GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN F_7 POPULATION OF *Brassica napus* L

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CERTIFICATE

*This is to certify that the thesis entitled, "**GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN F_7 POPULATION OF Brassica napus L**" submitted to the Faculty of Agriculture, Sher-e Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by JARIN FAIRUJ, Registration No. 15-06375 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2022
Place:Dhaka, Bangladesh

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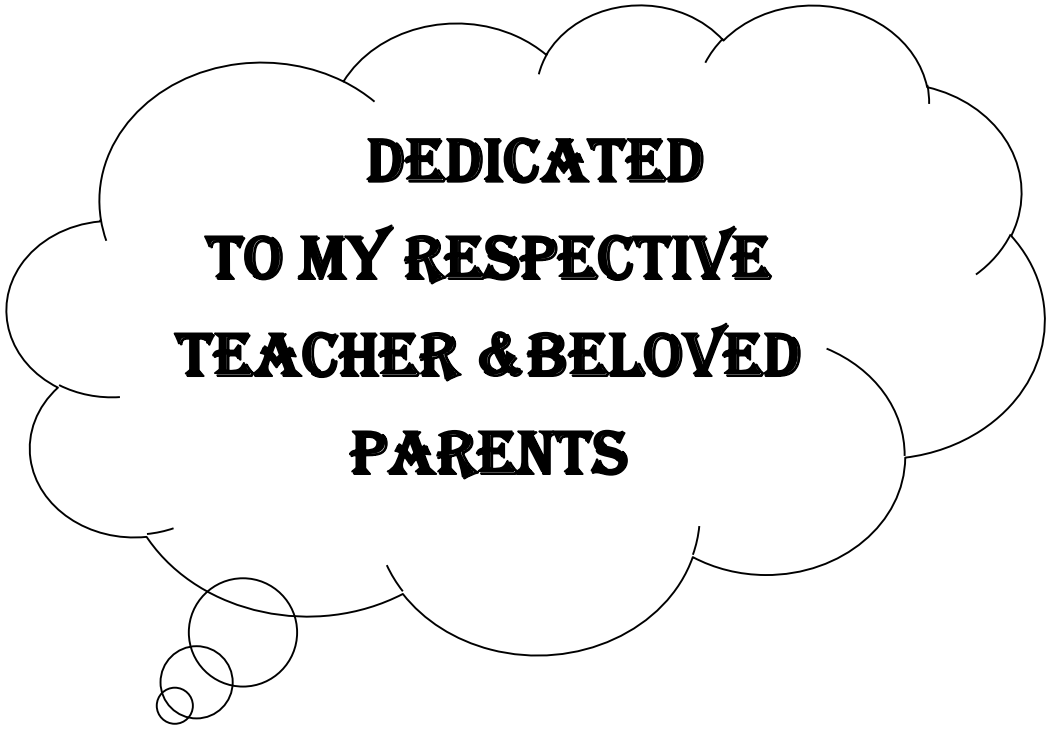
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TO MY RESPECTIVE
TEACHER &BELOVED
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GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN F_7 POPULATION OF *Brassica napus* L

By

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ABSTRACT

The experiment was conducted using 38 promising genotypes of *Brassica napus* L. during November 2019 to March 2020 at the experimental field of Sher-e Bangla Agricultural University, Dhaka. The study focused on correlation between eleven yield-contributing traits, direct and indirect impacts of several characters on yield per plant, heritability, genetic advance in order to evaluate genotypes. Significant differences were found for all of the variables after doing a variance analysis. Days to first flowering, number of primary branches per plant, number of secondary branches per plant, siliqua length (cm), seeds per siliquae, thousand seeds weight (g), and seeds yield per plant all showed the smallest difference between phenotypic and genotypic variation. The number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, and yield per plant all showed substantial genotypic and phenotypic coefficient of variation . The number of secondary branches per plant had the highest genotypic co-efficient of variation (42.39) and phenotypic co-efficient of variation (46.93). In number of siliqua per plant, high heritability (68.91) was combined with high genetic advance (55.72), indicating that this quality was under additive gene action and that selection for genetic improvement would be effective. In terms of correlation, the number of secondary branch per plant, siliqua length (cm), seeds per siliqua, and thousand seeds weight (cm) all had positive significant genotypic and phenotypic correlations with yield per plant. Days to 50% flowering (0.236), days to maturity (0.396), plant height (0.552), number of siliquae per plant (0.113), siliqua length (0.474), and seeds per siliquae (2.256) all had a positive and direct effect on yield per plant, indicating that they were the most important contributors to seed yield per plant. The path coefficient analysis was carried out using the correlation coefficient to determine direct and indirect influence. The most promising genotypes for a future research program were chosen after taking into account the genetic parameter, other agronomic characteristics, and the achievement of the objectives. These genotypes were G8, G9, G18, G21, and G14.

LIST OF CONTENTS

LIST OF TABLES

LIST OF TABLES (CONT'D)

LIST OF FIGURES

LIST OF PLATES

LIST OF PLATES (CONT'D)

LIST OF APPENDICES

SOME COMMONLY USED ABREVIATIONS

FULLWORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Agricultural	Agril.
And others	et al.
Accessions	ACC
Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Biological	Biol
Centimeter	cm
Co-efficient of Variation	CV
Ecology	Ecol.
Etcetera	etc.
Environmental variance	$\delta^2 e$
Figure	Fig.
Food and Agricultural Organization	FAO
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	$\delta^2 g$
Gram	g
Heritability in broad sense	$h^2 b$
Journal	J.
Kilogram	Kg
Meter	M
Mean Sum of Square	MSS
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta^2 p$
Randomized Complete Block Design	RCBD
Replication	R
Research	Res.
Science	Sci.
Sher-e-Bangla Agricultural University	SAU
Tripol super phosphate	TSP

CHAPTER I
INTRODUCTION

The family Brassicaceae, generally referred to as the mustard family, includes the significant oil seed crop known as *Brassica napus* L. Brassica vegetables include several types of seeds, as well as foods like cabbage, cauliflower, broccoli, and brussel sprouts. The genus is exceptional for having the highest number of significant horticultural and agricultural crops of any other genus. While many are annual or biennial, some are little shrubs.

Brassica plants have picked many scientists' interests because of their value in agriculture. By joining the chromosomes of three diploid species (*Brassica oleracea*, *Brassica nigra* and *Brassica rapa*), three significant species (*Brassica carinata*, *Brassica juncea*, and *Brassica napus*) are created as described by the Triangle of U theory.

Rapeseed (*Brassica napus* L.) is an amphidiploid (AACC genome, 2n=38) and inter-specific hybridization between diploid *Brassica rapa* L. (AA genome, 2n=20) and *Brassica oleracea* L. (CC genome, 2n=18) are liable for its production.

A large amount of energy and fat-soluble vitamins A, D, E, and K are also provided by it. Oil from oilseeds is used in both industrial and culinary applications. Vegetable fats and oils are an important part of the human diet. Animal-sourced oils are inferior to plant-sourced oils in terms of nutrients.

There are seven oilseed crops grown in Bangladesh but mustard alone occupies about 70% of the oilseed land. In Bangladesh the area under mustard cultivations are 814000 acres and the productions are 397000mT (BBS, 2021). In Bangladesh Comilla, Tangail, Jessore, Faridpur, Pabna, Rajshahi, Dinajpur, Kushtia, Kishoregonj, Rangpur and Dhaka are the major mustard growing districts (BBS, 2021). There is a huge chaos about the unexpected price hike of soybean oil. But we can easily turn Bangladesh into a self-dependent country in terms of edible oil production. In the good old days, even during in 1970s, mustard oil used to be main cooking oil here. The improved mustard seeds contain almost 39-44 per cent oil. Hence, improvement of yield and oil content are the major breeding objectives in case of mustard. It contains oleic acid, which is excellent for cooking oil because of its thermostability, and linoleic acid, which is desirable for nutritional reasons.

Though mustard is an important crop its production area is shrinking day by day due to long termed T. Aman and more holding boro rice. We could successfully grow it between the Aman and Boro rice rotations without changing the current cropping pattern if we can create new lines. After the harvest of Aman rice and before the transplantation of Boro rice, lands are open for the cultivation of gap-filling crops within 70–80 days. Therefore, in order to choose suitable mustard genotypes and increase our cropping intensity, we must develop short duration varieties and their responses.

The yield has a complicated nature and is reliant on numerous other physical qualities, most of which are inherited quantitatively. In order to focus more on the traits that have the biggest impact on seed yield, it is crucial to study the contributions of each attribute (Tuncturk and Ciftci, 2007). Numerous researchers have established the significance of genotypic and phenotypic variation, heritability, and character association for further genetic advancement (Ali *et al*., 2002). Additionally, Gosh and Gulati (2001) demonstrated that traits with high heritabilities are governed by additive genes and can be effectively used for plant selection based on phenotypic performance.

In general, correlation coefficients display correlations between variables and the degree of their linear relationships.

To decide on the appropriate selection criteria for a breeding program, it is crucial for plant breeders to understand the relationships between pairs of characteristics. The knowledge of genetic variability provides a reliable tool to the breeder for crop development. For breeders who want to increase Brassica output and quality, a higher genetic diversity and character association between yield and yield components are crucial criteria.

Therefore, the path coefficient analysis has been used by numerous researchers for a more and complete determination of impact of independent variable on dependent one. The path coefficient analysis helps the breeders to explain direct and indirect effects and widely used in breeding work in different crop species by various researchers (Ali *et al.,* 2013).

Considering the importance of developing a successful breeding program for further varietal improvement, an experiment was carried out with following

Objectives:

1. to study the variability among the F_7 populations
2. to find out the relationship among the different traits and their contribution to the yield and
3. to select promising genotypes considering early maturity and high yield.

CHAPTER II
REVIEW OF LITERATURE

Brassica napus is significant both economically and genetically because of its great nutritional value and market demand. As a result, the species of Brassica has gained a lot of attention in a number of its production and use-related areas. It is one of the most significant oil crops for several nations worldwide, including Bangladesh. With that in mind, various strategies are applied to various rapeseed kinds and cultivars in order to produce better results. Additionally, substantial research on Brassica breeding has been done in numerous nations in order to improve quality, yield, and its contributing characteristics. Numerous studies on the variability, correlation, and path analysis of the yield and the yield-contributing traits of Brassica that were carried out in various contexts are currently available. Environments have been created here to list the research's conclusions that apply to the current experiment. The entire review section has been broken into the following sections for the sake of this investigation:

2.1 Origin and geographical distribution

2.2 Genetic variability, heritability, and genetic advance

2.3 Correlation among different characters

2.4 Path co-efficient analysis

2.1 Origin and geographical distribution

Brassica sp. has been a matter of huge scientific interest because of their both agricultural importance and economical values. Six particularly Brassica species that have the highest agricultural importance are recognized as ‘crop Brassicas’. Primarily, *B. rapa* (AA, n=10), *B. nigra* (black mustard, BB, n=8) and *B. oleracea* (CC, n=9) these three ancestral diploid species have been existed. After that, through spontaneous hybridization followed by chromosome doubling, three amphidiploid species emerged, those are *B. napus* (AACC, n=19), *B. carinata* (BBCC, n=17), and *B. juncea* (AABB, n=18) as described by the Triangle of U-theory.

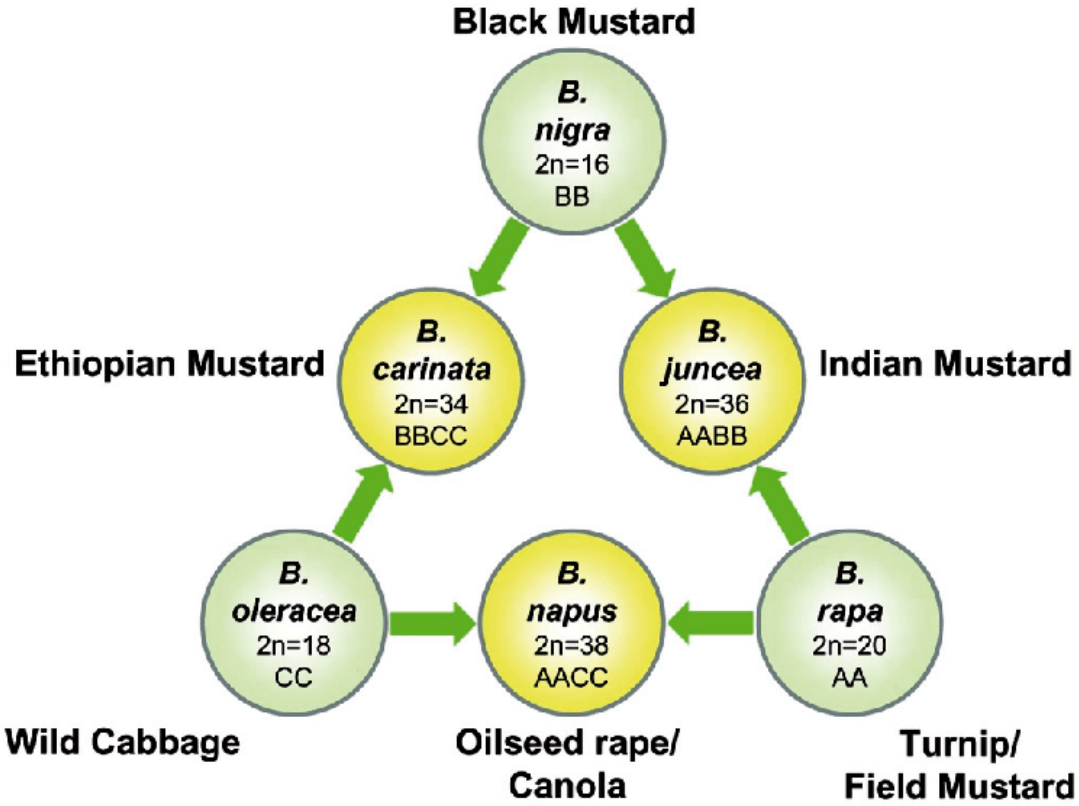

Plate 1. The "triangle of "U" diagram, representing the genetic relationships between the six species of the genus *Brassica.*

The genus is native to the wild in Western Europe, the Mediterranean and subtropical to temperate regions of Asia. In addition to the cultivated species, which are grown worldwide, many of the wild species produced as weeds, especially in North America, South America, and Australia. Reviewing the information and knowledge on performance of different genotypes, extent of genetic diversity, relationship among yield with other yield contributing characters, genotype-environmental relations, heritability, selection index and molecular marker-based analysis in mustard for yield and yield contributing characters are important for future breeding programs for developing short duration high yielding genotypes. It is necessary for us to take better steps for production and quality improvement of our local cultivars. In that respect, so many strategies and programs are conducted for the betterment of quality and yield of different varieties and cultivars to gain improved quality production. Due to application of different techniques in breeding process, remarkable improvement has been brought in productivity and quality of edible oil for using it in human diet. A huge number of

literary materials are available on variability, genetic diversity, correlation and path analysis of yield and yield contributing characters of Brassica grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. A reliable tool for crop development is provided to the breeder by knowledge of genetic variability. Breeders who want to increase Brassica production and quality must first meet two fundamental requirements: higher genetic variability and a link between yield and yield components. The degree to which different genotypes of the same trait tend to differ from one another is known as genetic variability. Variability, as opposed to genetic diversity, refers to the degree of variation within a given population. There are several books and articles accessible about the variation among *Brassica* spp.

