall average of the F₂ populations (40.83). The remaining backcrosses, including (P2×P6) ×P2= (37.67), (P3×P6) ×P3= (35.43), and (P4×P6) ×P4= (40.67), demonstrated the need for more days than their respective F₂ population required. Backcrossing appeared promising for this trait because (P1×P6) ×P1, (P5×P6) ×P5 and (P7×P6) ×P7 showed less mean for days of initial 50% blooming (Figure 2).

For this characteristic, the phenotypic variance (11.56) was marginally higher than the genotypic variance (10.01). Because the gap between genotypic and phenotypic variance appears to be small, it suggested that the genes governing this trait are not much influenced by the environment. The coefficients of variation for genotype and phenotype were 7.75 and 8.32, respectively. This minuscule variation between phenotypic and genotypic coefficients of variation determines that the majority of the current variation was created by genes, with the environment having the least impact. The GCV and PCV values showed that the genotypes for the characteristics showed significant variation. The inheritance of days to 50% blooming is controlled by an additive gene, according to a characteristic with a high heritability (86.64%) and a moderate genetic advance as a percentage of the mean (14.86%), and this trait would be beneficial if chosen for genetic development (Table 14).



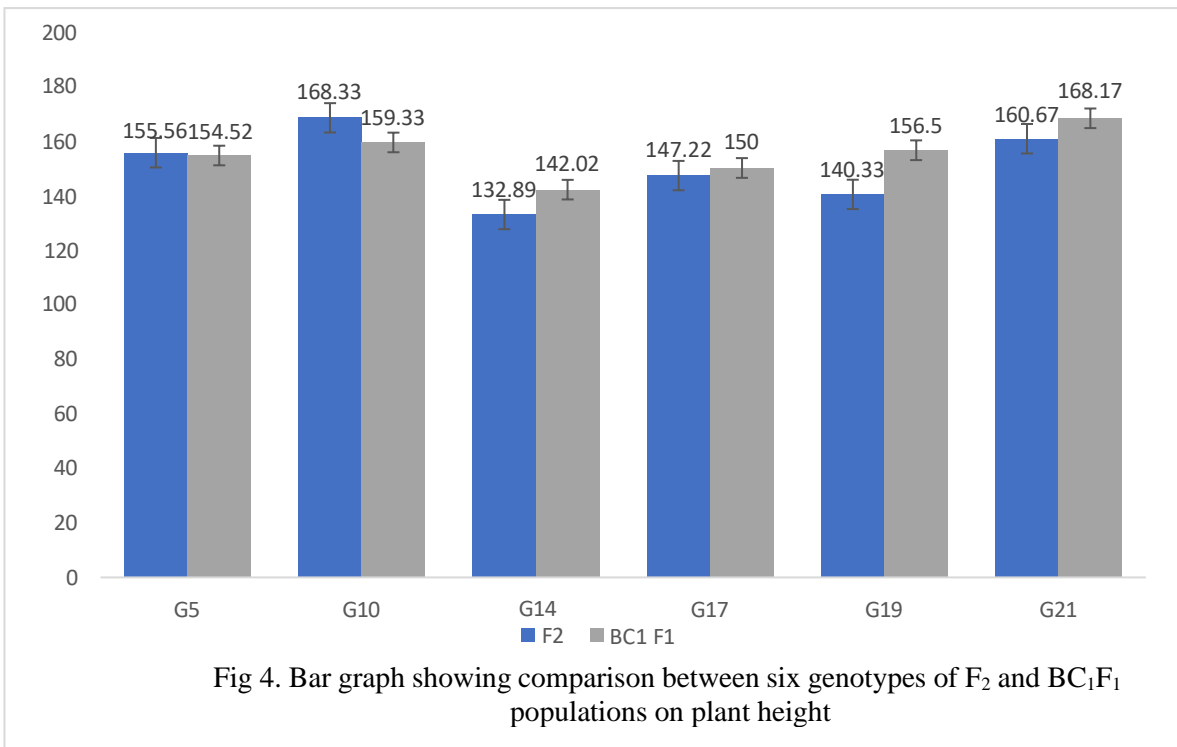
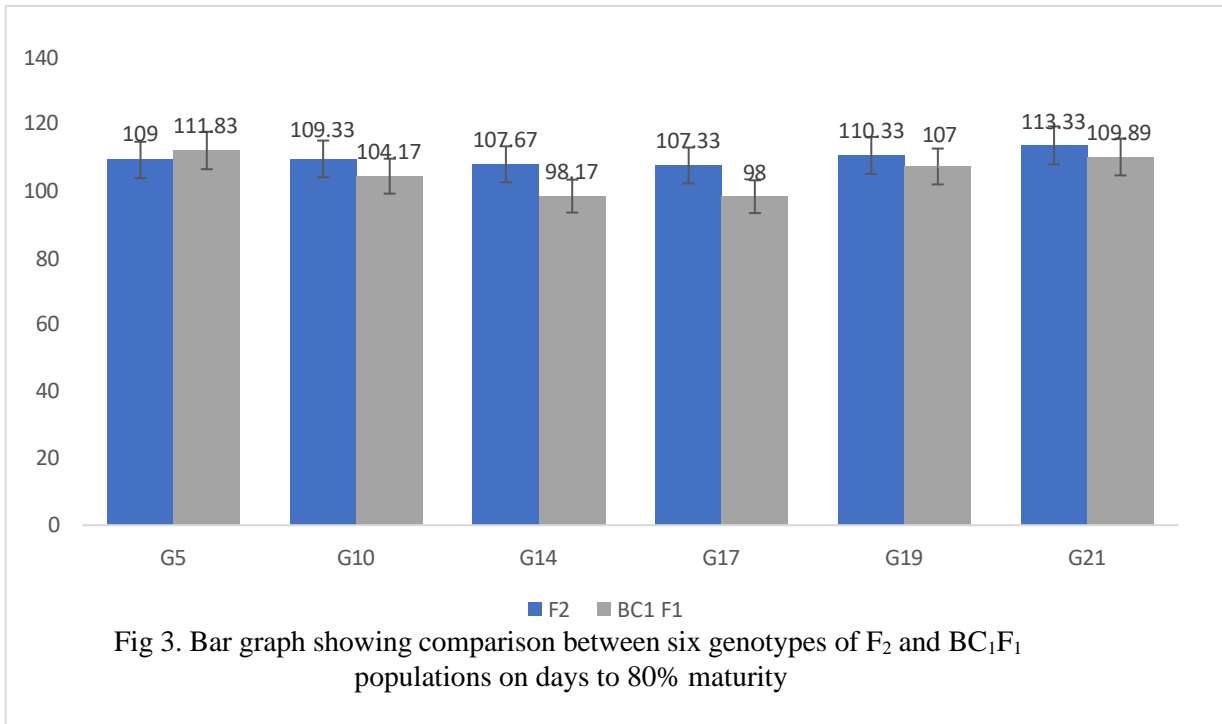
4.3.3.3. Days to 80% siliqua maturity

The mean performance for days to 80% siliqua maturity in the instance of six backcrosses BC₁F₁ populations revealed that (P1×P6) × P1= (108.56), (P2×P6) ×P2= (104.17), (P3×P6) ×P2= (100.83), (P4×P6) × P4= (104.67), (P5×P6) ×P5= (108.33) and (P7×P6) × P7= (109.50) displayed comparative earliest to their respective F₂ populations of (P1×P6=109), (P2×P6=109.33), (P3×P6=107.67), (P4×P6=109) (P5×P6=109.35) and (P7×P6=113.33) (Table 14). On the top of that the average of the six backcrosses as a whole (106.07) was also less than the average of the F₂ populations as a whole (107.14) (Figure 3). So, all the back crosses are suitable to be carried on.

Similar to the preceding two traits, this characteristic had about equal phenotypic and genotypic variance in terms of numbers. While the genotypic and phenotypic variation coefficient were 3.56 and 3.81, respectively, the genotypic and phenotypic variance were 10.51 and 14.32, respectively. The very small amount of variation between phenotypic and genotypic coefficients of variation and the difference between them suggest that the genes that control a trait are not significantly influenced by the environment. The GCV and PCV values showed that the genotypes for the characteristics showed significant variation. The trait's high heritability (73.38%) and low genetic advance (5.72%) as a proportion of the mean (5.39%) imply that days to 80% of Siliqua maturity are inherited under the control of a non- additive gene, and hence choosing this feature in terms of genetic growth would be ineffective (Table 14).