2.2 Genetic variability, heritability and genetic advance

It is crucial to have knowledge of the genetic variation, heritability, and anticipated genetic progress of various traits in a group of mustard populations because it has been suggested that these genetic parameters are affected by the growing environment. The extent of genetic variation, heritability, and genetic advance for the same character was actually reported by different researchers. These genetic characteristics were also evaluated in this current research on mustard, and the results will be useful for breeding initiatives.

Walle *et al.* (2014); carried out a study with thirty-six genotypes of Ethiopian mustard (*Brassica carinata*) and result revealed that there was significant difference in days to 50% flowering, plant height and primary branches per plant. PCV has always been higher than GCV for all yield related characters studied. High heritability with high genetic advance was observed in plant height, number of secondary branches per plant and days to 80% maturity.

Aytac and Kinaci (2009) conducted an experiment with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for two years.

Mekonnen *et al.* (2014); evaluated thirty-six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The PCV ranged from 8.3% to 91.7% and GCV ranged from 4.3% to 44.14% . Comparatively high GCV estimates were observed for number of siliquae per plant, primary and secondary branches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in primary branches per plant. Higher GCV and PCV for seed yield, number of siliquae per plant, primary and secondary branches which indicated that, it might provide better scope for improvement through selection. Besides these, higher heritability along with higher genetic advance was observed in days to maturity, days to flowering, grain-filling period, number of siliquae per plant, secondary branches per plant, plant height, seed yield/plot and hectare and lowest one was in primary branches per plant.

Using 26 F_4 populations of certain intervarietal crosses of *Brassica rapa*, Alam (2010) conducted a study to examine the variations present in various traits for their heritability, genetic progress etc. Significant differences were built into those characters. Plant height, the number of primary and secondary branches per plant, number of siliquae per plant all demonstrated high heritability in conjunction with significant genetic advance and extremely significant genetic advance in percentage of mean. However, the length of the siliqua exhibited low heritability.

Sheikh *et al.* (2009) implemented research on the induction of genetic variability in Ethiopian mustard (*Brassica carinata*) for quality traits through inter-specific hybridization. The result revealed that inter-specific hybridization was used to increase the spectrum of genetic variability in mustard for edible oil with meal quality traits from quality lines of *Brassica juncea*.

Thakral (2004) reported significant variation in his study on variation for yield and yield contributing characters in rapeseed. They observed strong PCV and GCV for the characteristics of plant height and seed output.

For 36 genotypes of Indian mustard, Ghosh and Gulati (2001) investigated genetic variability and associations of yield components. For all the parameters except plant height, the genotypic and phenotypic coefficients of variability were high in magnitude. With the exception of plant height, all the examined features had small discrepancies between the PCV and GCV and good heritability's, demonstrating the value of phenotypic selection in enhancing these traits. The number of primary branches, the number of siliquae on the main shoot, the length of the main shoot, and the number of seeds per siliqua all showed strong heritability along with high genetic progress. This finding points to the significance of additive gene action for their inheritance.

While working with various *B. napus* strains, Malik *et al.* (2000) noted extremely high broad sense heritability (h2 b>90%) for the quantity of primary branches per plant, days to 50% flowering, and oil content . Additionally, they noted low heritability (50%) for plant height, siliquae number/plant, number of seeds/siliqua, and seed output.

An experiment in *Brassica napus* conducted and heritability was stidied by Afrin *et al.,* (2011) . The plant height showed the highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliqua, number of siliquae per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

2.3 Interrelationship of characters

In a breeding program, it is vital to analyze the link between various qualities. There are a lot of books on the relationships between the traits of Brassica spp. Here is a review of some of these texts:

The nature and strength of any relationship between any two quantifiable qualities can be ascertained using correlation coefficient analysis. It converts complicated relationships between events into a straightforward form of association. However, the measure of correlation does not take into account how much one variable depends on another. It is impossible to distinguish between pure correlation studies and the direct contribution of each component to the yield and the indirect effects it has due to its association with other components. For this study, path coefficient analysis is successful. It was first developed and described by Wright (1921), as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components.

According to research by Ejaz-Ul-Hasan *et al.* (2014), there is a strong and statistically significant phenotypic association between plant height and the number of seeds produced per plant in *Brassica napus*.

Uddin *et al.* (2013) carried out an experiment using *Brassica rapa* with seven parental and twenty-one F_2 progenies to study the correlation between various yield components. The results showed that the yield per plant had a high significant positive correlation with the number of primary branches per plant, secondary branches per plant, and siliqua per plant at both phenotypically and genotypically, as well as a significant positive correlation at genotypically with days to flowering and days to maturity.

Rameeh (2012) aimed at finding out the planting date effect on yield associated traits and also determining the variations of correlations among the traits in different planting dates of rapeseed genotypes. Significant planting dates and genotypes effect for phonological traits, yield components, seed yield and oil percentage revealed significant differences of planting dates genotypes for these traits. The variation of correlation between duration of flowering and siliquas per plant was less than the correlation of duration of flowering to other traits in different planting dates.

Maurya *et al*. (2012); carried out an experiment with one hundred genotypes of *Brassica juncea* and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50% flowering.

Twelve yield related traits in 15 genotypes of *B. napus* and *B. campestris* were studied by Kumar *et al*. (2009). For most characters studied, genotypic correlation coefficient was higher in magnitude than this corresponds phenotypic correlation coefficients. Seed yield was positively correlated with plant height and 1000 seed weight.

In an experiment Mahmud *et al.* (2008); found highly significant positive association of seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant.

Parveen (2007) conducted an experiment with F_2 population of *Brassica rapa* to study the correlation and observed that yield per plant had non-significant positive association with plant height, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant, days to 50% flowering and length of siliqua.

Akbar *et al.* (2007) evaluated eight advanced lines and two check variety of *Brassica juncea* in Pakistan and reported that siliqua per plant had strong positive correlation with the seed yield followed by plant height while no significant correlation with thousand grain weight was found. But significantly negative correlation was present in siliqua per plant and primary branches per plant.

Khan *et al*. (2006) conducted research on correlation for some quantitative traits relating to yield and quality in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2002-2003. Eleven accessions of *Brassica napus* L. along with DGL as a standard variety were studied. A wide range of genetic variation existed among all the characters under study except 1000-grain weight were found out by them. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). It was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. They also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

According to a study by Ghosh and Gulati (2001), seed yield showed a substantial positive correlation with yield-contributing features such plant height, the number of secondary branches, the number of siliquae on the main shoot, and oil content. These

elements showed a strong positive association with one another. These appeared to be the most important selection parameters for increasing seed yield in Indian mustard, and the results suggest that selection for one of these characters may automatically accumulate the other variables.

2.4 Path co-efficient analysis

The path analysis aids in identifying the features' direct and indirect contributions to yield. Wright (1921) created and originally characterized it as a tool for genetic analysis that separates the direct effects of the characteristics on yield through other components from their indirect impacts on yield. Here, a number of researchers that have researched the relationship between different traits in rapeseed and mustard and the direct and indirect effects of a variable over the dependent variable are discussed.

In the study of 14 genotypes of mustard, Afroz *et al*. (2004) found that the number of siliquae per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight, and number of siliquae shattering per plant all had the most direct beneficial influence on plant height.

Zahan, (2006) reported that siliquae/plant had positive direct effect on yield/plant. And days to 50% flowering had negative direct effect on yield/plant.

A study was conducted by Tusar *et al., (*2006) to assess the nature and extent of variability of 11 yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliquae per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Path coefficient analysis revealed that the number of siliquae per plant had the greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliquae per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive direct effect on yield, but its correlation with yield was insignificant and negative.

Parveen, (2007) conducted an experiment with F_2 population of *Brassica rapa* to study the path analysis and observed that number of seeds per siliqua showed the highest direct effect on yield per plant.

When working with five parental genotypes of *Brassica rapa* and their ten F_3 offspring, including reciprocals, Hosen's (2008) path co-efficient analysis showed that thousand seed weight had the highest positive direct effect, followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity, and number of seeds per siliqua.

Afrin *et al.*, (2011) studied with *Brassica napus* to identify the path co-efficient among the characters. The plant height had the highest positive and direct effect on seed yield per plant followed by number of siliquae per plant and siliqua length.

Uddin (2013) conducted an experiment with seven parental and twenty-one F_2 progenies of *Brassica rapa* to study path coefficient and reported that days to 50% flowering, number of primary branches per plant, number of 19 secondary branches per plant, number of siliquae per plant, siliquae length, seed per siliqua and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association.

Ejaz-Ul-Hasan *et al*., (2014) conducted an experiment on *Brassica napus* and studied path coefficient. The result revealed that the highest direct positive effect of seeds per plant on yield followed by days to maturity, days to flowering, seeds per siliqua, siliqua length and thousand seed weight while plant height had direct negative effect on the yield per plant.

Siddikee, (2006) conducted and experiment on oleiferous *Brassica campestris* L. to study the path analysis and revealed that thousand seed weight had the highest positive direct effect on seed yield per plant.

Sharafi *et al.* (2015); were evaluated 28 winter rape seed cultivars and results showed that number of siliquae per plant, number of seeds per siliqua, and 1000 seed weight had positive direct effect on seed yield.

CHAPTER III

MATERIALS AND METHOD

This portion contains the information involved to the research methodology that was done in this experiment. It bears a short illustration of the location of the experimental site, climatic condition, characteristics of soil, planting materials, preparation of main field, layout and design of the experiment, manuring and fertilizing, seed sowing, intercultural operations, harvesting, data recording procedure, and statistical analysis etc.

3.1 Experimental period

The experiment was conducted during the period from 12 November 2019 to March 2020 (Rabi season).

3.2 Experimental site

The research work was conducted in the research field of Sher-e-Bangla Agricultural University, Dhaka-1207.

3.3 Geographical location

The research work was done 23°74' N latitude and 90°35' E longitude with an elevation of 8 meter from sea level (Anonymous, 2014). The experimental field belongs to AEZ-28, the Agro-ecological zone called the Madhupur tract. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.4 Climatic and soil condition

The experimental site was placed in the subtropical climatic zone. The data on temperature, humidity and rainfall during the time of experiment were collected from the Bangladesh Meteorological Department, Agargaon, Dhaka and noted in Appendix II. Clay loam soil with common fine to medium noticeable dark yellowish-brown mottles had an olive gray color and a clay loam texture. The organic carbon content is 0.82% and the pH ranges from 5.47 to 5.63. Appendix III details the physicochemical characteristics of the soil of experiment site.

3.5 Planting materials

Total thirty eight mustard genotypes were used for this research. The genetically pure seeds of these genotypes were collected from Sher-e-Bangla Agricultural University (SAU), Department of Genetics and Plant Breeding.

The purity and germination percentage were tested as around 80 to 100. The experimental genotypes are showed in Table 1.

Table 1. List of genotypes along with their sources

SL NO.	Genotypes Name	Accession Code	Source
1	G1	Nap9908 × Nap206	SAU
2	G2	Nap205 × Nap2037	SAU
3	G3	Nap248 × Nap9904	SAU
4	G4	Nap9908 × Nap2012	SAU
5	G5	Nap9905 × Nap206	SAU
6	G6	BS-13 × Nap2066	SAU
7	G7	Nap205 × Nap2013	SAU
8	G8	Nap248 × Nap0130	SAU
9	G9	Nap108 × Nap206	SAU
10	G10	Nap 9908 × Nap2037	SAU
11	G11	Nap248 × Nap2037	SAU
12	G12	Nap205 × Nap2022	SAU
13	G13	Nap248 × Nap206	SAU
14	G14	B-13 × Nap179	SAU
15	G15	B-13 × Nap0130	SAU
16	G16	Nap248 × Nap9901	SAU
17	G17	Nap205 × Nap0130	SAU
18	G18	Nap108 × Nap2057	SAU
19	G19	BS-13 × Nap2013	SAU
20	G20	Nap9908 × Nap2057	SAU
21	G21	B-13×Nap2022	SAU
22	G22	B-13×Nap2012	SAU
23	G23	Nap9908 × Nap0130	SAU
24	G24	Nap9908 × Nap9901	SAU
25	G25	Nap205 × Nap2037	SAU
26	G26	BS-13 × Nap9901	SAU
27	G27	B-13 × Nap0130	SAU
28	G28	BS-13 × Nap2001	SAU
29	G29	Nap 9905 × Nap2037	SAU
30	G30	Nap248 × Nap2012	SAU
31	G31	Nap9905 × Nap2001	SAU
32	G32	Nap205 × Nap179	SAU
33	G33	Nap9906 × Nap206	SAU
34	G34	Nap205 × Nap206	SAU
35	G35	Nap205 × Nap940061	SAU
36	G36	Nap9906 × Nap0136	SAU
37	G37	B-13 × Nap2937	SAU
38	G38	B-13 × Nap2057	SAU

3.6 Land preparation

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

3.7 Application of manures and fertilizers

Urea, Triple Super Phosphate (TSP), Muriate of potash (MOP), Gypsum, Zinc oxide and Boric acid were applied to the field at proper rate and proper time. The half amount of urea, total amount of Cowdung, TSP, MOP, Gypsum, Zinc Oxide and Boric acid were applied during final land preparation as basal dose. The remaining amount of urea was applied as top dressing 25 days after sowing.

3.8 Design and layout of the experiment

After final land preparation field lay out was carried out. The study was performed in Completely Randomized Block Design (RCBD) with three (3) replications The total area of the experiment was 19m×13m = 247m^2. Each replication size was 19m×3m and distance between replication to replication was 1m. The spacing between line to line was 30cm and plant to plant was 10 cm.

Table 2. List of fertilizers and manures with doses and procedures of application

Sl. No.	**Fertilizers/ manures**	**Dose**		**Procedures of application**
		Applied in the plot	**Quantity/ha**	
1	Cowdung	150kg	5 ton	As basal
2	Urea	7 kg	250 kg	50% basal and 50% at the time of flower initiation
3	TSP	4.5kg	170 kg	As basal
4	MOP	2.5 kg	75 kg	As basal
5	Gypsum	4 kg	150 kg	As basal
6	ZnO	80g	3kg	As basal
7	Boric acid	300g	10 kg	As basal

3.9 Seed sowing

By avoiding the empty seeds, pure and healthy seeds were chosen. In November 2019, seeds were planted along rows in the experimental plots, keeping the soil depth at 1.5 cm. After sowing, the seeds were carefully covered with dirt to ensure that there were no clods that would prevent the seeds from germinating. Three to four days after seeding, seed germination began. The pictorial view of experimental field during seed sowing is presented in plate 2 and the pictorial view of experimental field during tagging is shown in plate 3.

3.10 Irrigation and drainage

After the seeds were sown, irrigation was applied with a sprinkler to keep the soil's proper moisture level and guarantee uniform seed germination. Second watering was administered before the flowering process began (22 DAS). When the pod emerged 40 days after sowing, the third irrigation was administered. Sixty days after planting, as the seeds started to form pods, a fourth irrigation was applied. To remove the extra water, a good drainage system was kept up. When irrigation was being done, extra caution was needed to avoid the water pressure.

3.11 Intercultural operations, insect and disease control

To guarantee that the plants grew and developed normally, several intercultural operations were carried out, such as thinning and weeding. The initial weeding was completed after fifteen days of seeding. Thinning was done simultaneously to preserve 10 cm between plants and 30 cm between lines. The second round of weeding was completed twenty-five days after sowing. There were no notable pest or disease. The pictorial view of experimental field during weeding is presented in plate 5.

Plate 2. The pictorial view of experimental field during seed sowing

Plate 3. The pictorial view of experimental field during tagging

Plate 4. The pictorial view of experimental field during growth stage

Plate 5. The pictorial view of experimental field during weeding

3.12 Crop harvesting

Depending on the maturity, harvesting took place March, 2020. The crop was judged to be mature when 80% of the plants showed signs of maturity, such as straw-colored siliquae, leaves, stems, and desirable seed color in the matured siliqua. From the progressed lines in each replication, ten plants were chosen at random for morphological study and analysis. The plants were uprooted and collected after being properly labelled. Data on many factors were gathered from these plants. The pictorial view of experimental field during pre-harvesting is presented in plate 5.

Plate 6. Pictorial view of a plant showing flowering

3.13 Data collection

Eleven characteristics of ten plants, including days to first flowering, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliquae, number of seeds per siliqua, thousand seed weight and seed yield per plant, were taken into consideration for the study of various genetic parameters and their interaction.

Plate 7. The pictorial view of experimental field during supervision by supervisor

3.14 Data collection methods

The data were recorded on ten selected plants from 38 F_7 population on the following parameters-

3.14.1 Days to 1st flowering

Days to 1st flowering were recorded from sowing date to the date of 1st flowering of every entry.

3.14.2 Days to 50% flowering

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

3.14.3 Days to maturity

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

3.14.4 Plant height (cm)

This measurement was taken in centimeter (cm) from the base of the plant to the tip of the longest inflorescence.

3.14.5 Number of primary branches per plant

The total number of branches arisen from the main shoot of a plant was counted as the number of primary branches per plant.

3.14.6 Number of secondary branches per plant

The total number of branches arisen from the primary branch of 10 randomly selected plant was counted as the number of secondary branches per plant.

3.14.7 Number of siliquae per plant

Total number of siliquae of each 10 randomly selected plant was counted and averaged and considered as the number of siliquae per plant.

3.14.8 Siliquae length (cm)

This measurement was taken in centimeter (cm) from the base to the tip of a siliqua of the five representative siliquae.

3.14.9 Number of seeds per siliqua

Well filled seeds were counted from five siliquae and averaged which was considered as the number of seeds per siliqua.

3.14.10 Thousand seeds weight (g)

Ten plants from each cross were selected. Weight in grams of randomly counted thousand seeds of each entry was recorded.

3.14.11 Yield per plant (g)

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

3.15 Statistical analysis

To investigate the mustard genotype in relation to yield and yield-contributing traits, the gathered data from 38 genotypes for various characters were statistically evaluated. Using the R software (variability, agricolae), the analysis of variance (ANOVA), mean values for all the characters, and the statistically significant difference between the treatment means were calculated.

3.15.1 Analysis of variance (ANOVA)

In order to evaluate the genetic variability, the analysis of variance (ANOVA) for each character was evaluated individually using mean data. Using the F test, the level of significance was estimated at 5% and 1%.

Source of variation	**df**	**MSS**	**EMSS**	**F-Ratio**
Replication (r)	r-1	M1		M1/M3
Genotypes (g)	g-1	M2	$\delta e^2+\delta g^2$	M2/M3
Error (e)	(r-1)(g-1)	M3	δe^2	

Where,

r = Number of replications

g = Number of genotypes

df = degree of freedom

MSS = Mean sum of square

EMSS = Expected values of MSS

3.15.2 Estimation of variability parameters

Genotypic and phenotypic variations were calculated using the following formula from Johnson *et al.* (1955):

- **Genotypic variance,**

$$\sigma_g^2 = \frac{\text{MSG}-\text{MSE}}{\text{r}}$$

Where,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

- **Phenotypic variance**,

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

σ_p^2= Phenotypic variance

σ_g^2= Genotypic variance

σ_e^2= Environmental variance = Mean square of error

3.15.3 Estimation of genotypic and phenotypic coefficient of variation

The following formula is used to determine the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for each character. Burton provided the formula in 1952:

$$\text{GCV} = \frac{\sigma_g \times 100}{\bar{x}}$$

$$\text{PCV} = \frac{\sigma_p \times 100}{\bar{x}}$$

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

Phenotypic and genotypic coefficients of variation are classified as follows by Sivasubramanian and Madhavamenon (1973)

- Low (0-10%),
- Moderate (10-20%) and
- High (>20%)

3.15.4 Estimation of heritability in broad sense

Singh and Chaudhary proposed the following formula to calculate broad sense heritability (1985).

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where, h^2_b=Heritability in broad sense

σ^2_g= Genotypic variance

σ_p^2 = Phenotypic variance

3.15.5 Estimation of genetic advance

The formula provided by Allard (1960) was used to calculate the projected genetic advance for the various study characters:

$$GA = \frac{\sigma_g^2}{\sigma_p^2} . K . \sigma_p$$

Where,

GA = Genetic advance

σ_g^2 = Genotypic variance

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

K= Standard selection differential which is 2.06 at 5% selection intensity.

3.15.6 Estimation of genetic advance in percentage of mean

Comstock and Robinson (1960) provided the following formula to estimate genetic advance as a percentage of the mean:

GA in percent of mean = $\frac{\text{GA}}{\text{Grand mean}} \times 100$

Johnson *et al.* (1955) suggested the following categories of genetic advance in percent of mean:

- Less than 10% as- Low
- 10-20% as -Moderate and
- More than 20% High

3.15.7 Correlation coefficient analysis

The correlation coefficients were calculated to determine the degree of association between various features and yield. The variance and covariance components were used to calculate the genotypic and phenotypic correlation coefficients between fifteen characters, following the advice given by Al-Jibouri *et al* (1958).

$$r_g(xy) = \frac{Cov_g\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$$

$$r_p(xy) = \frac{Cov_p\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$$

Where,

$r_g(xy)$- The genotypic correlation coefficient and

$r_p(xy)$- The phenotypic correlation coefficient.

Cov_g & Cov_p are the genotypic and phenotypic covariance of xy, respectively.

σ^2_g & σ^2_p and are the genotypic and phenotypic variance of x and y, respectively.

The estimated value of "r" was compared with the table "r" value with n-2 degrees of freedom at a 5% and 1% level of significance, where "n" stands for the number of observational pairs. As a result, relevant statistical analysis was performed on the data from a variety of experimental goals in order to make defensible conclusions on the genetic divergence of mustard genotypes.

3.15.8 Path coefficient analysis

The method described by Dewey and Lu (1959), which was also cited by Singh and Chaudhary (1985) and Dabholkar (1992), involved doing Path coefficient analysis

using straightforward correlation values. In route analysis, the dependent variable's direct and indirect independent variables are divided by the correlation coefficient.

ryx1 = Pyx1 + Pyx2rx1x2 + Pyx3rx1x3

ryx2 = Pyx1rx1x2 + Pyx2 + Pyx3rx2x3

ryx3 = Pyx1rx1x3 + Pyx2rx2x3 + Pyx3

Assuming that x1, x2, and x3 all give y, a set of simultaneous equations (three equations in this example) must be stated as follows in order to evaluate the direct and indirect effects of the linked characters:

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

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

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

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

The residual effect (R) of the characters was determined by applying the following formula after determining their direct and indirect effects (Singh and Chaudhary, 1985):

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

Where,

$P_{RY}^2 = (R^2)$

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$

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

r_{iy}=Correlation of the character with yield

Categories:

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

CHAPTER IV
RESULTS AND DISCUSSION

The goal of the current experiment was to examine variation among 38 populations of *B. napus*. The study aimed to determine the phenotypic, genotypic, and environmental variance, phenotypic and genotypic coefficient of variation, heritability, genetic advance, genetic advance in percent of mean, correlation coefficient, and path coefficient. The data were recorded on the basis of different characters such as days to first flowering, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length (cm), seeds per siliqua, thousand seeds weight (g) and seeds yield per plant (g). of 38 populations of *B. napus*. The data were statistically analyzed and thus acquired results are described below under the following headings:

4.1 Genetic variability of the populations
4.2 Heritability, genetic advance and genetic advance in percentage of mean
4.3 Correlation analysis
4.4 Path coefficient analysis

4.1 Genetic variability of the genotypes

The results of the analysis of variance of the various yield-contributing traits of 38 populations of *Brassica napus* L. are shown in Table 3. Depending on the level of genetic variability existing in the population, crop enhancement programs will either succeed or fail. The degree of genetic variability can influence how quickly and how much a population will improve genetically through selection or hybridization followed by selection. Table 4 displays the average value of each of the eleven characters of 38 F_7 genotypes which represents presence of variation. It also reflects genotypic variance, which measures the magnitude of variation resulting from differences within genotypic values and phenotypic variance measures the magnitude of variation coming out of differences in phenotypic values.. Numerous researchers, including Shalini *et al.* (2000), Thakral *et al.* (2004), Uddin *et al.* (2005), Khan *et al.* (2006), Parveen (2007), Zebarjadi *et al.* (2011), and Walle *et al*. (2014), found significant variations between the genotypes.

Table 3. Analysis of variance for eleven characters of 38 genotypes of *Brassica napus*

Characters	Mean sum of square			CV (%)
	Replication (r-1) = 2	Genotype (g-1) = 37	Error (r-1) (g-1) = 74	
DFF	2.01	10.01**	2.24	5.37
DFPF	0.64	41.36**	3.86	5.6
DM	4.90	39.49**	6.98	2.88
PH	46.18	483.72**	67.87	6.73
NPBP	2.38	7.48**	0.88	21.29
NSBP	0.06	10.21**	0.71	20.12
NSPP	1547.96	7996.44**	1045.42	21.89
SL	0.10	2.73**	0.18	5.11
SPS	19.26	28.26*	16.07	15.94
TSW	0.54	1.68**	0.14	8.76
SYPP	0.76	10.76**	0.17	6.55

*, 5% level of significance **, 1% level of significance
DFF=Days to first flowering, DFPF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seed yield per plant (g), CV= Coefficient of variation

Table 4. Mean analysis of yield and yield contributing parameters of 38 genotypes of *B. napus*

Genotype	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	SYPP
G1	25.33jk	32.33k-m	94.33a-e	138.00 b	3.33i-l	3.55g-j	148.67d-k	8.37g-m	22.94c-i	5.58ab	7.06hi
G2	25.33jk	32.67k-m	87.67hi	101.33l-n	3.67h-l	3.77f-i	268.83ab	8.70f-i	29.57ab	4.85d-g	9.16ab
G3	28.33c-h	42.67a	82.67j	121.70c-j	3.00j-l	1.53mn	193.67cd	7.87l-o	29.22a-c	5.50a-c	8.51b-d
G4	30.33a-c	31.67lm	94.00a-e	128.47b-g	4.33g-j	2.80i-m	174.67de	7.90k-o	23.71a-i	4.43d-i	7.11hi
G5	27.67d-j	32.33k-m	94.00a-e	114.67h-l	2.50kl	7.53a	144.90d-l	8.87e-i	27.43a-g	4.48d-i	8.46c-e
G6	27.33e-j	32.33k-m	93.33a-g	129.47b-g	2.83j-l	2.23j-n	194.00cd	8.90d-h	27.87a-f	4.97b-e	8.84bc
G7	25.33jk	31.33lm	94.00a-e	99.33n	2.80kl	2.13k-n	166.63d-f	8.20i-m	20.40ij	4.38e-i	4.68o-r
G8	24.33k	31.00lm	87.00i	121.33d-j	3.00jkl	4.47e-h	153.23d-i	8.40g-m	28.21a-e	3.25jk	5.46l-n
G9	25.67i-k	30.67m	93.67a-f	128.00b-h	4.33g-j	1.83l-n	132.00e-m	8.23h-m	28.57a-d	5.01b-d	9.58a
G10	29.33a-e	32.33k-m	95.00a-c	123.00c-i	4.33g-j	2.63i-m	228.10bc	9.57b-d	24.56a-i	4.60d-h	7.16g-i
G11	28.00c-i	32.33k-m	94.00a-e	129.27b-g	3.33i-l	2.70i-m	297.10a	9.47b-e	23.68a-i	4.51d-h	6.65ij
G12	29.00a-f	32.33k-m	95.67ab	102.67l-n	2.67kl	5.13c-f	112.17g-m	9.13b-f	27.48a-g	4.57d-h	8.80bc
G13	30.33a-c	31.67lm	94.33a-e	124.17c-i	3.00jkl	2.17k-n	136.67e-l	9.60bc	23.30b-i	4.30f-i	5.23l-o
G14	29.00a-f	40.67a-d	97.00a	103.00l-n	8.33a	2.27j-n	297.33a	9.67b	30.01a	5.93a	9.61a
G15	29.33a-e	41.33a-c	94.00a-e	118.97f-j	3.17i-l	5.00c-f	98.00j-m	8.97c-g	27.01a-h	4.30f-i	4.62op-r
G16	31.33a	42.33ab	91.33c-h	113.00i-m	4.00h-k	1.97k-n	109.33g-m	7.97j-n	26.16a-i	4.10hi	4.17q-s
G17	30.00a-d	39.33b-e	89.67f-i	122.67c-i	3.17i-l	2.20j-n	97.67k-m	8.67f-i	26.64a-i	4.63d-h	5.47l-n
G18	28.00c-i	35.33g-k	81.33j	109.00j-n	4.33g-j	3.17h-l	122.67e-m	7.10q-t	27.78a-g	4.29fg-i	4.60o-r

DFF=Days to first flowering, DFPF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seed yield per plant (g)

Table 4. (Cont'd.)