4.3.3.4. Plant height (cm)

The mean performance of the case of six backcrosses BC₁F₁ populations, plant height showed that (P1×P6) × P1= (151.50), (P2×P6) ×P2= (155.33), (P3×P6) ×P3= (132.67), (P4×P6) × P4= (145.33) and (P7×P6) × P7= (149.59) displayed comparative earliest to their respective F₂ generation combinations of (P1×P6=155.56), (P2×P6=168.33), (P3×P6=132.89), (P4×P6=147.22) and (P7×P6=160.67). But, the average of the six backcrosses combined (150.68) was higher than the average of the entire F₂ generation. (148.66). Therefore, what we can see is all the back crosses except (P5×P6) ×P5= (160.44) was showing lower value than their corresponding F₂



combination mean, while $(P5 \times P6) = 140.33$ (Figure 4). So, the backcrosses showed earliness than their respective F_2 combinations.

Plant height had a genotypic variance of 104.31 and a phenotypic variance of 113.73, with a moderate level of environmental variance (9.42), indicating that the environment had a significant impact on the gene controlling this feature. The phenotypic and genotypic coefficient variances were 7.06 and 6.77, respectively, with barely any difference between them. High heritability (91.72%) and modest genetic progress (13.73) as a percentage of mean are present for the characteristic. Because plant height expression was governed by additive genetic action and had a high heritability with a moderate genetic advance as a percentage of the mean, selection for this characteristic may be successful in transforming it into acceptable height (Table 14).

4.3.3.5. Number of primary branches

The grand mean value for number of primary branches in F_2 populations was 5.08 (Table 15) while the grand mean for backcross BC_1F_1 populations was 5.26 which is seemingly higher than F_2 generation and implies that the number of primary branches was on increase while backcross was done. This increasing rate in cases of number of primary branches was the target for keeping the yield as the main trait to be increased. All the backcross BC_1F_1 populations $(P1 \times P6) \times P1 = (4.70)$, $(P4 \times P6) \times P4 = (5.28)$, $(P5 \times P6) \times P5 = 5.44$ and $(P7 \times P6) \times P7 = (5.70)$ except $(P2 \times P6) \times P2 = (4.72)$, $(P3 \times P6) \times P3 = (4.44)$, $(P5 \times P6) \times P5 = 5.44$ were responsive in increasing their number of primary branches which will possibly make the yield higher. As Their respective F_2 populations were showing lower mean than them $(P1 \times P6 = 4.67)$, $(P4 \times P6 = 6.00)$ and $(P7 \times P6 = 4.89)$ (Table 15).

Table 15. Mean performance of six selective BC₁F₁ and six F₂ populations in *B. juncea* L.

COMBINATIONS	NPB	NSB	SL	SPS	SPP	HI
F ₂ (P1× P6)	4.67	8.67	3.77	11.89	226.00	23.99
BC ₁ [(P1× P6) ×P1]	4.70	7.89	4.18	11.50	193.26	24.33
F ₂ (P2× P6)	4.78	8.11	4.56	14.45	204.00	25.81
BC ₁ [(P2× P6) ×P2]	4.72	8.39	4.32	14.50	204.85	26.89
F ₂ (P3× P6)	3.89	8.89	5.13	12.66	189.33	27.00
BC ₁ [(P3× P6) ×P3]	4.44	7.17	4.03	13.03	193.72	24.75
F ₂ (P4× P6)	6.00	14.33	4.74	12.22	257.17	22.13
BC ₁ [(P4× P6) ×P4]	5.28	10.22	4.08	12.56	220.33	29.82
F ₂ (P5× P6)	4.33	10.67	4.73	11.78	239.44	28.72
BC ₁ [(P5× P6) ×P5]	5.44	12.33	4.32	10.44	251.53	23.56
F ₂ (P7× P6)	4.89	11.33	4.97	13.42	268.33	28.53
BC ₁ [(P7× P6) ×P7]	5.70	7.63	4.41	13.28	190.54	29.47
F ₂ (Mean)	5.08	9.82	4.43	13.13	237.69	27.01
F ₂ (CV%)	5.49	4.06	2.25	1.66	3.56	1.53
BC ₁ (Mean)	5.26	8.31	4.61	12.53	190.06	27.29
BC ₁ (CV%)	3.51	3.31	1.74	1.97	2.38	2.93

Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% siliqua maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).



(P1×P6) × P1



(P2×P6) × P2



(P3×P6) × P3



(P4×P6) × P4



(P5×P6) × P5



(P7×P6) × P7

Plate 14. Vegetative stage of 6 BC₁F₁ populations

Their total mean for backcross being higher than the F₂ generation mean also indicated the acceleration. The genotypic and phenotypic variances for the number of major branches were 0.28 and 0.46, respectively. The difference between phenotypic and genotypic variation was essentially negligible, suggesting that the environment has little effect on the gene controlling this feature. The fact that this characteristic displayed a moderate range of phenotypic coefficient variation (12.21) and genotypic coefficient variation (9.54) suggested that the varieties' inherent variability existed. This characteristic was combined with poor genetic progress and high heritability (61.1%). more genetic advance as a proportion of the mean (15.37) reveals that the number of primary branches' legacy is controlled by an additive gene, and that selecting this attribute for genetic development purposes would be productive (Table 14).

4.3.3.6. Number of secondary branches

The grand mean for the number of secondary branches per plant in the F₂ population was 9.82 (Table 15), whereas the grand mean for backcross BC₁F₁ populations was 8.31. Since backcross appeared to be greater than the F₂ generation, this suggested that the number of secondary branches has been increasing. The goal was to maintain yield as the major attribute that needed to be improved while the number of primary branches was increased. (P₂×P₆) ×P₂= (8.39), (P₅×P₆) × P₅= (12.33), were responsive in increasing their number of secondary branches, which may result in a higher yield. As Their respective F₂ combinations (P₂×P₆=8.11), (P₅×P₆=10.67) showed lower means than they did. Their backcross total being larger than the F₂ generation total mean indicating acceleration in addition to number of more secondary branch. But the rest crosses show no improvement in terms of this trait than the F₂ generation (Table 15).

The number of secondary branches showed that the genotypic and phenotypic variances were 2.91 and 3.58, respectively. The discrepancy between phenotypic and genotypic variance was essentially preventable, which suggested that the environment had a minimal influence on the gene governing this feature. The presence of inherent variability across the types was shown by screening a moderate array of phenotypic co- efficient variation (18.73) and genotypic coefficient variation (16.89) by this trait. This characteristic had minimal genetic advance, high heritability (81.36%), and a larger

genetic advance as a percentage of the mean (31.39) suggested that the number of secondary branches was regulated by additive gene action, and that the trait would become the ideal number of branches if it were chosen for genetic growth (Table 14).

4.3.3.7. Siliqua length (cm)

The mean performance of the case of six backcrosses for siliqua showed that except $(P1 \times P6) \times P1 = (4.18)$, $(P4 \times P6) \times P4 = (4.87)$, all the other combination displayed comparative larger length in their respective F_2 generation combinations than backcross combination. The average of the combined six backcrosses, however, (4.61), was greater than the average of the entire F_2 generation. (4.43) (Table 15). As a result, all of the rest back crossings except for mentioned one, exhibited values that were lower than the equivalent F_2 combination.

For this characteristic, a minute value of genotypic variance and phenotypic variance was found to be 0.104 and 0.12, respectively, with the difference between the two variances being almost 0. The presence of inherent variability across the types was shown by screening a moderate array of phenotypic coefficient variation (7.55) and genotypic coefficient variation (7.00) by this trait. The least divergence in both situations demonstrates how little environmental factors affect genes that determine traits, with genotypes taking the lead instead. This characteristic is highly heritable (85.8%) and has a low genetic advance with a moderate genetic advance as a percentage mean (13.35) (Table 14), which suggests that the additive gene effect is under control for this trait. If this feature selected for in breeding, the additive gene impact guarantees the formation of big siliquae.