Genotype	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	SYPP
G19	28.67b-g	36.00f-j	81.67j	132.10b-f	2.33l	1.23n	82.93m	6.47t	14.41j	2.48l	3.69s
G20	27.67d-j	36.33e-i	90.67d-i	133.43b-d	3.33i-l	4.33e-h	135.90e-l	7.83l-p	27.01a-h	4.63d-h	8.07d-f
G21	31.00ab	40.33a-d	89.67f-i	161.70a	7.00a-d	6.00b-d	112.83g-m	8.43g-l	23.72a-i	3.87ij	4.30q-s
G22	31.33a	43.33a	94.67a-d	124.67b-i	4.67f-i	5.00c-f	129.00e-m	9.77b	24.30a-i	4.53d-h	4.11rs
G23	28.33c-h	37.00e-h	92.67b-g	124.10cd-i	4.33g-j	3.33g-k	139.00e-l	10.60a	20.76h-j	4.37e-i	8.90bc
G24	29.00a-f	38.67c-f	89.33g-i	133.17b-e	6.00c-f	7.33ab	115.67f-m	6.67r-t	22.60d-i	2.79kl	4.46p-r
G25	29.00a-f	37.67d-g	93.33a-g	127.77b-h	6.33b-e	7.00ab	117.50f-m	8.43g-l	26.87a-i	4.53d-h	5.70kl
G26	26.00h-k	34.00h-l	94.33a-e	134.77bc	3.67h-l	6.33a-c	144.33d-l	7.73m-q	26.80a-i	4.23g-i	5.50lm
G27	25.33jk	33.00j-m	94.33a-e	116.47g-k	5.00e-h	5.33c-e	107.67h-m	7.17p-s	24.93a-i	2.73kl	4.82n-q
G28	26.67f-k	31.67lm	91.33c-h	123.87c-i	5.67d-g	6.00b-d	160.83d-g	8.63f-j	21.86e-i	4.63d-h	7.79e-g
G29	29.33a-e	36.67e-h	92.67b-g	119.77e-j	5.67d-g	7.333ab	101.11i-m	7.37n-q	26.813a-i	4.64d-h	6.27jk
G30	27.00e-j	36.33e-i	92.33b-g	132.40b-e	7.33a-c	2.83i-m	118.33f-m	8.77f-i	26.31a-i	4.10hi	7.67f-h
G31	26.33g-k	35.33g-k	91.33c-h	104.13k-n	6.00c-f	6.00b-d	149.67d-k	8.60f-j	24.43a-i	4.30f-i	3.76s
G32	27.00e-j	32.33k-m	94.00a-e	121.33d-j	7.67 ab	7.33ab	137.33e-l	8.80e-i	25.37a-i	4.03hi	4.53p-r
G33	27.00e-j	37.00e-h	92.67b-g	100.10mn	7.00a-d	5.33c-e	150.00d-k	7.17p-s	21.43f-i	4.47d-i	5.01m-p
G34	26.00h-k	33.33i-m	93.33a-g	125.30b-i	3.33i-l	4.00e-i	140.33e-l	6.53st	25.85a-i	4.53d-h	4.66op-r
G35	26.00h-k	33.33i-m	90.33e-i	128.00 b-h	4.00h-k	5.00c-f	150.33d-j	7.23o-r	24.54a-i	4.90c-f	9.03a-c
G36	27.67d-j	32.67k-m	91.67b-h	112.50i-n	4.33g-j	4.67d-g	156.83d-h	8.57f-k	25.17a-i	4.30f-i	7.01hi
G37	27.67d-j	31.67lm	93.00a-g	129.13b-g	4.00h-k	4.00e-i	94.00lm	7.47n-q	21.34g-i	2.57l	4.15rs
G38	28.33c-h	32.00lm	93.33a-g	138.07b	3.67h-l	4.00e-i	94.67lm	8.37g-m	26.80a-i	4.43d-i	5.71kl

DFF=Days to first flowering, DFPF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seed yield per plant (g)

Table 4. (Cont'd.)

Genotype	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	SYPP
Min	24.33	30.67	81.33	99.33	2.33	1.23	82.93	6.47	14.41	2.48	3.69
Max	31.33	43.33	97.00	161.70	8.33	7.53	297.33	10.60	30.01	5.93	9.61
Mean	27.87	35.18	91.70	122.80	4.45	4.21	149.85	8.33	25.01	4.33	6.34
SE	1.22	1.60	2.16	6.73	0.77	0.69	26.40	0.35	3.27	0.31	0.34
LSD	2.44	3.19	4.30	13.40	1.53	1.37	52.60	0.69	6.52	0.62	0.67

DFF=Days to first flowering, DFPF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seed yield per plant (g)

Table 5. Estimation of genetic parameters in eleven characters of 38 genotypes of *Brassica napus*

Parameters	Mean	σ^2p	σ^2g	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic Advance (5%)	Genetic Advance (% of mean)
DFF	27.88	4.83	2.59	2.24	7.88	5.77	2.11	53.57	2.43	8.70
DFPF	35.09	16.36	12.50	3.86	11.53	10.08	1.45	76.43	6.37	18.15
DM	91.83	17.82	10.84	6.98	4.60	3.58	1.01	60.80	5.29	5.76
PH	122.39	206.49	138.62	67.87	11.74	9.62	2.12	67.13	19.87	16.24
NPBP	4.41	3.08	2.20	0.88	39.83	33.66	6.17	71.42	2.58	58.59
NSBP	4.20	3.88	3.17	0.71	46.93	42.39	4.53	81.61	3.31	78.90
NSPP	147.73	3362.43	2317.01	1045.42	39.25	32.58	6.67	68.91	82.31	55.72
SL	8.32	1.03	0.85	0.18	12.21	11.09	1.12	82.49	1.73	20.75
SPS	25.15	20.14	4.06	16.07	17.84	8.01	9.83	20.17	1.86	7.41
TSW	4.34	0.66	0.51	0.14	18.69	16.50	2.18	78.00	1.30	30.03
SYPP	6.32	3.70	3.53	0.17	30.42	29.71	0.71	95.37	3.78	59.76

σ^2p: Phenotypic variance
σ^2g: Genotypic variance
σ^2e: Environmental variance
PCV: Phenotypic coefficient of variation
GCV: Genotypic coefficient of variation
ECV: Environmental coefficient of variation
GA (5%): Genetic advance
GAM: Genetic advance (% of mean)
CV (%) = coefficient of variation

4.1.1 Days to first flowering

Highly significant variation was found among the genotypes in case of days to first flowering with the mean sum of square 10.01** (Table 3). It was varied from 24.33 days to 31.33 days with a mean value of 27.87 days (Table 4). The highest duration for days to first flowering was recorded in G22 and G16 (31.33 Days) followed by G21 (31.00Days), G13 (30.33 Days) and G17 (30.00 Days) where G8 required 24.33 Days to take first flowering, the lowest among the genotypes (Table 4). The phenotypic variance was (4.83) slightly higher than the genotypic variance (2.59) and genotypic and phenotypic coefficient of variations were 5.77 and 7.88, respectively (Table 5). This minor difference between phenotypic and genotypic coefficient of variation explored that the present variation was mainly contributed by the genotypes as the environmental influences were negligible.

4.1.2 Days to 50% flowering

Highly significant variations were observed in days to 50% flowering among the 38 advanced populations of *B. napus* (41.36**) (Table 3). The minimum duration to days to 50% flowering was found in G9 with 30.67 days followed by G28 and G37 with 31.67 days indicating that 50% flowers appeared earlier in G9, G28 and G37 than other advanced populations after sowing. The earliness of 50% flowering of population indicated that the plants matured early. G22 took maximum period for 50 % flowering with 43.33 days (Table 4). Mean value was recorded as 35.18 days. Pictorial view of a plant showing flowering is presented in plate 8. *Ali et al.* (2002) found days to 50% flowering for parents which was ranged from 39 to 46 days. The phenotypic variance (16.36) was higher than genotypic variance (12.50) and difference between them was moderate indicating that environment had moderate influence for the expression of the character (Table 5). The Genotypic coefficient of variation and Phenotypic coefficient of variation were moderate with value of 10.08 and 11.53per cent, respectively (Table 5)

Plate 8. The pictorial view of experimental field during pre-harvesting

4.1.3 Days to maturity

The mean sum of squares for days to maturity was 39.49** which indicates high amount of variation among the genotypes (Table 3). The average days required to be matured of the siliqua was 91.70 ranged from 81.33days to 97.00 days (Table 4). For days to maturity, 97.00 days were required for G14 which was the highest duration for days to followed by G12 (95.67 DAS), however, the lowest days to siliqua maturity was observed in G18 (81.33 DAS) followed by G19 and G3 required 81.67 and 82.67 DAS respectively (Table 4). Mean performance of days to maturity in 38 genotypes of *B. napus* is shown in Figure 1 through line graph. Days to siliqua maturity exhibited moderate genotypic variance (10.84) and phenotypic variance (17.82) along with lower phenotypic coefficient of variation (4.60) and genotypic coefficient of variation (3.58). Difference between phenotypic variance and genotypic variance indicating environmental factors slightly influenced in the expression of this trait. (Table 5; Figure 9).

4.1.4 Plant height (cm)

Considerable variation among the genotypes was observed in plant height. ANOVA revealed the mean sum squares for plant height was 483.72** (Table 3). The maximum plant height was 161.70 cm and the lowest was 99.33 cm (Table 4) with a mean value of 122.80. The highest plant height was observed in G21 (161.70 cm) followed by G38 (138.07 cm) and G1 (138.00 cm). The lowest plant height was found in G7 (99.33 cm) (Table 4). Mean performance of plant height in 38 genotypes of *B. napus* is shown in Figure 2 through line graph. For plant height, genotypic and phenotypic variance was recorded as 138.62 and 206.49 respectively (Table 5) with a high environmental influence (67.87). The highest genotypic, phenotypic and environmental variances were observed in plant height as reported by Khan *et al.,* (2013). Phenotypic and genotypic coefficient of variation for this trait was moderate 11.74 and lower 9.62 respectively (Table 5; Figure 9).

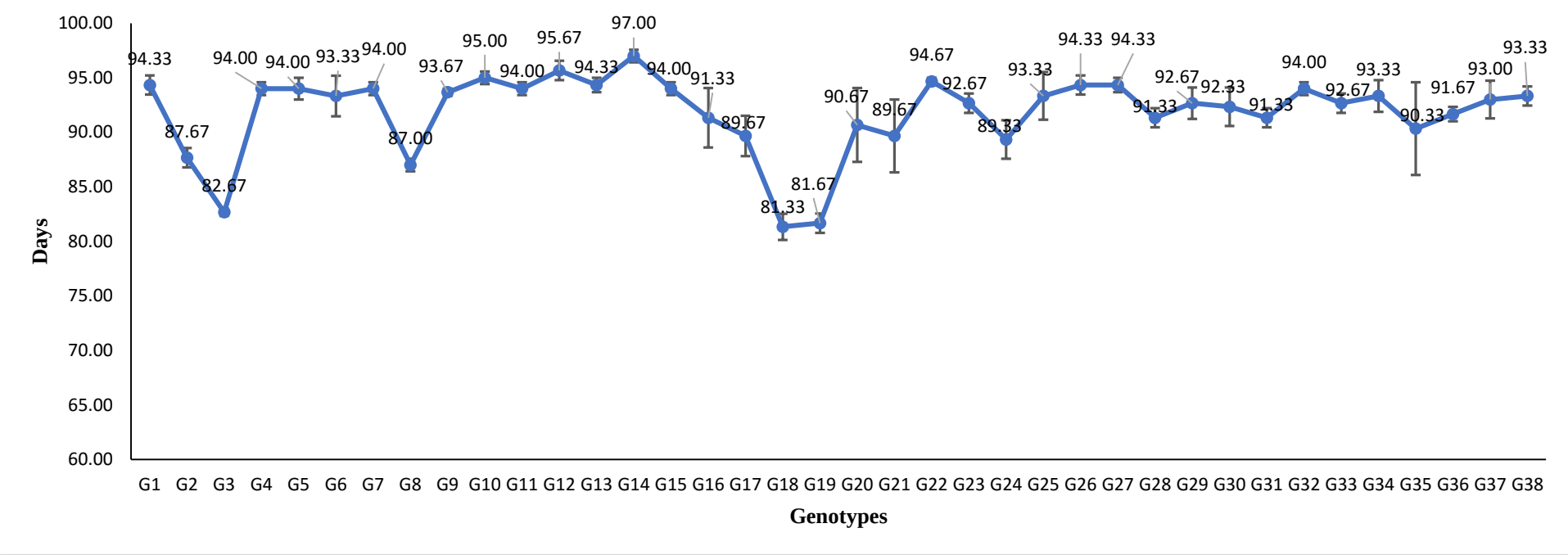

Figure 1. Mean performance of days to maturity in 38 genotypes of *B. napus*

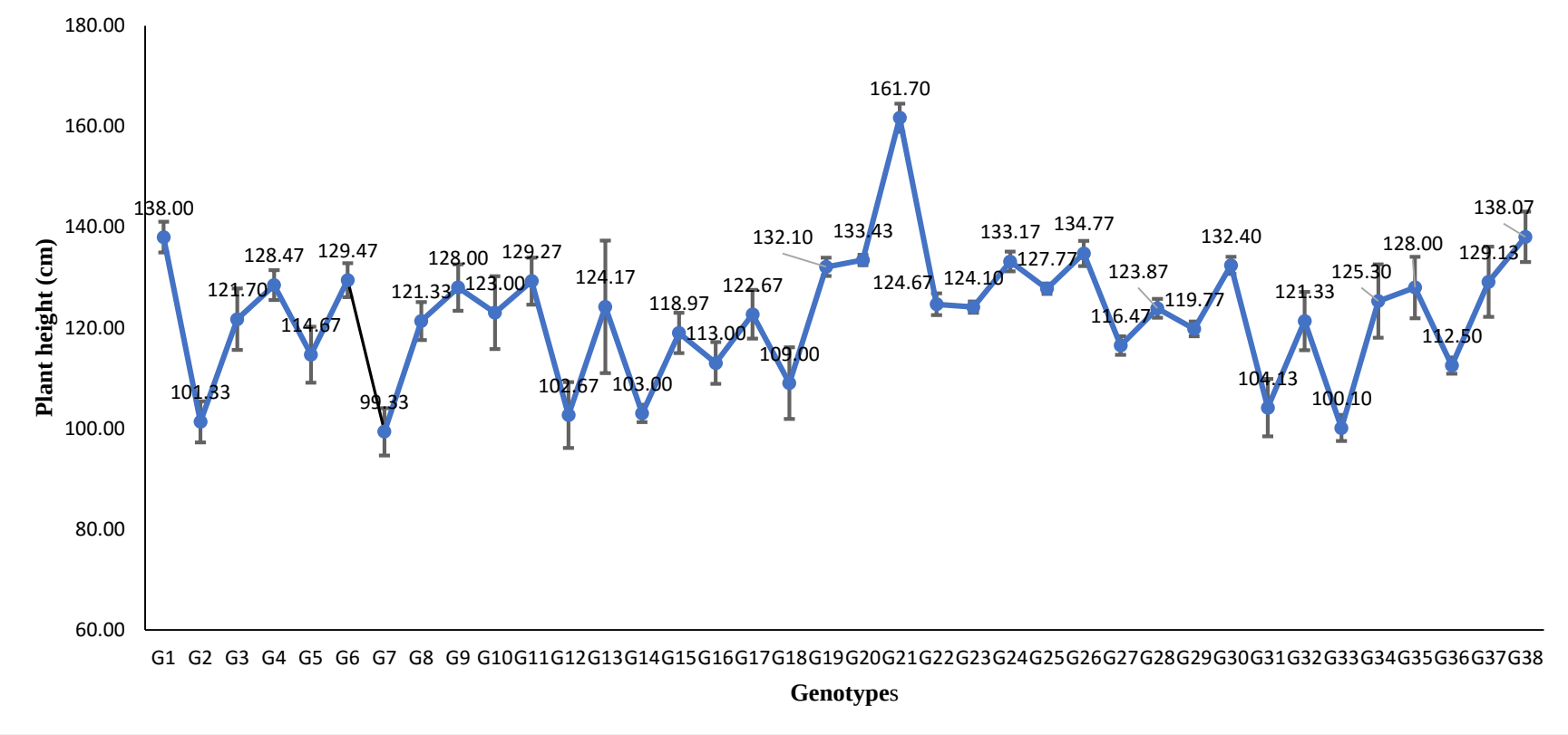

Figure 2. Mean performance of Plant height (cm) in 38 genotypes of *B. napus*

4.1.5 Number of primary branches per plant

Number of primary branches per plant showed highly significant variations among the tested advanced populations (7.48**) (Table 3). Maximum number of primary branches per plant was noticed in G14 (8.33) followed by G33 (7.67) and G30 (7.33) and minimum number of primary branches per plant were found in G19 (2.33) followed by G5 (2.50), G12 (2.67), G7 (2.80) and G6 (2.83) (Table 4). The mean value was 4.45 (Table 4). G14 showed maximum no. of primary branches per plant (8.33) indicating more siliquae than the other populations which ultimately increased yield per plant. Mean performance of number of primary branches per plant in 38 genotypes of *B. napus* is presented in Figure 3 through line graph. The genotypic and phenotypic variance was recorded as 2.20 and 3.08 percent, respectively which suggested that there was less influence of environment on this character (Table 5). Naznin *et al.* (2015) showed least differences between the phenotypic variance (1.27) and genotypic variance (0.86) in case of number of primary branches per plant. Findings of Hosen *et al.* (2008) was also agreed with this result. The values of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) was high, 33.66 and 39.83 percent (Figure 9), respectively.

4.1.6 Number of secondary branches per plant

Significant variations were observed for the number of secondary branches per plant (10.21**) suggesting that large variations are present among the tested advanced populations (Table 3). The maximum number of secondary branches were found in G5 (7.53) followed by 7.33 in G24, G29 and G32 respectively. The minimum number of secondary branches per plant were found in G19 (1.23). Mean value was 4.21 (Table 4). Mean performance of number of secondary branches per plant in 38 advance genotypes of *B. napus* is presented in Figure 4 through line graph. The genotypic and phenotypic variance were recorded as 3.17 and 3.88 respectively and phenotypic variance was slightly higher than genotypic variance which indicates the differences among population was mainly determined by the differences of genotypes. The value of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) were high, 42.39 and 46.93 percent, respectively (Table 5; Figure 9). Sikarwar *et al.* (2017) reported high phenotypic coefficient of variation (PCV) and

genotypic coefficient of variation (GCV) for number of secondary branches per plant. Naznin *et al.* (2015) showed the same findings.

4.1.7 Number of siliquae per plant

The mean sum of squares for number of siliquae per plant was 7996.44** revealed that highly significant variation was present among the selected genotypes (Table 3). The maximum siliquae production was recorded as 297.33 while the lowest value was 82.93 with a mean value of 149.85 siliquae per plant. The highest number of siliquae was observed in G14 (297.33) which was statistically similar with G11 (297.10) whereas the lowest number of siliquae was found in G19 (82.93) (Table 4). In case of *Brassica juncea* siliquae number was ranged from 215.66 to 350.66, estimated by Patel *et al.*, (2021). Mean performance of number of siliqua per plant in 38 genotypes of *B. napus* is shown in Figure 5 through line graph. The phenotypic variance (3362.43) and genotypic variance (2317.01) was higher with a large environmental variance (1045.42) was found for the selected trait. However, the higher genotypic coefficient of variance (32.58) and phenotypic coefficient of variance (39.25) was recorded (Table 5; Figure 9) for this trait. For number of siliquae per plant, the lower GCV (7.49) and moderate PCV (11.38) was supported by Yadava *et al.*, (2011). The larger difference between phenotypic variance and genotypic variance indicates higher environmental influences on the expression of the trait. Similar results were observed by Khan *et al.*, (2013).

4.1.8 Siliqua length

The mean sum of square for this trait was highly significant (2.73**) which indicated considerable amount of variation for this trait in the varieties (Table 3). Siliqua length ranged from 6.47 cm to 10.60 cm with the mean value of 8.33 cm (Table 4). The maximum siliqua length was observed in the genotype G22 (10.60 cm) while the minimum was observed in the genotype G19 (6.47 cm) (Table 4). The genotypic and phenotypic variance for siliqua length was seen as value of 0.85 and 1.03, respectively. Siliqua length exhibited low GCV (11.09%) and PCV (12.21%) values (Table 5; Figure 9). As PCV is higher than GCV thus we can conclude that the trait is controlled by its genotype as well as influence of environment.

4.1.9 Seeds per siliquae

The mean sum square for this trait was recorded as 28.26* which showed highly significant variation present in the character among the 38 genotypes of *B. napus.* (Table 3). Number of seeds per siliqua ranged from 14.41 to 30.01 with an average of 25.01 among the different genotypes (Table 4). The maximum number of seeds was found in G14 (30.01) which was statistically similar with G2 (29.57) and G3 (29.22) while the lowest number of seeds were estimated in G19 (14.41). According to Patel *et al.* (2021) seeds per siliqua was varied from 11.80 to 16.46. Mean performance of seeds per siliqua in 38 genotypes of *B. napus* is shown in Figure 6 through line graph. The genotypic and phenotypic variance for the trait was 4.06 and 20.14, respectively with an environmental variance 16.07 indicating the environmental effect on this character was high (Table 5; Figure 9). Lower case of genotypic coefficient of variance (8.01) and moderate phenotypic coefficient of variance (17.84) was observed for the trait. Yadava *et al.* (2011) revealed the similar genotypic and phenotypic coefficient of variance (1.11 and 2.03, respectively). Higher phenotypic variance with considerable environmental variance indicated that expression of the character was also associated with the environmental interaction and variation is less controlled by the differences in genotype.

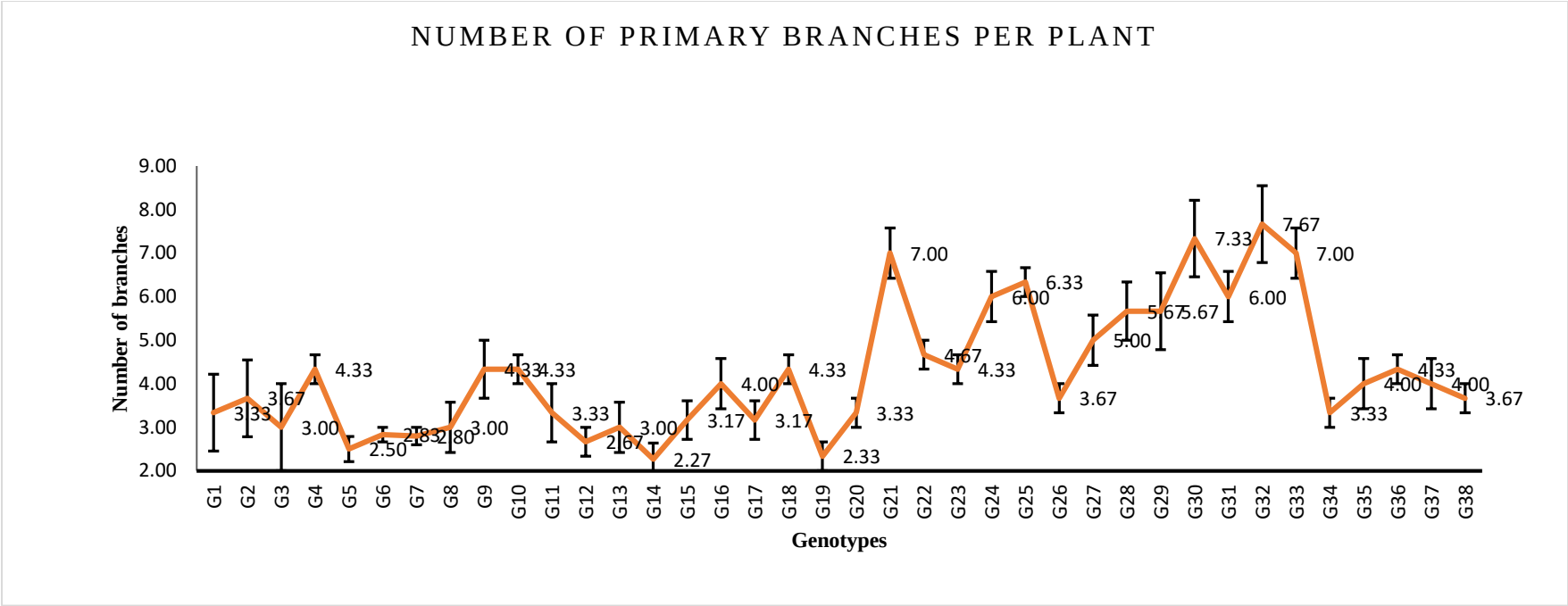

Figure 3. Mean performance of number of primary branches per plant in 38 genotypes of *B. napus*

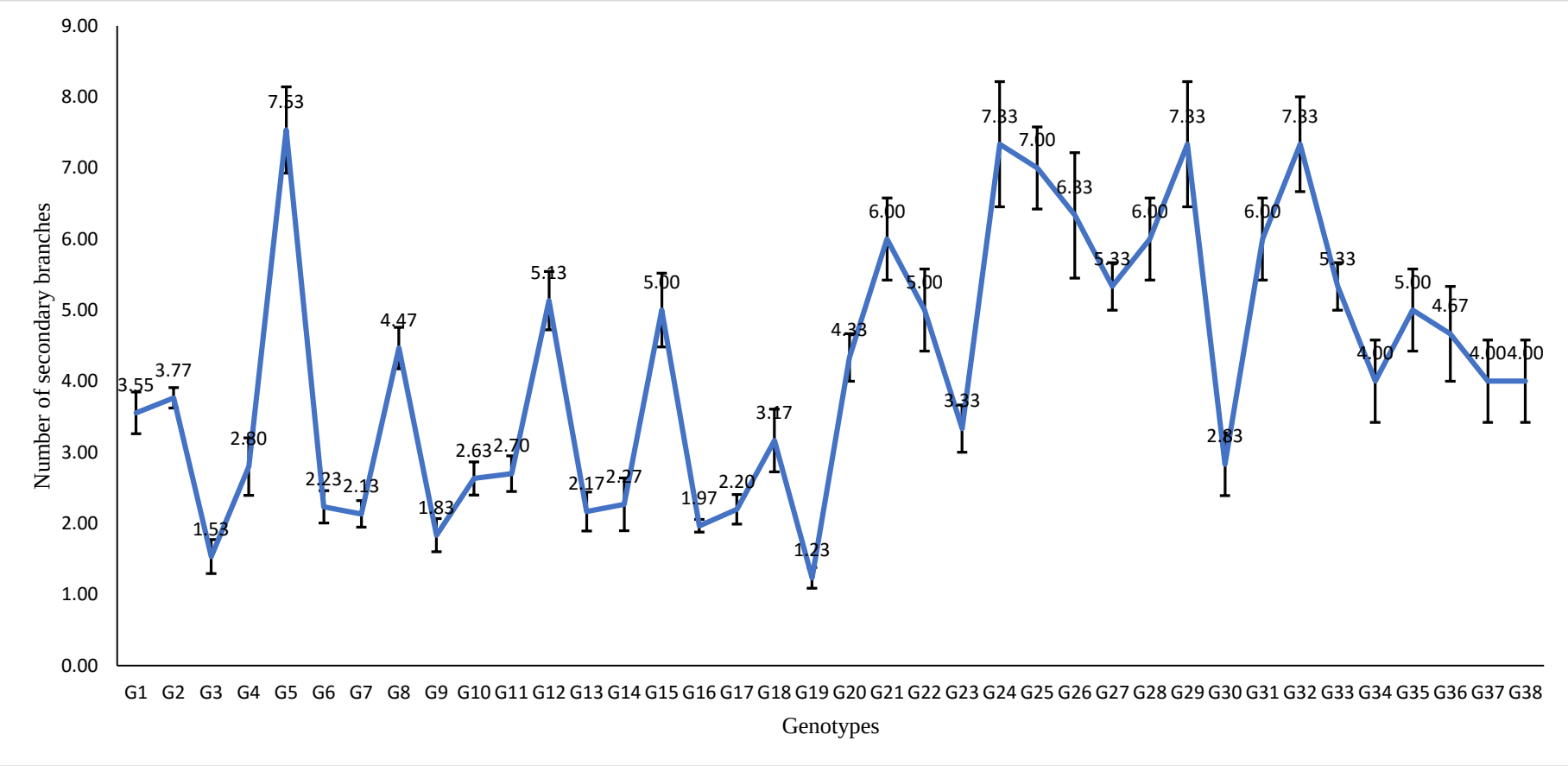

Figure 4. Mean performance of number of secondary branches per plant in 38 genotypes of *B. napus*