4.3.3.8. Seeds per siliqua

In the F_2 populations, the grand mean for seeds per siliqua was 13.53, whereas the grand mean for backcross was 13.13 (Table 15). BC_1F_1 populations were greater than the respective F_2 populations, indicated that there were more seeds per siliqua in BC_1F_1 populations than there were in F_2 counterparts. While there are more seeds per siliqua, the chance of more yield was to be enhanced. All of the backcross combinations $(P1 \times P6) \times P1 = (11.50)$, $(P2 \times P6) \times P2 = (14.50)$, $(P3 \times P6) \times P3 = (13.03)$, $(P4 \times P6) \times P4 = (12.56)$ responded on increasing the seeds per siliqua on their plants, which could lead to a better yield, since their corresponding F_2 combinations $(P1 \times P6 = 11.89)$, $(P2 \times P6 = 14.45)$, $(P3 \times P6 = 12.66)$, $(P4 \times P6 = 12.22)$ displayed lower means. The fact that

their backcross mean was higher than the mean for the F₂ generation indicates acceleration of more seeds per siliqua. which exhibits improvement in this feature over the F₂ generation (Table 15)

For this characteristic, the genotypic and phenotypic variances were found to be minute, with values of 0.86 and 1.21, respectively. However, the difference between the two variances was essentially insignificant and not worth mentioning. The presence of inherent variability across the genotypes was revealed by screening a low assortment of phenotypic coefficient variance (8.13) and genotypic coefficient variance (6.85) by this attribute. The least divergence in both situations demonstrates how little environmental factors affect genes that determine traits, with genotypes taking the lead instead. This characteristic exhibit high heritability (70.91%), low genetic advance (11.87%), and moderate genetic advance as a percentage of the mean, which suggests that additive gene impact is the trait's regulator. If this characteristic is selected to boost yield in the breeding program, additive gene effect ensures that the desired count of seeds per siliquae will be generated. (Table 14)

4.3.3.9. Siliqua per plant

The higher the siliqua, the higher the seed count. The backcross BC₁F₁ populations had higher mean in terms of this traits, are (P₂×P₆) ×P₂= (204.85), (P₃×P₆) ×P₃= (193.72), (P₅×P₆) ×P₅=251.46 than their F₂ populations (P₂×P₆=204.00), (P₃×P₆=189.33), (P₅×P₆=239.44). The rest of the backcrosses like (P₁×P₆) × P₁= (193.26), (P₄×P₆) × P₄= (257.17), (P₇×P₆) × P₇= (251.53) could not exceed their respective F₂ populations in siliqua count (P₁×P₆=226), (P₄×P₆=297.78) and (P₇×P₆=268.33) (Table 15). This indicates the deceleration in terms of siliqua count per plant which was opposite of our target. So, (P₂×P₆) ×P₂, (P₃×P₆) ×P₃ and (P₅×P₆) ×P₅ shows desirability for this trait.

For the trait number of Siliqua per plant, considerable genotypic variation (1085.81) and phenotypic variance (1181.52) were found together with noticeably high environmental variance (95.7), which denotes the significant environmental influence on the trait-controlling gene rather than genotypic influence. The presence of inherent variability among the genotypes was shown by screening a low assortment of phenotypic coefficient variance (15.11) and genotypic coefficient variance (14.49) by this attribute. This variable has a high genetic advance as a percentage of the mean (28.62) and a high

heritability (91.9%), which suggests that the additive gene effect was under control. If this characteristic chosen in a breeding program, the additive gene impact ensures that a greater number of siliquae will emerge (Table 14).

4.3.3.10. 1000 seeds weight (gm)

The grand mean for the total number of primary branches in the F₂ populations was 2.8 (Table 13), yet the grand mean for the backcross BC₁F₁ populations was 3.4, which seems to be greater than the F₂ populations and suggested that the weight of 1000 seeds climbed while the backcross was in progress. The objective was to retain yield as the major attribute that needs to be improved while the number of primary branches increased. All of the backcross combinations (P1×P6) × P1= (3.62), (P2×P6) × P2= (2.99), (P3×P6) × P3= (3.10), (P4×P6) × P4= (3.03), (P5×P6) × P5=3.99 and (P7×P6) × P7= (3.68) were responsive in increasing their 1000 seeds weight, which may result in a higher yield. As Their respective F₂ combinations (P1×P6=3.16), (P2×P6=2.63), (P3×P6=2.56), (P4×P6=2.30) (P5×P6=3.80) and (P7×P6=3.31) showed lower means than backcrosses did (Figure 5). Their backcross total mean exceeding the F₂ generation mean also suggests an acceleration.

The phenotypic and genotypic variations of thousand seed weight, respectively, were 0.18 and 0.17, which ostensibly demonstrates the minute difference between the variances. The discrepancy indicates that genotypic influence was the main promoter here and that the gene determining the characteristic has the least environmental influence. The genotypic and phenotypic coefficient variation were respectively 12.23 and 12.33. This characteristic exhibit high heritability (98.52%), modest genetic advance (25.02%) and moderate genetic advance as a fraction of the mean, which suggests that additive gene impact is the trait's regulator (Table 14). If desired for this trait to increase yield in the breeding program, additive gene effect ensures that the desired weight of 1000 seeds would be produced.

4.3.3.11. Yield per plant (gm)

The grand mean value for number of primary branches in F₂ populations was 9.54 (Table 15) while the grand mean for backcross BC₁F₁ populations was 10.3, which was seemingly higher than F₂ populations and implied that yield per plant was on increase

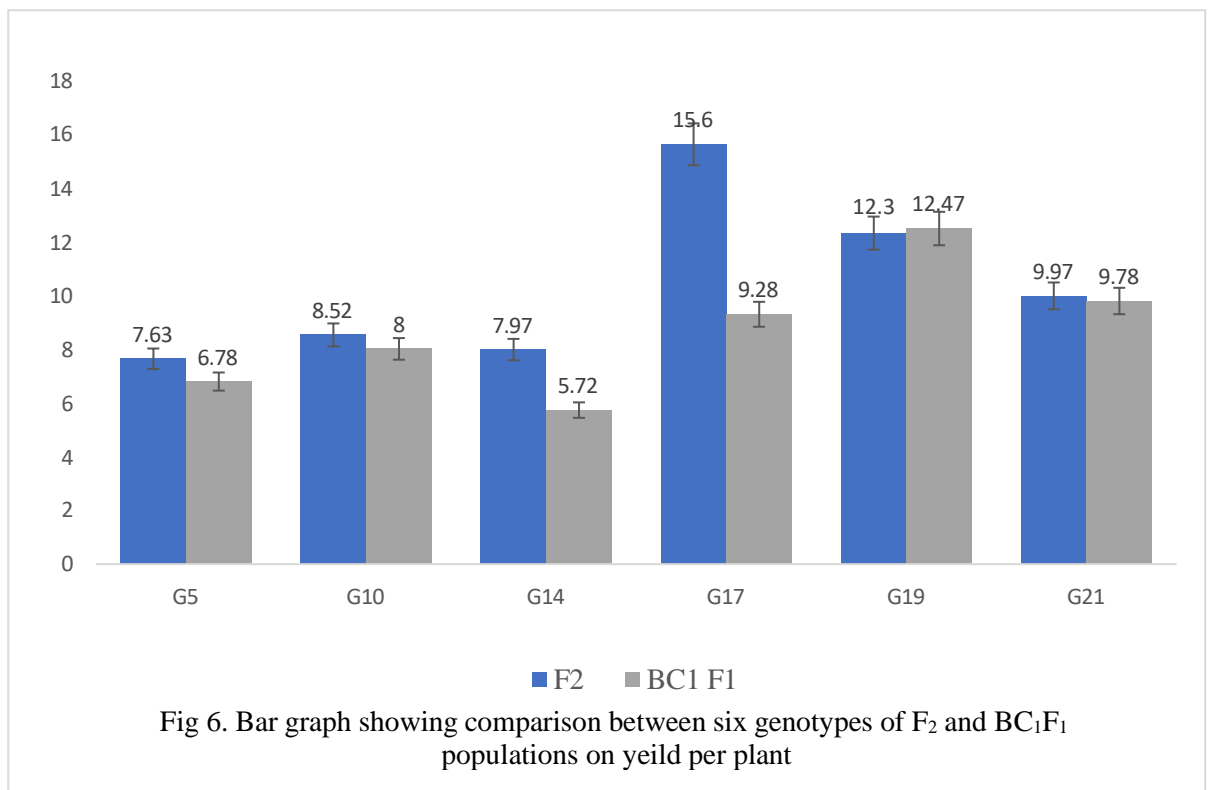
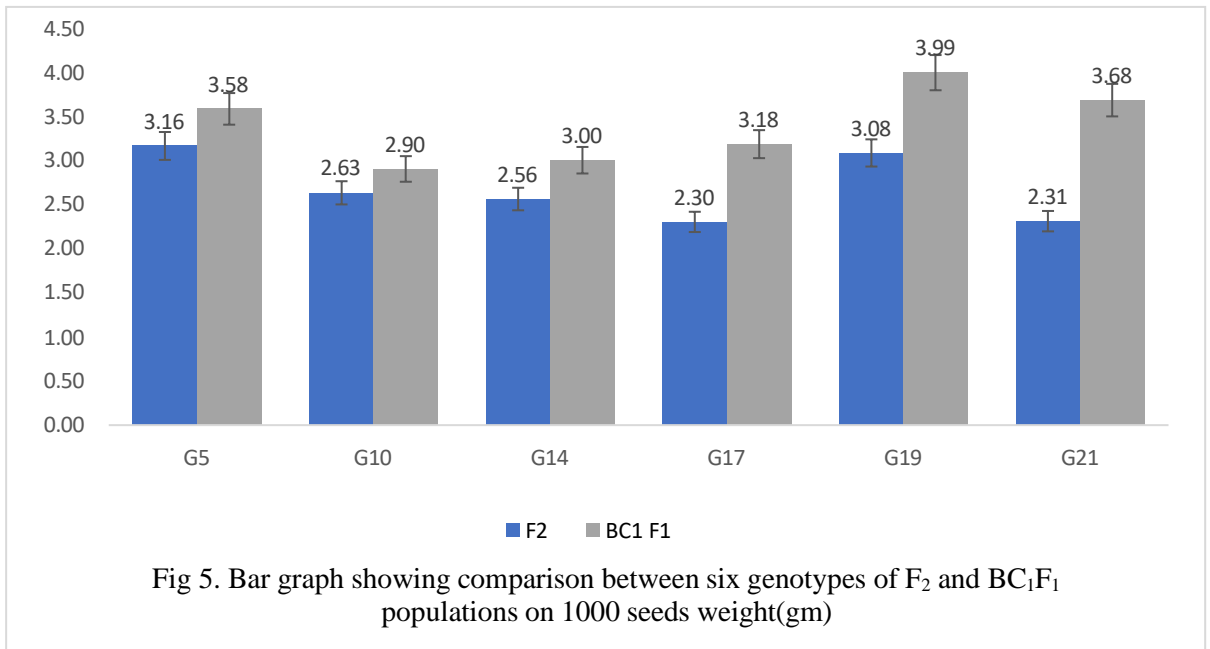
rate while backcross took place. All the backcross combination $(P1 \times P6) \times P1 = (10.78)$, $(P2 \times P6) \times P2 = (8.91)$, $(P3 \times P6) \times P3 = (9.73)$, $(P5 \times P6) \times P5 = (12.37)$ and $(P7 \times P6) \times P7 = (11.78)$ except $(P4 \times P6) \times P4 = (12.27)$ were responsive in increasing their number of primary branches which will possibly make the yield higher. As Their respective F₂ combination were showing lower mean than them $(P1 \times P6 = 7.63)$, $(P2 \times P6 = 8.52)$, $(P3 \times P6 = 7.97)$, $(P4 \times P6 = 15.60)$ $(P5 \times P6 = 12.30)$ and $(P7 \times P6 = 9.97)$. Their total mean for backcross being higher than the F₂ generation mean also shows the progress. (Figure 6).