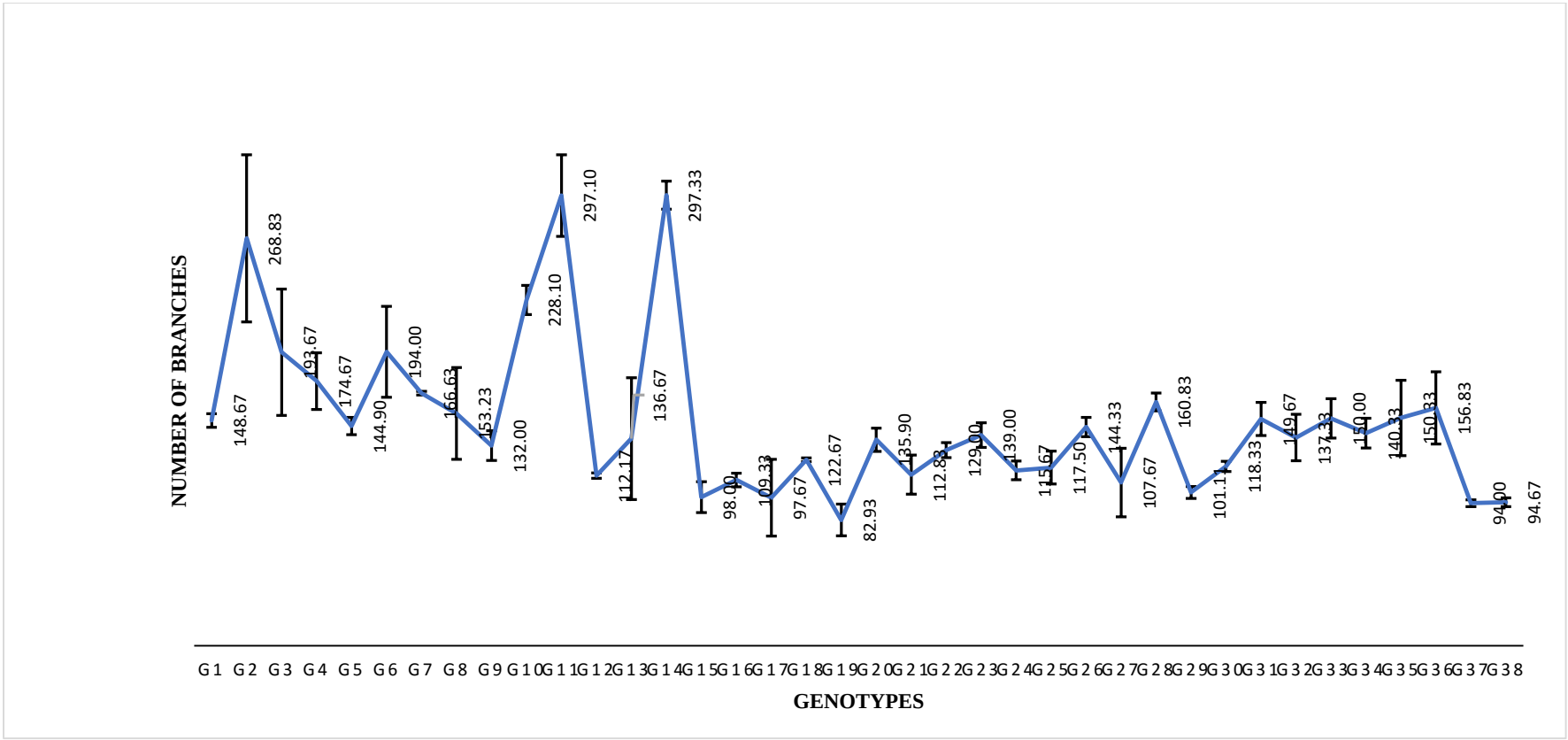

Figure 5. Mean performance of number of siliqua per plant in 38 genotypes of *B. napus*

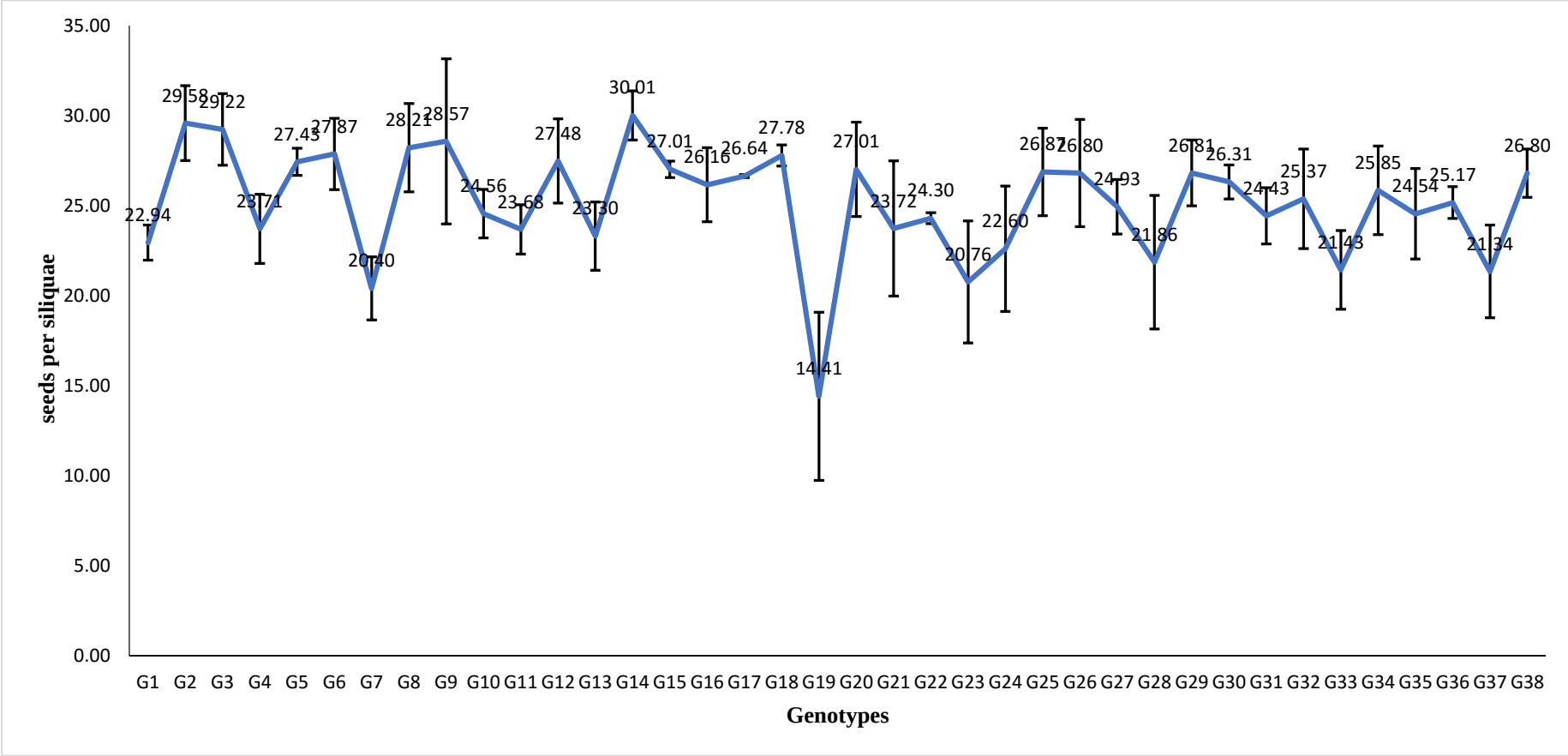

Figure 6. Mean performance of seeds per siliquae in 38 genotypes of *B. napus*

4.1.10 Thousand seeds weight (g)

Thousand seeds weight (g) showed significant variations (1.68**) among the tested genotypes (Table 3). Maximum thousand seeds weight (g) was found in G14 (5.93 g) which increased the possibility of higher yield and ultimately highest yield was found in G14 (9.61 g) whereas minimum thousands seed weight (g) was found in G19 (2.48 g) followed by G37 (2.57 g), G27 (2.73 g) and G24 (2.79 g) (Table 4). The mean value was 4.33 (Table 4). Mean performance of thousand seeds weight of 38 advanced genotypes of *Brassica napus* L. is embellished in Figure 7 through line graph. The values of phenotypic variance and genotypic variance were 0.66 and 0.51, respectively. The little difference between them indicates the less influence of environment on this trait. The values of GCV and PCV was moderate, 16.50 and 18.69 percent, respectively (Table 5; Figure 9).

4.1.11 Yield per plant (g)

Significant variation was observed among the varieties and the mean sum of square for yield per plant was 10.76** (Table 3). The estimated result revealed that yield per plant was varied from 3.69 g to 9.61 g with an average 6.34 (Table 4). The highest value was observed in G14 (9.61 g) which was statistically similar with G9 (9.58 g), G2 (9.16 g) and G35 (9.03 g). However, variety G19 was recorded for the lowest yield value as 3.69 g followed by G31 (3.76 g). Mean performance of thousand seeds weight in 38 advanced genotypes of *Brassica napus* L. is embellished in Figure 8 through line graph. Yield per plant exhibited the lowest value for genotypic (3.53) and phenotypic variance (3.70) whereas the environmental variance was negligible. The estimated phenotypic coefficient of variance (30.42) and genotypic coefficient of variance (29.71) was high (Table 5; Figure 9), indicating high variations were exhibited by genotype for yield per plant that could be beneficial for selecting the segregating lines in next. While Patel *et al.* (2019) found moderate phenotypic coefficient of variation for seed yield per plant (16.42)

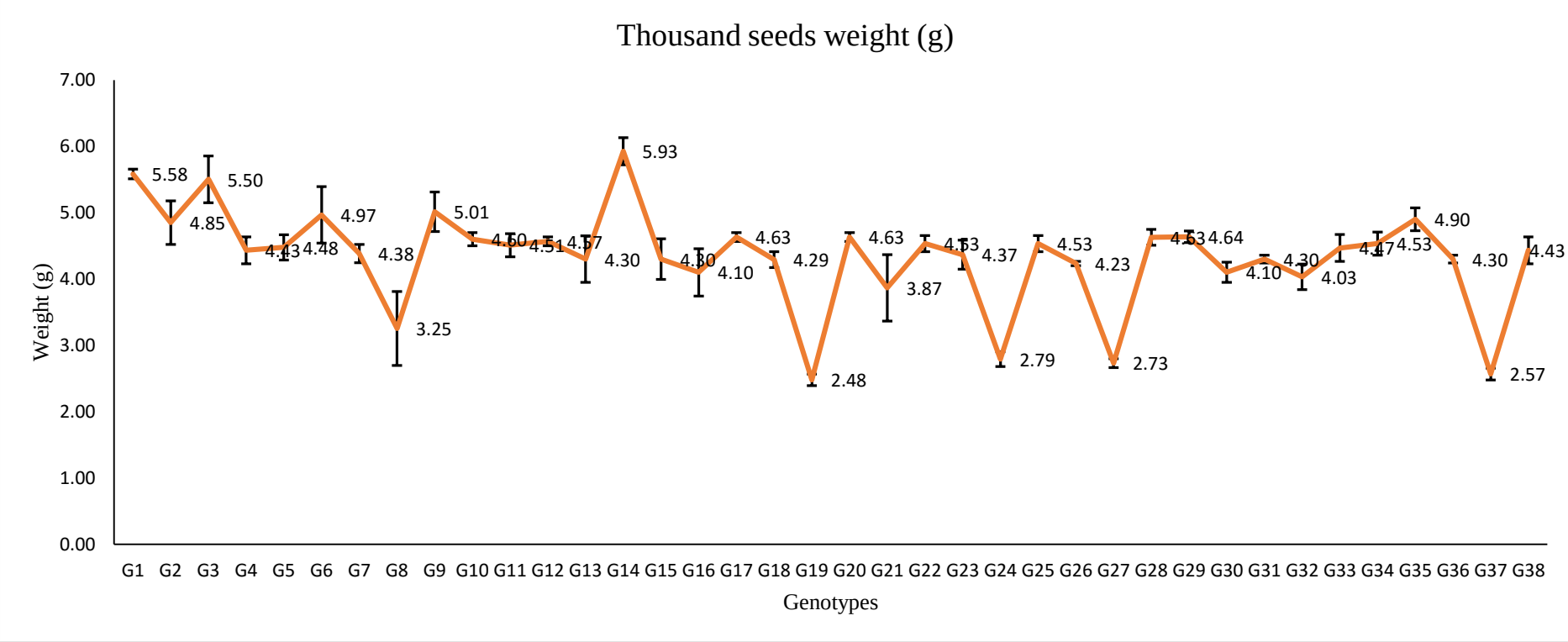

Figure 7. Mean performance of thousand seeds weight (g) in 38 genotypes of *B. napus*

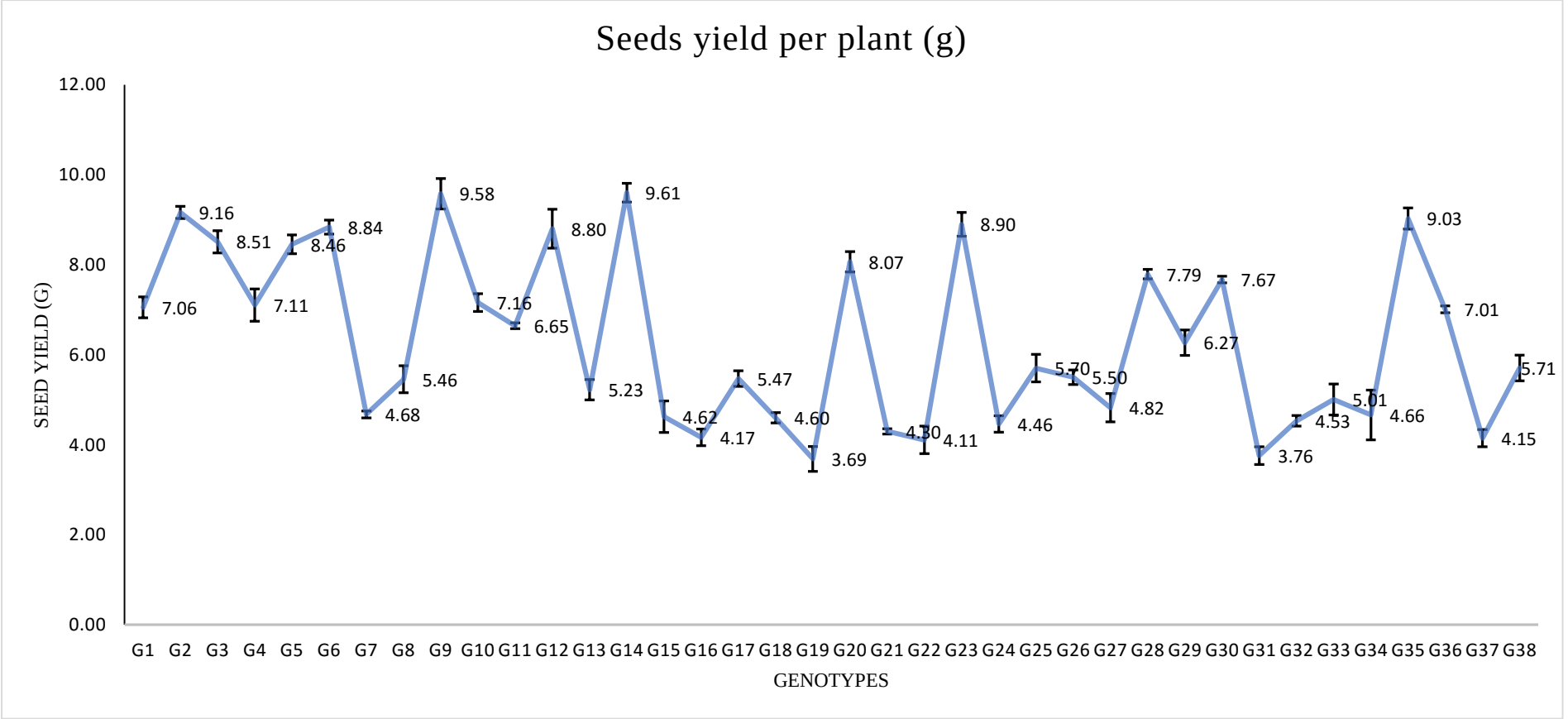

Figure 8. Mean performance of yield per plant in 38 genotypes of *B. napus*

4.2 Heritability, genetic advance and genetic advance in percentage of mean

4.2.1 Days to first flowering

Days to first flowering showed the moderate heritability (53.57%) with low genetic advance (2.43%) and low genetic advance as percentage of mean (8.70%) indicated, inheritance of days to first flowering might be controlled by the non-additive gene effects suggested that hetreosis breeding could be rewarding and simple selection may not be effective (Table 5; Figure 10).