The lowest genotypic (4.95) and phenotypic (5.07) variance values were found in yield per plant, while the environmental variance was minimal. The low environmental variance demonstrates the low environmental influence on the trait-controlling gene and the substantial genotypic influence. The high genotypic and phenotypic coefficients of variation were 21.60 and 21.85, respectively. The GCV and PCV values showed that the genotypes for the characteristics showed significant variation. For yield per plant, Salam *et al.* (2017) also discovered a moderate level of GCV and PCV. Given that yield per plant had a high heritability of 97.67% and a low genetic progress as a percentage of the mean (43.97%), the inheritance of yield per plant might be regulated by additive gene effects. (Table 14).

4.3.3.12. Harvest index

Except $(P3 \times P6) \times P3$, $(P5 \times P6) \times P5$, the other backcrosses $(P1 \times P6) \times P1 = (24.33)$, $(P2 \times P6) \times P2 = (26.89)$, $(P4 \times P6) \times P4 = (29.82)$ and $(P7 \times P6) \times P7 = (29.47)$ has higher mean value than their corresponding F₂ populations $(P1 \times P6 = 23.99)$, $(P2 \times P6 = 25.81)$, $(P4 \times P6 = 22.13)$, and $(P7 \times P6 = 28.53)$. The grand mean of backcross (27.29) was also higher than the respective F₂ populations mean value (27.01), which was a positive mark for breeding purpose.

With little environmental variance (0.36), genotypic variance (4.05) and phenotypic variance (4.45) were estimated (Table 14). The coefficients of variation for genotype and phenotype were respectively, 7.41 and 7.73. This slight variation in the coefficients of variation between genotype and phenotype determines that the majority of the current variation was driven by genes, with the environment having a minor influence. The GCV and PCV values showed that there was a lot of diversity among the genotypes for the characteristics. High heritability (91.93%) and a moderate genetic advance as a proportion of the mean



(14.65%) imply that the additive gene controls how the days to harvest index is inherited, and this attribute would be beneficial if chosen for genetic development (Table 14).

4.4 Gene action and genetic components analysis of F₂ populations through Hayman's approach

The outcomes of the Hayman's ANOVA trailed by Morley Jone's modification for all the intended characters in F₂ populations are presented in Table 16. Here 'a and b' express additive genetic affect and dominance affect, respectively. In the F₂ populations the additive genetic effects (a) were significant at high or moderate level for all the characters in F₂ populations. As the value of 'a' is higher than 0 for every described trait it shows the presence of partial dominance. The dominance effects (b) were also highly significant in F₂ populations for the characters. When the both 'a and b' value are significant, it indicates the inclusion of the both additive and dominant components in the inheritance of these traits. Additive effect was more prevailing here for the traits siliqua maturity, plant height, number of primary branches, number of secondary branches, siliqua per plant, seeds per siliquae as the extent of 'a' was much higher than 'b' in the corresponding generation, indicated greater importance of additive effects (Table 16). In terms of days to first flowering, days to 50% flowering, siliqua length, 1000 seeds weight, yield per plant and harvest index, the magnitude of 'a' is lower than the magnitude of 'b' which is the indication of presence of dominance effect.

In diffraction through the sub-component of 'b', the average heterosis deviation (b1) was significant in F₂ populations were highly significant followed by the interaction of the alleles present in the same locus (dominance deviation) due to the asymmetrical gene frequencies (b2) and the residual dominance effects (b3) for all the characters (Table 16). In F₂ populations, the magnitude of b1 for days to first flowering, siliqua maturity, number of primary branches and harvest index smaller in comparison with b2 and b3 representing reduced heterosis due to inbreeding in this generation while the rest of the trait has higher value for b1 than b2, and b3 which showed increased heterosis due to the negative inbreeding depression. The significance of b2 (asymmetry of dominant genes) described the main share of the dominance effects (b)

Table 16. Hayman's analysis of variance for 12 traits of F₂ populations in 7×7 diallel of *B. juncea* L.

	Df	DFE	D50%F	DSM	PH	NPB	NS	SL	SPP	SPS	TSW	YPP	HI
a	6	9.80*	29.16**	29.35**	612.01**	4.39**	15.18**	0.58	5363.59**	9.23**	0.82**	12.03**	8.05**
b	21	31.98**	38.35**	12.01*	360.26**	1.55**	13.21**	0.64	2498.09**	6.47**	0.90**	19.87**	45.91**
b1	1	17.81**	40.48**	2.89	602.12**	1.02**	71.57**	3.90**	3253.26**	3.69**	1.07**	163.46**	3.27**
b2	6	36.49**	22.36**	15.44*	217.18**	1.37**	8.12**	0.59	2860.84**	1.24**	0.87**	8.90**	38.17**
b3	14	31.05**	45.05**	11.19*	404.31**	1.67**	11.22**	0.44	2288.68**	8.91**	0.90**	14.31**	52.28**
Error	54	9.43	7.70	5.87	90.82	0.39	1.61	0.08	616.81	1.80	0.01	1.03	3.87

Note:

DF=Degree of freedom, DFE=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g) and HI=Harvest index, a= additive dominance effect, b= dominance effect, b₁= average deviation, b₂= dominance deviation and b₃= residual dominance effect.

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

in the parents for all of the traits. Also, the significance of b_3 (residual dominance effects) reported for the chief r proportion of the dominance effects (b) in the parents for number of branches per plant. The asymmetry of dominant genes (b_2) was non-significant in F_2 populations for silique length (Table 16). Therefore, the results indicated that the significant dominant effects were due to mid-parental dominance, asymmetry of gene distribution and a residual dominance effect for majority of the characters studied except siliquae length. The genetic components of variation of F_2 generation are presented in Table 17.

The genetic components of all of the traits under study in the F_2 populations (Table 17) showed that the estimate of the additive component (D) was highly significant, demonstrating the significance of additive variation in the inheritance of these features. The values of H_1 and H_2 scores of characters were also extremely significant indicated that they were responsible for dominance variation. H_2 for the characters had a significant and favorable value, which indicated the presence of dominant influences. Significant H_2 positive score suggested that this feature had dominant effects. For all traits across the F_2 populations, the dominance gene effect (H) was higher than the additive values (D) with the exception of the days to 80% siliqua maturity, which suggested heterosis breeding would be effective. The genetic components D and H identified the parent that concentrates the majority of the genes or favorable alleles for the trait. Therefore, the considerable positive D showed a predominate additive influence, whereas the significant negative D indicated that additive gene activity was not controlling the transmission of these traits. Similar to the substantial positive H , which suggested a dominant influence that was predominate and recommended delaying selection until heterozygosity was decreased, the significant negative H indicated that dominance effects were confined by parents who carried alleles that were associated with low value for the qualities.

Table 17. Genetic components of variation for eleven horticultural traits in a 7×7 half diallel population of *B. juncea* L.

Components	DFF	D50F	DSM	PH	NPB	NSB	SPS	SL	SPP	TSY	YPP	HI
E	9.43**	7.70**	5.87**	90.81**	0.39	1.61	1.80*	0.08	616.81**	0.01	1.03*	3.87**
D	0.19	3.25	5.53	4.30	2.9	0.00	0.00	0.17*	0.00	0.09	0.70	0.00
F	2.72*	2.854*	4.35	0.00	0.00	0.00	0.00	0.24*	0.00	0.16	0.58	5.84*
H ₁	22.76**	32.92**	2.61	254.39**	1.21	12.68	3.84**	0.63**	2054.61**	1.31**	20.77**	57.13**
H ₂	18.32**	31.58**	2.08	252.77**	1.07	11.34	4.75**	0.51**	1619.42**	1.04	18.78**	48.20**
h ²	0.27	3.78	0.00	67.86*	0.00	12.57	0.00	0.69	304.91	0.20	30.00	0.00
Allied components												
(H ₁ /D) ^{0.05}	2.41	3.18	0.69	7.69	2.02	#DIV/0!	#DIV/0!	1.92	#DIV/0!	3.91	5.45	#DIV/0!
H ₂ /4H ₁	0.20	0.24	0.20	0.25	0.22	0.22	0.31	0.20	0.20	0.20	0.23	0.21
[(4DH ₁) ² +F]/ [(4DH ₁) ² -F]	-1.00	1.32	3.68	1.00	1.00	#DIV/0!	#DIV/0!	2.14	#DIV/0!	1.64	1.16	-1.00
h ₂ /H ₂	0.00	0.12	0.00	0.27	0.00	1.11	0.00	1.35	0.19	0.19	1.60	0.00
h ² _n	0.06	0.05	0.12	0.02	0.25	0.13	0.00	0.11	0.18	0.26	0.16	0.09
h ² _b	0.37	0.53	0.19	0.42	0.55	0.69	0.29	0.65	0.50	0.98	0.85	0.78

*p<0.05; **p<0.01, E=Environment component, D=Additive component, F= Mean cov. Of D and H₁, H₁= Dominant component, H₂= ratio of +/- gene, h²=Heritability, h²_n = Narrow sense heritability and h²_b =Broad sense heritability, h²/H₂= Number of dominant gene blocks, H₂/4H₁= ratio of gene with ± effects, [(4DH₁)²+F]/ [(4DH₁)²-F] = Ratio of dominant and recessive gene, (H₁/D)^{0.5} = Men degree of dominance Note: DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g) and HI=Harvest index (%).

All of the traits in this characteristic displayed positive H signals that indicated direct dominance (Table 17). It is stated that significant additive and dominance gene with greater magnitude of non-additive gene action indicated the presence of both additive and non-additive gene with greater magnitude of non-additive gene for inheritance of characters. Gupta *et al.*, (2015) and Amkha *et al.*, (2014) reported additive and dominance gene action with greater magnitude of non-additive gene action for inheritance of traits. The high magnitude of dominance effect would have diminished. For all of the traits, the additive and additive effects are found to be significant. Positive additive \times additive interaction demonstrated allele association, while the negative form demonstrated allele dispersion in the parents. As a result, alleles relationship in parents was demonstrated by positive significant values of D in all traits in this study.

In addition to additive gene effects, dominance (H) and dominance \times dominance gene effects had also high contributions in controlling traits, Gene interaction is considered to be complementary when the dominance(H) and dominance \times dominance have same sign what all of the trait showing. In duplicate epistasis variability in segregating generations might be reduced which hinder in the selection process (Pattanaik *et al.*,2014) so it was difficult to utilize them in breeding program. Therefore, selection with duplicate type of epistasis must be delayed to advance generation to benefit from the reduction of digenic epistasis variation and exploit transgressive segregants. Duplicate type of non- allelic interactions was also reported for different yield contributing character Singh *et al.*, (2007), Dashti *et al.*, (2010), Kabdal and Singh (2010), Singh *et al.*, (2012). The result was also matched with Philanim *et al.*, (2019).

The direction of F confirmed that the dominant alleles in the parents were distributed symmetrically. Highly substantial positive value of F for days to 1000 seeds weight suggested that dominant alleles for this feature were more common in the parents than recessive alleles. In terms of F, if it is equal to 0, it means balanced distribution of dominant and recessive gene. Among twelve traits described here, all traits show dominant alleles was more frequent than recessive alleles their F value was higher than 0. $F > 0$ for these 3 traits signifies prevalence of dominant alleles in parents. For all the characters, the environment had a significant impact. For all of the traits

examined, the environment had a major impact since component E proved to be significant.

For days to 80% siliqua maturity, the mean degree of dominance as determined by $(H_1/D) 0.5$ was less than 1 (Table 17), showing the occurrence of partial dominance for the inheritance of the feature. Hence, the ratio was greater than 1 for all the attribute except plant height, over-dominance was seen for the inheritance of the 11 traits (eliminating plant height) among the twelve traits studied here. The $H_2/4H_1$ ratio measures the proportion of dominant genes that have both positive and negative impacts across all loci. The value of $H_2/4H_1$ for all characters deviated from the expected value of 0.25, demonstrating asymmetry in the distribution of genes. The ratio of parents' dominant genes ($H_2/4H_1$) that had positive or negative impacts. When $p = q$ at all loci equals 0.5, means symmetrical distribution of positive and negative dominant gene in parents.

When $p \neq q$, a deviated from 0.25, asymmetrical distribution of positive and negative dominant gene in parents would result. In other words, if this ratio is less than 0.25, then the spread of the parents' positive and negative dominant genes is symmetrical; otherwise, it is asymmetrical. (Al-Timimi *et al.*, 2020)

The ratio of $[(4DH_1) \frac{1}{2} + F] / [(4DH_1) \frac{1}{2} - F]$ was greater than 1 for all the traits except days to first flowering, plant height, number of primary branches and harvest index indicating the total number of dominant genes were in excess than the total number of recessive genes and minority of recessive allele in the parents for these characters. Whereas, the ratio was less than 1 for days to first flowering (-1.00) and harvest index (-1.00) showed reverse effect that means minority of dominant allele and excess of recessive allele. $[(4DH_1) \frac{1}{2} + F] / [(4DH_1) \frac{1}{2} - F] = 1$ for plant height and number of primary branches means nearly equal number of dominant and recessive allele.

The total number of groups of genes which control the character and exhibited dominance was measured by h^2/H_2 . The estimated value of h^2/H_2 was positive for all the characters indicated that the characters were controlled by a number of genes or gene groups which exhibited dominance effect. Heritability estimates in both broad and narrow sense for the studied attributes were computed according to Mather and Jinks (1971).

High values for heritability in broad sense were obtained for all traits revealing that most phenotypic variability in each trait was due to genetic causes. High heritability values in broad sense along with medium or low ones in narrow sense were exhibited, indicating that most genetic variances were due to non-additive genetic effects. These findings support the aforementioned results on genetic components in which H_1 estimates played a greater role in the inheritance of these characters. Therefore, the bulk method program for improving such traits might be promising proposed by Bakhsh *et al.*, (2003); Allah *et al.*, (2010); Kennedy *et al.*, (2011).

4.4.1 Days to first flowering

The components $H_1(22.76)$ and $H_2(18.32)$ are significant while D is not significant for days to first flowering (Table 17). This gives the signal of importance of dominance effect of genes in the inheritance of flowering. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was much higher than D , signifying the majority of dominance type of gene action for this trait. Highly substantial positive value of F for days to first flowering suggested that dominant alleles for this feature were more common in the parents than recessive alleles. Dominance effect was found positive and non-significant. The $[(H_1 / D)0.5]$ value was greater than 1 indicating overdominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.20) which was smaller than the expected value of 0.25. The ratio of $[(4DH_1) \frac{1}{2} + F] / [(4DH_1) \frac{1}{2} - F]$ was less than unity, suggesting majority of recessive alleles and lesser dominant alleles. The analysis gives narrow sense heritability as 6% and broad sense heritability 37% (Table 17).