4.2.2 Days to 50% flowering

High heritability of 76.43% with low genetic advance (6.37%) was noted for the character and the value of genetic advance in percent of mean was moderate (18.15%) (Table 5; Figure 10). High heritability having low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective. Akter (2010) reported high heritability (88.86%) and low genetic advance (2.06) for days to 50% flowering which was similar to this findings. Heterosis breeding, family selection on progeny testing method could be rewarding for this character.

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4.2.3 Days to maturity

A high heritability (60.80%) was observed for the trait including, lower value of genetic advance (5.29%) and genetic advance as percentage of mean (5.76%) indicated non-additive gene action was involved in the inheritance of this trait. Ara *et al.* (2010), Jahan (2008) and Hussain *et al*. (2014) found high heritability with low genotypic advance in percent of mean for days to siliqua maturity, therefore, selection for this trait might not be rewarding. It was also supported by Tewachew and Mohammed (2018), who estimated heritability for days to maturity which was moderate. Heterosis breeding, family selection on progeny testing method could be rewarding for this trait.

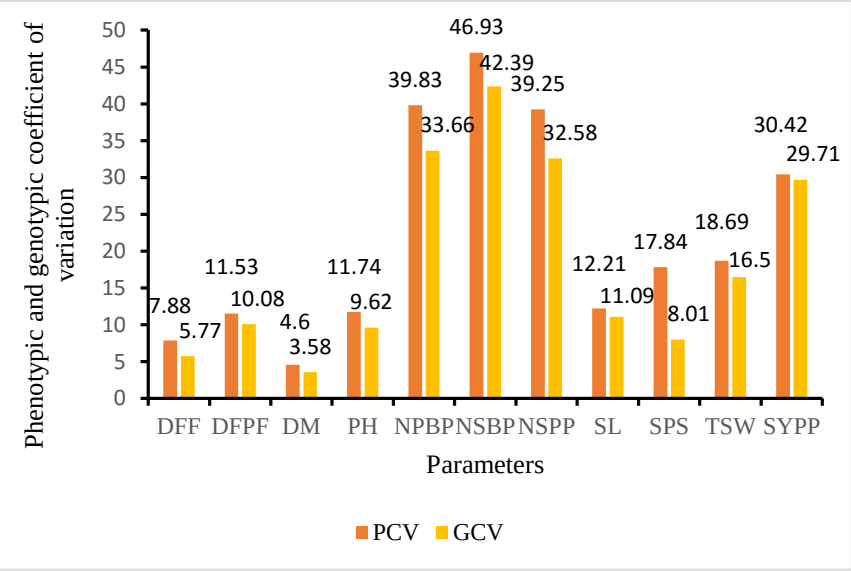

Figure 9. Phenotypic and genotypic coefficient of variation of 11 characters of *B. napus*

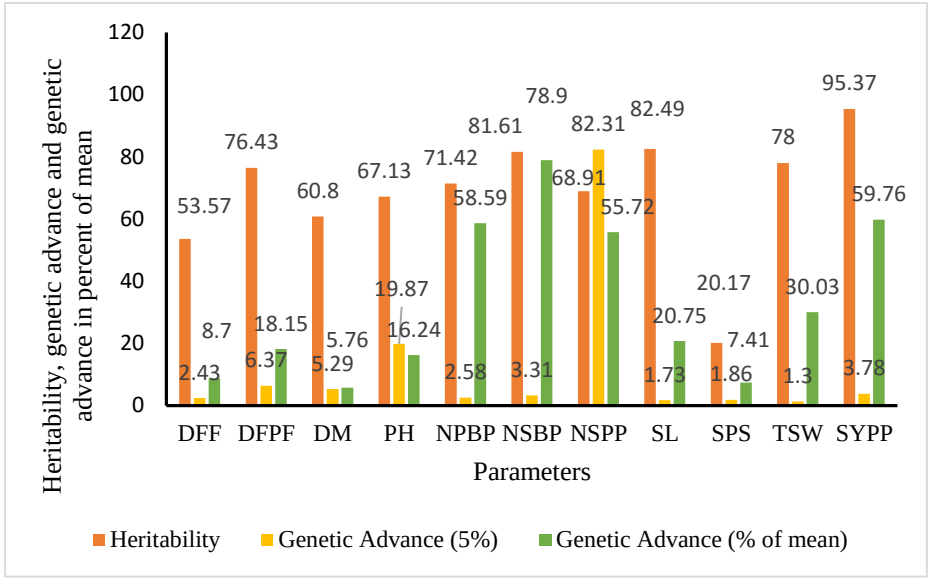

Figure 10. Heritabilitity, genetic advance and genetic advance in percentage of mean of 11 characters of *B. napus*

4.2.4 Plant height (cm)

High heritability (67.13%) with the moderate value of genetic advance (19.87%) and moderate genetic advance as percentage of mean (16.24%) were observed for plant height (Table 5). Similar results were found in Patel *et al.* (2019) findings, revealed plant height was expressed high heritability (89.72%) with moderate genetic advance as per cent of mean (14.62%). Mekonnen *et al.* (2014), Bibi *et al.* (2016) and Gupta *et al.* (2019) reported high heritability with high genetic advance as percentage of mean for plant height. High heritability with moderate genetic advance as percent of mean revealed that expression of plant height was controlled by non additive gene action, hence, selection for this trait may be effective to get shorter plant of *Brassica napus.* Heterosis breeding, family selection and progeny testing methods could be used for the improvement of this trait.

4.2.5 Number of primary branches per plat

High heritability (71.42%) along with low genetic advance (2.58%) and high genetic advance in percent of mean (58.59%) (Table 5; Figure 10) indicating the presence of additive gene action which was responsible for the effectiveness of the selection for this trait (Figure 10).

4.2.6 Number of secondary branches per plant

High heritability (81.61%) along with low genetic advance (3.31%) and high genetic advance in percent of mean (78.90%) (Table 3; Figure 10) indicating the presence of additive gene action which was responsible for the effectiveness of the selection for this trait.

4.2.7 Number of siliquae per plant

The heritability estimated for this trait was higher (68.91%) along with higher genetic advance (82.31%) and a high genetic advance as per centage of mean (55.72%), expressing additive gene effect presence in the character so direct selection may be effective based on the character (Table 5; Figure 10). Mandal *et al.* (2022) similarly observed high heritability (80.61%) with moderate genetic advance (14.36%). So, this trait could be exploited for further improvement by the selection procedure.

4.2.8 Siliqua length (cm)

A high heritability estimates of 82.49%, low genetic advance 1.73% and a high genetic advance as percent of mean 20.75% were observed (Table 5; Figure 9) for silique length. High heritability with combination of high genetic advance as percent of mean suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non- additive genetic effects for the control of this character.

4.2.9 Seeds per siliqua

A low heritability (20.17%) besides lower genetic advance (1.86%) and low genetic advance as percentage of mean (7.41%) indicating, the character is governed by non-additive gene actions. Improvement of the character required further selection procedure to the extended generations may be ineffective (Table 5) (Figure 9). High heritability (86.00%) and moderate genetic advance (10.81%) was narrated by Hussain *et al.* (2014) and Czern (2020).

4.2.10 Thousand seeds weight (g)

High heritability (78.00%) along with low genetic advance (1.30%) (Table 5,Figure 10) indicating the presence of additive gene action which was responsible for the effectiveness of the selection for this trait whereas genetic advance in percent mean was recorded high (30.03%) (Table 5; Figure 10). High heritability with low genetic advance in thousand seed weight was observed by Parveen *et al*. (2015) which indicated the possibility of non-additive gene action.

4.2.11 Yield per plant (g)

The highest heritability (95.37%) was recorded for this character along with low genetic advance (3.78%) and high genetic advance as percentage of mean (59.76%). Therefore, selection might be effective as the expression was controlled by the additive genetic effects (Table 5; Figure 10). Afrin *et al.* (2017), Rout *et al.* (2019) and Aktar *et al.* (2019) observed high heritability coupled with high genetic advance as percentage of mean for seed yield of *Brassica juncea.*

A

B

Plate 9. Pictures showing (A) Highest siliqua length of genotype G23, (B) lowest siliqua length of genotype G19

4.3 Correlation analysis

Indirect selection through other characters can be used to improve a certain trait in all breeding operations. This requires an in-depth knowledge of the relationships between various characters and the target character as well as between the various characters themselves. Estimates of the yield's association with other characters for which the genotype could be visually determined are required. The coupling phase of linkage, which results in a positive correlation, and the repulsion phase, which results in a negative correlation, are between the genes controlling various qualities. If there is no association, the relevant genes are either spread out over various chromosomes or are positioned widely apart on the same chromosome. Given its complexity, yield is controlled by several different genes. With a view to determining the amount and kind of correlations existing between yield and yield attributing characters, correlation studies could be used to determine the influence of each character on yield. Therefore, Table 6 shows the values of the genotypic and phenotypic correlation co-efficient for 11 traits across the advance population of *Brassica napus* that were examined.

4.3.1 Days to first flowering

Days to first flowering exhibited highly significant and positive correlation with days to 50% flowering (r_g = 0.659**, r_p = 0.528**), plant height (cm) (r_g = 0.241**) and siliqua length (cm) (r_g = 0.303**), pointing out a possible increase in days to 50% flowering, plant height (cm) and siliqua length (cm) by increasing days to first flowering. It exhibited highly significant and negative correlation with number of siliqua per plant (r_g = -0.209*) and yield per plant (g) (r_g = -0.232*) which indicated a possible increase in number of siliqua per plant and yield per plant (g) by decreasing days to first flowering. It also showed insignificant and positive correlation with days to maturity (r_g = 0.047^{NS}, r_p = 0.049^{NS}), plant height (cm) (r_p = 0.154^{NS}), number of primary branches per plant (r_g = 0.130^{NS}, r_p = 0.076^{NS}), siliqua length (cm) (r_p = 0.182^{NS}), seeds per siliqua (r_g = 0.021^{NS}) and thousand seeds weight (g) (r_p = 0.049^{NS}). It also showed insignificant and negative correlation with number of secondary branches per plant (r_g = -0.127^{NS}, r_p = -0.026^{NS}), number of siliquae per plant (r_p = -0.132^{NS}), , seeds per siliqua (r_p = -0.131^{NS}),

Table 6: Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different advance population of *Brassica napus*

Character		DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW
DFPF	r_g	0.659**									
	r_p	0.528**									
DM	r_g	0.047^{NS}	-0.251**								
	r_p	0.049^{NS}	-0.162^{NS}								
PH	r_g	0.241**	0.057^{NS}	-0.034^{NS}							
	r_p	0.154^{NS}	0.026^{NS}	-0.069^{NS}							
NPBP	r_g	0.130^{NS}	0.304**	0.232*	0.002^{NS}						
	r_p	0.076^{NS}	0.253**	0.153^{NS}	0.003^{NS}						
NSBP	r_g	-0.127^{NS}	-0.024^{NS}	0.248**	0.086^{NS}	0.404**					
	r_p	-0.026^{NS}	0.024^{NS}	0.158^{NS}	0.012^{NS}	0.353**					
NSPP	r_g	-0.209*	-0.165^{NS}	0.209*	-0.365**	0.110^{NS}	-0.305**				
	r_p	-0.132^{NS}	-0.097^{NS}	0.069^{NS}	-0.175^{NS}	0.016^{NS}	-0.244**				
SL	r_g	0.303**	0.037^{NS}	0.508**	-0.117^{NS}	0.054^{NS}	-0.130^{NS}	0.450**			
	r_p	0.182^{NS}	0.038^{NS}	0.392**	-0.057^{NS}	0.035^{NS}	-0.140^{NS}	0.312**			
SPS	r_g	0.021^{NS}	0.150^{NS}	0.201*	-0.278**	0.102^{NS}	0.089^{NS}	0.419**	0.320**		
	r_p	-0.131^{NS}	0.083^{NS}	0.034^{NS}	-0.130^{NS}	0.006^{NS}	0.058^{NS}	0.172^{NS}	0.125^{NS}		
TSW	r_g	-0.031^{NS}	0.092^{NS}	0.306**	-0.195*	0.004^{NS}	-0.222*	0.569**	0.465**	0.871**	
	r_p	0.049^{NS}	0.119^{NS}	0.180^{NS}	-0.181^{NS}	0.061^{NS}	-0.173^{NS}	0.433**	0.341**	0.282**	
SYPP	r_g	-0.232*	-0.228*	0.179^{NS}	-0.107^{NS}	-0.091^{NS}	-0.214*	0.543**	0.386**	0.691**	0.671**
	r_p	-0.162^{NS}	-0.183^{NS}	0.128^{NS}	-0.085^{NS}	-0.066^{NS}	-0.178^{NS}	0.445**	0.355**	0.272**	0.571**

*, 5% level of significance **, 1% level of significance NS, Non-significance

DFF=Days to first flowering, DFPF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seed yield per plant (g)

thousand seeds weight (g) (r_g = -0.031^{NS}) and yield per plant (g) (r_p = -0.162^{NS}). Insignificant association of these traits revealed that the combination between these traits was largely influenced by environmental factors (Table 6).

4.3.2 Days to 50% flowering

Days to 50% flowering exhibited highly significant and positive correlation with number of primary branches per plant (r_g = 0.304**, r_p = 0.253**) pointing out a possible increase in number of primary branches per plant by increasing days to 50% flowering. It exhibited highly significant and negative correlation with days to maturity (r_g = -0.251**) and yield per plant (g) (r_g = -0.228*) which indicated a possible increase in days to maturity and yield per plant (g) by decreasing days to 50% flowering. It also showed insignificant and positive correlation with plant height (cm) (r_g = 0.057^{NS}, r_p = 0.026^{NS}), number of secondary branches per plant (r_p = 0.024^{NS}), siliqua length (cm) (r_g = 0.037^{NS}, r_p = 0.038^{NS}), seeds per siliqua (r_g = 0.150^{NS}, r_p = 0.083^{NS}) and thousand seeds weight (g) (r_g = 0.092^{NS}, r_p = 0.119^{NS}). It also showed insignificant and negative correlation with days to maturity (r_g = -0.251**, r_p = -0.162^{NS}), plant height (cm) (r_g = 0.057^{NS}, r_p = 0.026^{NS}), , number of secondary branches per plant (r_g = -0.024^{NS}, r_p = 0.024^{NS}), number of siliqua per plant (r_g = -0.165^{NS}, r_p = -0.097^{NS}) and yield per plant (g) (r_g = -0.228*, r_p = -0.183^{NS}). Insignificant association of these traits suggested that the interrelationship between these traits was largely influenced by environmental factors (Table 6).