4.4.2 Days to 50% flowering

The components $H_1 (32.76)$ and $H_2 (31.58)$ are significant while $D (3.25)$ is not significant for days to 50% flowering (Table 17). This indicates the importance of dominance effect of genes in the inheritance of flowering. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was much higher than D , signifying the majority of dominance type of allele for this trait. Highly substantial positive value of $F (2.85)$ for days to 50% flowering suggested that dominant alleles for this feature were more common in the parents than recessive alleles. Dominance effect was found positive

and non-significant. The $[(H_1/D)^{0.5}]$ value was greater than 1 representing overdominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.24) which was smaller than the expected value of 0.25. The ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 5% and broad sense heritability 53% (Table 17).

4.4.3 Days to 80% siliqua maturity

The components $H_1(2.61)$, $H_2(2.08)$ and $D(5.53)$ is not significant for days to 80% Siliqua maturity (Table 17). This implies that none of them is controlling the transmission of genes in the inheritance of maturity. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was less than D, signifying the majority of recessive type of allele for this trait. Lower value of F (2.85) for days to 50% flowering suggested that recessive alleles for this feature were more common in the parents than dominant alleles. Dominance effect was found positive and non-significant. The $[(H_1/D)^{0.5}]$ value (0.69) was less than 1 representing partial dominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.20) which was smaller than the expected value of 0.25. The ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 12% and broad sense heritability 19% (Table 17).

4.4.4 Plant height

The components $H_1(254.39)$, $H_2(252.77)$ are significant while $D(4.30)$ is non-significant for the trait plant height (Table 17). H_1 , H_2 being significant indicates the importance of dominance effect of genes in the inheritance of height. Environment component E (90.81) being significant proves the impact of environmental factors. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was way higher than D, signifying the majority of dominance type of allele for this trait. Dominance effect was found positive. The $[(H_1/D)^{0.5}]$ value (7.69) was greater than 1 representing overdominance for the character. Positive and negative

alleles showed symmetrical distribution, as indicated by $H_2/4H_1$ value (0.25) which was similar to the expected value of 0.25. The ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 2% and broad sense heritability 42% (Table 17).

4.4.5 Number of primary branches per plant

H_1 (1.21), H_2 (1.07) are significant while D (0.29) is non-significant for the trait plant height (Table 17). H_1 , H_2 being significant indicates the importance of dominance effect of genes in the inheritance of height. Environment component E (0.39) being non-significant proves the scarce impact of environmental factors. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was way higher than D (0.29), signifying the majority of dominance type of allele for this trait. The $[(H_1/D)^{0.5}]$ value (2.02) was greater than 1 representing overdominance for the respective character. Positive and negative alleles showed asymmetrical distribution, as indicated by $H_2/4H_1$ value (0.22) which was deviated from the expected value of 0.25. The ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 25% and broad sense heritability 55% (Table 17).

4.4.6 Number of secondary branches per plant

H_1 (12.68), H_2 (11.34) are significant for the trait plant height (Table 17). H_1 , H_2 being significant indicates the importance of dominance effect of genes in the inheritance of height. Environment component E (1.6) being non-significant proves the scarce impact of environmental factors. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was way higher than D , signifying the majority of dominance type of allele for this trait. Positive and negative alleles showed asymmetrical distribution, as indicated by $H_2/4H_1$ value (0.22) which was deviated from the expected value of 0.25. The analysis gives narrow sense heritability as 13% and broad sense heritability 69% (Table 17).

4.4.7 Seeds per siliqua

The components H_1 (3.84), H_2 (4.75) are significant for the trait seed per siliqua (Table 17). H_1 , H_2 being significant indicates the importance of dominance effect of genes in the inheritance of height. Environment component E (1.80) being non-significant proves the minimal impact of environmental factors. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was way higher than D, signifying the majority of dominance type of allele for this trait. Dominance effect was found positive. The $[(H_1/D)^{0.5}]$ value was greater than 1 representing overdominance for the character. Positive and negative alleles showed symmetrical distribution, as indicated by $H_2/4H_1$ value (0.31) which was deviated from the expected value of 0.25. The analysis gives broad sense heritability 29% (Table 17).

4.4.8 Siliqua length (cm)

H_1 (0.63), H_2 (0.51) are significant while D (0.17) is non-significant for the trait plant height (Table 17). H_1 , H_2 being significant indicates the importance of dominance effect of genes in the inheritance of height. Environment component E (0.08) being non-significant proves the scarce impact of environmental factors. Positive value of F (0.24) for siliqua length suggested that dominant alleles for this feature were more common in the parents than recessive alleles. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was way higher than D signifying the majority of dominance type of allele for this trait. The $[(H_1/D)^{0.5}]$ value (1.92) was greater than 1 representing overdominance for the respective character. Positive and negative alleles showed asymmetrical distribution, as indicated by $H_2/4H_1$ value (0.20) which was deviated from the expected value of 0.25. The ratio (2.14) of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 11% and broad sense heritability 65% (Table 17).

4.4.9 Siliquae per plant

H_1 (2054.61), H_2 (1619.42) are significant for the trait plant height (Table 17). H_1 , H_2 being significant indicates the importance of dominance effect of genes

in the inheritance of height. Environment component E (616.81) being non-significant proves the scarce impact of environmental factors. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was way higher than D signifying the majority of dominance type of allele for this trait. Positive and negative alleles showed asymmetrical distribution, as indicated by $H_2/4H_1$ value (0.20) which was deviated from the expected value of 0.25. The ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 18% and broad sense heritability 50% (Table 17).

4.4.10. Thousand seeds weight

The components $H_1(1.31)$ and $H_2(1.04)$ are significant while D (0.09) is not significant for 1000 seeds weight (Table 17). This gives the signal of importance of dominance effect of genes in the inheritance of flowering. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was much higher than D, signifying the majority of dominance type of gene action for this trait. Positive value of F (0.16) for 1000 seeds weight suggested that dominant alleles for this feature were more common in the parents than recessive alleles. Dominance effect was found positive and non-significant. The $(H_1/D)^{0.5}$ value (3.91) was greater than 1 indicating overdominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.20) which was smaller than the expected value of 0.25. The ratio (1.64) of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 26% and broad sense heritability 98% (Table 17).

4.4.11. Yield per plant (gm)

The components $H_1(20.77)$ and $H_2(18.78)$ are significant while D (0.7) is not significant for 1000 seeds weight (Table 17). This gives the signal of importance of dominance effect of genes in the inheritance of flowering. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was much higher than D, signifying the majority of dominance type of gene action for this trait. Positive value of F (0.58) for 1000

seeds weight suggested that dominant alleles for this feature were more common in the parents than recessive alleles. Dominance effect was found positive and non-significant. The $(H_1 / D)^{0.5}$ value (5.45) was greater than 1 indicating overdominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.23) which was smaller than the expected value of 0.25. The ratio (1.16) of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was greater than unity, suggesting majority of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritability as 16% and broad sense heritability 85% (Table 17).

4.4.12. Harvest Index

The components $H_1(57.13)$ and $H_2(48.20)$ are significant while $D (5.84)$ is not significant for harvest index (Table 17). This gives the indication of importance of dominance effect of genes in the inheritance of flowering. Positive H value suggested a dominant influence that was recommended delaying selection until heterozygosity was decreased. The magnitude of H_1 was much higher than D , signifying the majority of dominance type of gene action for this trait. Positive value of F (0.58) for 1000 seeds weight suggested that dominant alleles for this feature were more common in the parents than recessive alleles. Dominance effect was found positive and non-significant. The $(H_1 / D)^{0.5}$ value (5.02) was greater than 1 indicating overdominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.21) which was smaller than the expected value of 0.25. The ratio (-1.00) of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was less than unity, suggesting majority of recessive alleles and lesser dominant alleles. The analysis gives narrow sense heritability as 9% and broad sense heritability 78% (Table 17). Uddin and Newaz (1997) and Sarker (2000) observed high heritability for Siliqua yield

CHAPTER V

SUMMARY AND CONCLUSION

The current study, titled on "Genetic components and heterosis analysis of F₂ and BC₁F₁ populations in *B. juncea* L." was carried out with twenty-one (21) F₂ populations with their seven (7) parental lines and six (6) selected BC₁F₁ populations. In the current investigation the mean performance, genetic variability, correlation, heterosis, inbreeding depression, gene action and genetic component of F₂ and BC₁F₁ populations and their seven (7) parental lines were assessed.

This experiment was conducted on 2021 and 2022 at Sher- e- Bangla Agricultural University in Dhaka-1207 using RCBD design with three replications for 12 quantitative characters.

For each twelve attributes, there were detectable genotype-to-genotype differences. Mean performance for 21 F₂ populations along with 7 parental line showed significance difference. The F₂ population G19 (48DAS) needed the longest time for its first blooming while parental line BINA Sarisha- 7 (P1) (32.33DAS) needed the shortest period of time for first blooming. Days to 50% flowering reached its lowest point in F₂ population G20 (35.67 DAS), and G20 needed the longest days for 50% flowering to take place (48.00 DAS). Days to 80% of Siliqua's maturity were measured, with the minimum value being found in parent (P1) BINA-7 (102.67 DAS) and the highest value being found in F₂ population G21 (113.33 DAS). In F₂ populations G8 (172 cm), the tallest plant was discovered, while G12 had the shortest plant (126 cm). The primary branch yield in P4 (BARI sharish-16) was the lowest (3.22), but it was the F₂ populations G17 (14.33) which had the most secondary branches per plant, whereas P5 BARI sharish-16 (5.56) had the fewest secondary branches. Parental line P5 BARI sharish-16 had siliquae that were 3.05 cm shortest among all the genotype and parental lines and in G2(5.33) whose siliquae had recorded as the longest one. The highest number of Siliqua per plant was found in F₂ populations G17 (297.78), while the lowest amount was found in G2 (189.00 per plant). Significant variances were seen in the data for seed per siliquae. It got its peak in count in F₂ populations G13 (17.00), while G20 had the lowest value. (10.44). The maximum result for 1000 seeds weight was shared by F₂ populations G20 (3.99 gm) whereas G16 yielded the lowest 1000 seeds weight (2.10 gm). The most decisive

characteristic is yield, with G17 producing the maximum amount (15.6 gm) and P2 (Rye-5) producing the least amount (5.56 gm) for seed yield. The estimated harvest index reached its highest point in G13 (35.27%), while its lowest point was discovered in G7 (20.10%).

The amount of the phenotypic coefficient of variation among the traits was greater than the genotypic counterparts, indicating that environmental variance was only a small factor in regulating the expression. Plant height (92.55 and 101.71, respectively) and the number of Siliqua per plant were the two traits with the greatest genotypic and phenotypic variance. (251.57 and 279.26 respectively). Number of primary branches per plant (13.02, 11.68), number of secondary branches per plant (15.90, 15.22), and siliqua length all showed moderate phenotypic and genotypic coefficient of variation. (12.57 and 12.15). No trait displayed significant phenotypic and genotypic variation. Days to first flowering (82.50%), days to 50% flowering (79.52%), days to Siliqua maturity (73.70%), plant height (90.99%), number of primary branches per plant (86.53%), number of secondary branches per plant (91.71%), siliqua length (93.48%), seed per siliqua (82.27%), Siliqua per plant (90.09%), 1000 seeds weight (95.53%), yield per plant (97.45%) and harvest index (82.57%) showed the highest broad sense heritability. Only the number of Siliqua per plant (31.01) showed a higher genetic advance, although the number of primary branches per plant (31.99%), secondary branches per plant (30.02%), 1000 seeds weight (20.06), and yield per plant (36.65%) did. Days to first flowering (13.62), days to 50% flowering (13.83), plant height (12.41), Siliqua per plant (13.84), seeds per siliqua (16.34), and harvest index (11.60) all showed moderate genetic advance as a percentage of mean, along with high heritability, which made it easier to choose high yielding genotypes.

The genotypic correlation coefficients were greater than the corresponding phenotypic correlation coefficients for all of the characteristics. Given that the environmental variance was minimal, the differences between genotypic and phenotypic correlation coefficients were quite small. Consequently, choosing this feature may be a reliable choice for breeding program. Days to first flowering (0.81 and 0.73), days to 80% Siliqua maturity (0.84 and 0.68) were predicted to have positive and significant associations with days to 50% flowering at both the genotypic and phenotypic levels. Plant height has no positively significant connection with any trait at both levels. Days to first flowering (0.44), Days to 50% flowering (0.50), days to 80% Siliqua

maturity (0.44) and the number of Siliqua per plant (0.09) were associated with plant height positively and significantly at phenotypic level only. Siliqua per plant is strongly associated with number of primary branches (0.61 and 0.34), number secondary branches (0.84 and 0.50) and yield per plant (0.70 and 0.67) at both level in positive term and with 1000 seeds weight (0.66) at phenotypic level only. 1000 seeds weight has positively significant association with siliqua per plant (0.73 and 0.66), yield per plant (0.70 and 0.61) at both level and number secondary branches (0.47), siliqua per plant (0.66), harvest index (0.47). Yield per plant has positive significant correlation with number of primary branches (0.51 and 0.44), number secondary branches (0.66 and 0.60), siliqua per plant (0.70 and 0.67) at both index while siliqua length (0.52), harvest index (0.45) only at phenotypic index.

Out of 21 F₂ populations resulting from the half diallel cross from the 7 selected parents where one of the parents is check variety P7 BARI sharisha-11. The F₂ population G14 (-18.53%) showed the highest negative heterosis with strong significance for days to first flowering when compared to better parents, but it is also F₂ population G14 (-8.33%) which showed the same when it was compared to the check variety BARI sharisha-11. In terms of days to 50% flowering, F₂ population G14 (-20.71%) and G21 (-19.33%) both showed the largest negative heterosis while compared to better parents and check heterosis respectively. According to estimated data for days to 80% Siliqua maturity, the majority of F₂ population took longer to grow than their parents. The F₂ population G21 had the largest negative heterosis (-6.53%) compared to the control variety, whereas G1 had the lowest positive heterosis (0.64% and 0.31%, respectively) for both heterobeltiosis and standard heterosis.

In line with expectations, F₂ population G4 showed the largest significant and negative heterosis for plant height (-17.16% and -18.31% expressed by G19 and G12, respectively) for both the over-better parent and the check variety. G10 had the highest positive heterotic effect in terms of Siliqua per plant for both the better parent and the check variety (29.47%(G20) and 37.60%, (G17), respectively). For 1000 seeds weight, the F₂ population G8 (72.71%) and G20 (30.71) showed the highest positive heterosis both over the better parent and check variety respectively. According to data on yield per plant, F₂ population G17 (91.45% and 79.30), had the most positive heterotic impact above the better parent and reference variety. For both heterobeltiosis and standard heterosis, the most significant positive heterosis for the

harvest index was found in F₂ populations G19 (29.17%) and G13 (25.18%) above better parent and check variety heterosis.

In terms of inbreeding depression, days to first flowering, days to 50% flowering, days to 80% Siliqua maturity if show positive inbreeding depression expected to be the desired one and opposite depression is desired for siliqua per plant, 1000 seed yield, yield per plant, harvest index. The F₂ population G20 (22.14%) showed highest positive inbreeding depression for days to first flowering. The F₂ population G13(21.74%) was peak point of inbreeding depression for 50% flowering to take place. 6.29% was the highest depression shown by G1 for days to 80% Siliqua maturity. Highest inbreeding depression was 12.78% prevailed G18 for plant height. Highest negative depression which is highly significant is showed by -30.02% in F₂ population G8 for siliqua per plant. Yield per plant 1000 seeds weight showed highest negative inbreeding (-43.13) in F₂ population G2 and -29.23% in G17. Harvest index's highest negative inbreeding depression was portrayed by G13 which is - 17.84%.

Backcross BC₁F₁ analysis provided us with some expected and desirable combination. The BC₁F₁ line (P5×P6) ×P5 showed lowest count of days in case of days to first flowering (34das), days to fifty percent flowering (43.5DAS), days to eighty percent maturity found lowest for BC₁F₁ line (P4×P6) ×P4 (98DAS) and plant height was found shortest in BC₁F₁ line (P5×P6) ×P5 (140.33cm). Siliqua length (3.99cm), Seed per plant (285.99) and yield per plant (12.47) were found highest in BC₁F₁ (P5×P6) ×P5 among all the backcrosses.

For the majority of the traits, dominance variance was higher than additive variance, indicating that gene action is not fixable in nature. Selection for these traits must therefore be delayed until later generations. However, where additive variance was higher than dominance variance, selection would be highly successful because gene action is fixable in nature. Negative dominance variances may be the result of sampling error, genotype-environment interactions, or both. For the majority of the examined traits, the phenotypic variance was higher than the genotypic variance, showing that environmental variance predominates over genotypic variance. In most of the crosses, the degree of dominance(h/d) was more than one of the examined features, indicating over dominance effects. The presence of both additive and non-

additive gene effects for character inheritance were suggested by significant additive (D) and dominant (H) gene action with greater magnitude of non-additive gene action. With the exception of the days to 80% Siliqua maturity, the value of dominance gene action in this experiment was larger than the value of additive gene action, which encourages us to move toward heterosis breeding.

RECOMMENDATIONS

- i. The F₂ populations e.g., G9, G12, G13, G16 could be selected for early maturity variety and G4, G20, G17 in terms of yield might be recommended for selection considering mean performance of the population.
- ii. Based on the F₂ heterotic effect, the F₂ populations G4, G14, G21 and G8, G13, G17, G19, G20 might be used as a potential line for selecting individual plants having earliness and high yield in next generations.
- iii. The F₂ populations G1, G13, G18 and G20 showed the highest inbreeding depression for earliness and plant height. While the F₂ populations G2, G8, G13 and G17 had lowest inbreeding depression in terms of siliqua per plant, siliqua length and yield per plant. Therefore, these populations might be considered to get transgressive recombinant lines in next generations.
- iv. The backcross BC₁F₁ population (P5×P6) ×P5 showed the most desirable results in term of the maximum yield and contributing traits, so this BC₁F₁ line was selected.

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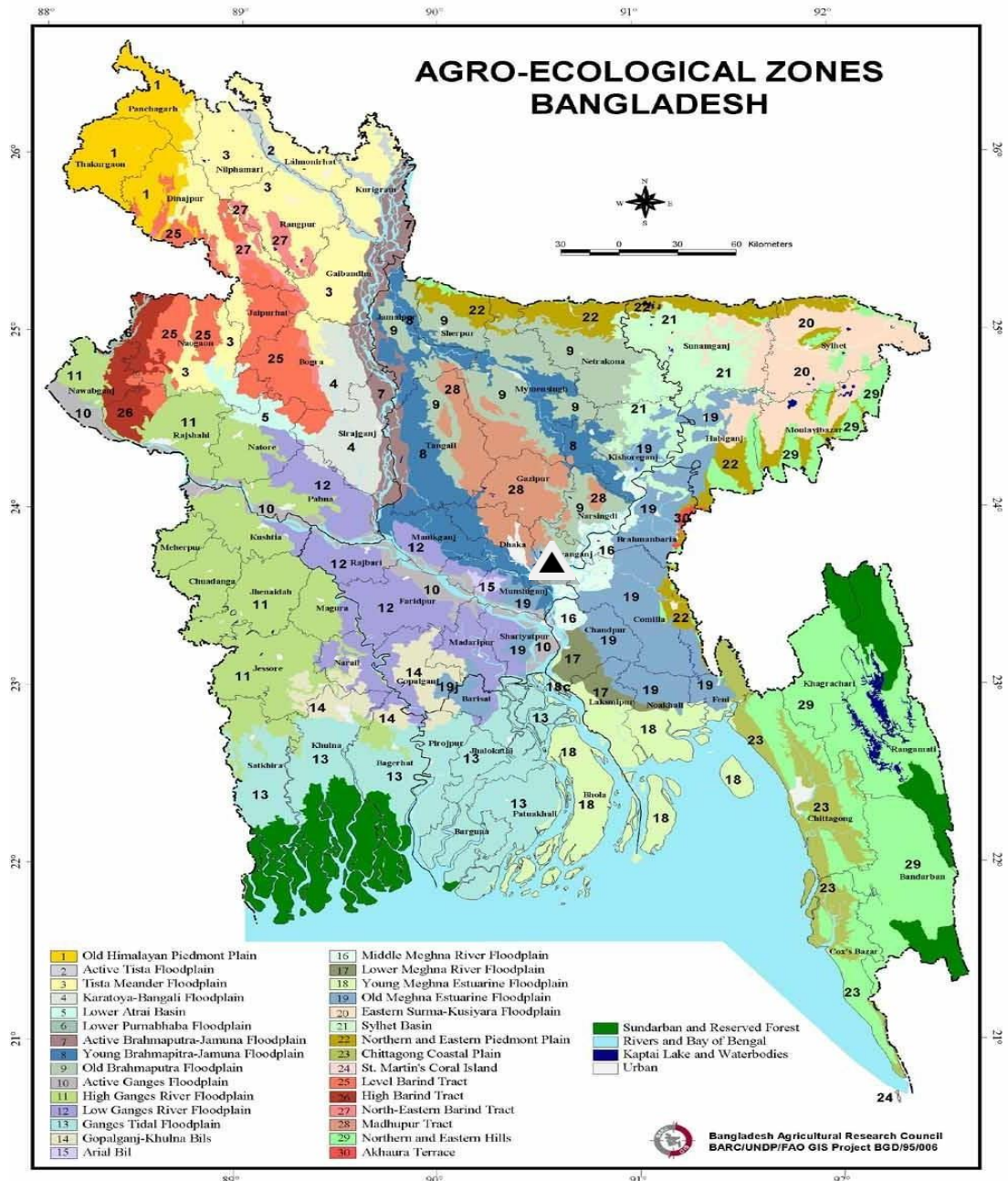
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APPENDICES

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.	2021	29.5	20.5	225	73	34.4	216
Dec.	2021	26.4	17	21.72	73	12.8	212
Jan.	2022	26	15.3	25.65	71	7.7	198
Feb.	2022	29.8	17.4	2360	64	28.9	225
Mar.	2022	34	21.3	27.6	62	65.8	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. The morphological, mechanical and chemical characteristics of soil of the experimental site as observed prior to experimentation (0 -15 cm depth).

A. Morphological characteristics of the experimental field

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

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 4. Mean data of 21 F₂ population of *Brassica juncea* L.

Genotype	Combination	DFF	D50%F	DSM	PH	NPB	NSB	SL	SPP	SPS	TSW	HI
G1	BINA7*Rye5	34.00	36.00	104.33	137.83	4.22	8.67	4.22	213.67	14.11	2.11	9.47
G2	BINA7*Daulat	42.00	44.00	109.67	143.33	4.67	7.33	5.33	189.00	15.00	3.82	9.97
G3	BINA7*BS10	37.00	41.33	108.00	159.33	6.00	11.00	4.66	227.78	14.08	2.38	9.47
G4	BINA7*BS16	38.00	37.00	106.00	158.00	5.33	12.00	4.45	287.56	14.00	2.56	13.87
G5	BINA7*BJ00	37.67	41.33	109.00	155.56	4.67	8.67	3.77	226.00	11.89	3.16	7.63
G6	BINA7*BS11	38.00	41.33	110.67	145.33	4.33	9.00	4.13	233.33	10.89	2.24	7.13
G7	Rye5*Daulat	34.00	36.33	105.33	136.22	4.33	6.33	4.22	195.11	12.44	2.31	8.47
G8	Rye5*BS10	43.00	43.00	106.33	172.00	7.00	13.34	4.40	274.33	10.92	2.19	8.57
G9	Rye5*BS16	34.00	38.00	107.67	136.67	4.67	10.00	4.79	211.44	12.89	2.89	10.47
G10	Rye5*BJ00	37.00	38.00	109.33	168.33	4.78	8.11	4.56	204.00	14.45	2.63	8.52
G11	Rye5*BS11	37.67	42.00	106.33	144.67	6.00	13.78	4.13	272.00	13.45	3.37	12.73
G12	Daulat*BS10	43.00	43.33	105.33	126.00	5.00	10.33	4.80	272.00	15.67	2.31	9.13
G13	Daulat*BS16	33.00	36.00	104.33	151.89	6.22	10.00	4.13	224.11	17.00	3.35	12.53
G14	Daulat*BJ00	33.00	36.67	107.67	132.89	3.89	8.89	5.13	189.33	12.66	2.56	7.97
G15	Daulat*BS11	37.00	38.67	105.33	128.78	5.00	10.78	4.89	233.17	14.00	2.48	8.97
G16	BS10*BS16	39.00	44.00	108.00	151.17	5.00	9.67	4.46	271.67	12.56	2.10	9.63
G17	BS10*BJ00	34.00	38.33	107.33	147.22	6.00	14.33	4.74	297.78	12.22	2.30	15.60
G18	BS10*BS11	37.00	37.67	106.00	143.56	6.44	11.34	4.60	271.33	14.33	2.54	11.63
G19	BS16*BJ00	39.00	48.00	110.33	140.33	4.33	10.67	4.73	239.44	11.78	3.80	12.30
G20	BS16*BS11	34.00	35.67	107.00	156.50	5.44	12.33	4.32	285.89	10.44	3.99	12.47
G21	BJ00*BS16	39.00	44.00	113.33	160.67	4.89	11.33	4.97	268.33	13.42	2.31	9.97

DFF=Days to first flowering, D50%F=Days to 50% flowering, DSM=Days to 80% maturity, PH= Plant height (cm), NPB=Number of primary branches per plant, NS=Number of secondary branches per plant, SL=Siliquae length (cm), SPP=Siliqua per plant, SPS=Seed per siliquae, TSW=1000 seeds weight (g), YPP=Yield per plant (g) and HI=Harvest index