4.3.3 Days to maturity

Days to maturity exhibited highly significant and positive correlation with number of primary branches per plant (r_g = 0.232*), number of secondary branches per plant (r_g = 0.248**), number of siliquae per plant (r_g = 0.209*), siliqua length (cm) (r_g = 0.508**, r_p = 0.392**), seeds per siliqua (r_g = 0.201*) and thousand seeds weight (g) (r_g = 0.306**) which indicated a possible increase in number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length (cm), seeds per siliquae and thousand seeds weight (g). It also showed insignificant and positive correlation with number of primary branches per plant (r_p = 0.153^{NS}), number of secondary branches per plant (r_p = 0.158^{NS}), number of siliquae per plant (r_p = 0.069^{NS}), seeds per siliqua (r_p = 0.034^{NS}) and thousand seeds weight (g) (r_p = 0.180^{NS}). It also showed insignificant and negative correlation with plant height (cm) (r_g = -0.034^{NS}, r_p =

-0.069^{NS}) indicating that indicated that environmental factors largely influenced on the association between these traits (Table 6).

4.3.4 Plant height (cm)

Plant height (cm) exhibited highly significant and negative correlation with number of siliquae per plant (r_g = -0.365**), seeds per siliqua (r_g = -0.278**) and thousand seeds weight (g) (r_g = -0.195*) which indicated a possible increase in number of siliquae per plant, thousand seeds weight (g) and seeds per siliqua decreases plant height (cm). It also showed insignificant and positive correlation with number of primary branches per plant (r_g = 0.002^{NS}, r_p = 0.003^{NS}) and number of secondary branches per plant (r_g = 0.086^{NS}, r_p = 0.012^{NS}) indicating that it had a very little contribution toward the increase in number of primary branches per plant, and number of secondary branches per plant. It also showed insignificant and negative correlation with number of siliqua per plant (r_p = -0.175^{NS}), siliqua length (r_g = -0.117^{NS}, r_p = -0.057^{NS}), seeds per siliqua (r_p = -0.130^{NS}), thousand seeds weight (g) (r_p = -0.181^{NS}) and yield per plant (g) (r_g = -0.107^{NS}, r_p = -0.085^{NS}) indicated that environmental factors largely influenced on the association between these traits (Table 6).

4.3.5 Number of primary branches per plant

Number of primary branches per plant exhibited highly significant and positive correlation with number of secondary branches per plant (r_g = 0.404**, r_p = 0.353**) which indicated a possible increase in number of secondary branches per plant increases the number of primary branches per plant. It also showed insignificant and positive correlation with number of siliquae per plant (r_g = 0.110^{NS}, r_p = 0.016^{NS}), siliqua length (cm) (r_g = 0.054^{NS}, r_p = 0.035^{NS}), seeds per siliqua (r_g = 0.102^{NS}, r_p = 0.006^{NS}) and thousand seeds weight (g) (r_g = 0.004^{NS}, r_p = 0.061^{NS}) indicating that it had a very little contribution toward the increase in number of siliquae per plant, siliqua length (cm), seeds per siliqua and thousand seeds weight (g). It also showed insignificant and negative correlation with yield per plant (g) (r_g = -0.091^{NS}, r_p = -0.066^{NS}) indicated that environmental factors largely influenced on the association between these traits (Table 6).

4.3.6 Number of secondary branches per plant

Number of secondary branches per plant exhibited highly significant and negative correlation with number of siliquae per plant (r_g = -0.305**, r_p = -0.244**), thousand seeds weight (g) (r_g = -0.222*) and yield per plant (g) (r_g = -0.214*) which indicated a possible increase in siliquae per plant, thousand seeds weight (g) and yield per plant decreases the number of secondary branches per plant. It also showed insignificant and positive correlation with seeds per siliqua (r_g = 0.089^{NS}, r_p = 0.058^{NS}) indicating that it had a very little contribution toward the increase in seeds per siliqua. It also showed insignificant and negative correlation with thousand seeds weight (g) (r_p = -0.173^{NS}), yield per plant (g) (r_p = -0.178^{NS}) and siliqua length (cm) (r_g = -0.130^{NS}, r_p = -0.140^{NS}) indicated that environmental factors largely influenced on the association between these traits (Table 6).

4.3.7 Number of siliquae per plant

Number of siliqua per plant showed highly significant and positive correlation with siliqua length (cm) (r_g = 0.450**, r_p = 0.312**), seeds per siliqua (r_g = 0.419), thousand seeds weight (g) (r_g = 0.569**, r_p = 0.433**) and yield per plant (g) (r_g = 0.543**, r_p = 0.445**) which indicates a possible increase in number of siliquae per plant increases the siliqua length (cm), seeds per siliqua, thousand seeds weight (g) and yield per plant (g). Naznin et al. (2015) also showed highly significant positive association of number of siliquae/plant with seed yield/plant. Rameeh (2011) also confirmed the same finding. Similar result was also discovered by Esmaeeli-Azadgoleh et al. (2009) and Marjanovic-Jeromela et al. (2007). It was also found that number of siliquae per plant showed non-significant and positive correlation with seeds per siliqua (r_p = 0.172) (Table 6).

4.3.8 Siliqua length (cm)

Highly significant and positive correlation of length of siliqua (cm) was observed with seeds per siliqua (r_g = 0.320**), thousand seeds weight (g) (r_g = 0.465**, r_p = 0.341**) and yield per plant (g) (r_g = 0.386**, r_p = 0.355**) which indicated a possible increase in length of siliqua (cm) increases the seeds per siliqua, thousand seeds weight (g) and yield per plant (g). It also showed insignificant and positive correlation with seeds per siliqua (r_p = 0.125) at phenotypic level stated that it had a very little association with seeds per siliqua (Table 6).

4.3.9 Seeds per siliqua

Seeds per siliqua showed significant and positive correlation with thousand seeds weight (g) (r_g = 0.871**, r_p = 0.282**) and yield per plant (g) (r_g = 0.691**, r_p = 0.272**) at both genotypic and phenotypic level indicates a possible increase in number of seeds per siliqua increases the yield per plant (g) (Table 6).

4.3.10 Thousand seeds weight (g)

Thousand seeds weight exhibited highly significant and positive correlation with yield per plant (g) (r_g = 0.671**, r_p = 0.571**) at both genotypic and phenotypic level indicating that an increase in thousand seeds weight tends to increase seed yield per plant. The similar result was also reported by Parveen *et al.* (2015) (Table 6).

4.4 Path coefficient analysis

Simple correlation does not take into account the intricate connections between the numerous characteristics associated to the dependent variable. Correlation coefficients illustrate relationships between independent variables and their linear relationship. When the causal relationship between variables is required, it is however insufficient to just explain these interactions. Some research has suggested that yield factors may affect seed yield directly, indirectly, or both. Therefore, understanding how yield components affected seed yield was crucial. As a result, the statistical technique most frequently applied for this purpose is path coefficient analysis. By using the other components, it is possible to calculate the direct and indirect effects of yield components on seed yield. Genotypic path was worked out in the present study (Table 7) considering yield per plant as dependent character and its attributes as independent characters viz., days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, length of siliqua (cm), no. of seeds per siliqua and 1000 seed weight (g). Each component has two path actions viz., direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.4.1 Days to first flowering

Path coefficient analysis revealed that days to first flowering had negative direct effect (-0.887) on yield per plant. This negative direct effect was minimized by the positive indirect effect on yield per plant via days to 50% flowering (0.156), days to maturity

Table 7. Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of *Brassica napus*

Trait	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	Genotypic correlation with SYPP
DFF	**-0.887**	0.156	0.019	0.133	-0.001	0.124	-0.024	0.144	0.047	0.057	-0.232*
DFPF	-0.584	**0.236**	-0.099	0.031	-0.002	0.023	-0.019	0.017	0.338	-0.171	-0.228*
DM	-0.042	-0.059	**0.396**	-0.019	-0.001	-0.244	0.024	0.241	0.453	-0.570	0.179NS
PH	-0.214	0.013	-0.013	**0.552**	-0.00001	-0.085	-0.041	-0.055	-0.626	0.363	-0.107^{NS}
NPBP	-0.115	0.072	0.092	0.001	**-0.005**	-0.397	0.013	0.026	0.231	-0.008	-0.091^{NS}
NSBP	0.112	-0.006	0.098	0.048	-0.002	**-0.982**	-0.035	-0.062	0.201	0.413	-0.214*
NSPP	0.186	-0.039	0.083	-0.201	-0.001	0.300	**0.113**	0.213	0.946	-1.058	0.543**
SL	-0.269	0.009	0.201	-0.064	-0.0003	0.128	0.051	**0.474**	0.722	-0.866	0.386**
SPS	-0.019	0.035	0.080	-0.153	-0.001	-0.087	0.048	0.152	**2.256**	-1.619	0.691**
TSW	0.027	0.022	0.121	-0.108	-0.00002	0.218	0.065	0.221	1.965	**-1.859**	0.671**
Residual effect 0.06											

*, 5% level of significance **, 1% level of significance NS, Non-significance

DFF=Days to first flowering, DFPF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seed yield per plant (g)

(0.019), plant height (cm) (.0133), number of secondary branches per plant (0.124), siliqua length (cm) (.144), seeds per siliquae (0.047) and thousand seeds weight (g) (0.057) however it had negligible negative indirect effect via number of primary branches per plant (-0.001) and number of siliqua per plant (-0.024). Finally, the trait showed negative genotypic correlation with seed yield per plant (-0.232) which was significant (Table 7). Result of this trait indicating that indiect selection could reduce negative direct effect as well as correlation with seed yield per plant.

4.4.2 Days to 50% flowering

Days to 50% flowering showed positive direct effect (**0.236**) towards yield per plant. The trait showed positive indirect effect on seed yield per plant via plant height (0.031), number of secondary branches per plant (0.023), siliqua length (cm) (0.017) and seeds per siliqua (0.338). The trait showed negative correlation with seed yield per plant (-0.228) indirect effect on seed yield per plant via days to first flowering (-0.584), days to maturity (-0.099), number of primary branches per plant (-0.002), number of siliqua per plant (-0.019) and thousand seeds weight (g) (-0.171). Finally, the trait showed negative genotypic correlation with seed yield per plant **(-0.228)** which was significant (Table 7) indicating that direct selection for this trait should not be practiced to reduce the undesirable negative effect.

4.4.3 Days to maturity

Days to 80% maturity showed positive direct effect **(0.396)** towards yield per plant. Naznin et al. (2015) reported positive direct effect of days to maturity towards yield per plant that was similar to the present finding. Rashid et al. (2013) showed the similar result. The trait showed positive indirect effect on seed yield per plant via number of siliqua per plant (0.024), siliqua length (cm) (0.241) and seeds per siliquae (0.453). The trait showed negative indirect effect on seed yield per plant via days to first flowering (-0.042), days to 50% flowering (-0.059), plant height (cm) (-0.019), number of primary branches per plant (-0.001), number of secondary branches per plant (-0.244) and thousand seeds weight (g) (-0.570). The trait had non-significant positive genotypic association with yield per plant **(0.179)** (Table 7)**.**

4.4.4 Plant height (cm)

Plant height exhibited positive direct effect **(0.552)** on yield per plant. Uddin et al. (2013) demonstrated that plant height had the negative direct effect on yield per plant

which supported the result. The trait showed positive indirect effect on seed yield per plant via days to 50% flowering (0.013) and thousand seeds weight (g) (0.363). The trait showed negative indirect effect on seed yield per plant via days to first flowering (-0.214), days to maturity (-0.013), number of primary branches per plant (-0.00001), number of secondary branches per plant (-0.085), number of siliqua per plant (-0.041), siliqua length (cm) (-0.055) and seeds per siliquae (-0.626). The trait had non-significant negative genotypic association with yield per plant **(-0.107)**. Direct effect **(0.552)** is positive and higher than the genotypic correlation coefficient **(-0.107)** which exhibited true relationship between them and direct selection for this trait will not be rewarding for yield improvement (Table 7).

4.4.5 Number of primary branches per plant

Number of primary branches per plant showed negative direct effect **(-0.005)** towards yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 50% flowering (0.072), days to maturity (0.092), plant height (cm) (0.001), number of siliqua per plant (0.013), siliqua length (cm) (0.026) and seeds per siliquae (0.231). The trait showed negative indirect effect on seed yield per plant via days to first flowering (-0.115) and number of secondary branches per plant (-0.397) and thousand seeds weight (g) (-0.008). The trait had negative genotypic association with seed yield per plant **(-0.091)** which was non-significant (Table 7).

4.4.6 Number of secondary branches per plant

Number of primary branches per plant showed negative direct effect **(-0.982)** towards yield per plant. Naznin et al. (2015) revealed that number of secondary branches per plant had high positive direct effect on yield/plant which supported the present finding. Khan (2010) also agreed to the finding. The trait showed positive indirect effect on seed yield per plant via days to first flowering (0.112), days to maturity (0.098), plant height (cm) (0.048), seeds per siliquae (0.201) and thousand seeds weight (g) (0.413). The trait showed negative indirect effect on seed yield per plant via days to 50% flowering (-0.006), number of primary branches per plant (-0.002), number of siliqua per plant (-0.035) and siliqua length (cm) (-0.062). The trait had significantly negative genotypic association with yield per plant **(-0.214)** (Table 7)**.**

4.4.7 Number of siliqua per plant

Number of siliquae per plant exhibited positive direct effect **(0.113)** on yield per plant. The trait showed positive indirect effect on seed yield per plant via days to first flowering (0.186), days to maturity (0.083), number of secondary branches per plant (0.300), siliqua length (cm) (0.231) and seeds per siliquae (0.946). The trait showed negative indirect effect on seed yield per plant via days to 50% flowering (-0.039), plant height (cm) (-0.201) and number of primary branches per plant (-0.001) and thousand seeds weight (g) (-1.058). The trait had significant positive genotypic association with seed yield per plant **(0.543)**. Direct effect **(0.113)** is positive and higher than the genotypic correlation coefficient **(0.543)** which exhibited true relationship between them and direct selection for this trait will be effective for yield improvement (Table 7).

4.4.8 Siliqua length (cm)

Length of siliqua showed positive direct effect **(0.474)** on yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 50% flowering (0.009), days to maturity (0.201), number of secondary branches per plant (0.128), number of siliqua per plant (0.051) and seeds per siliquae (0.722). The trait showed negative indirect effect on seed yield per plant via days to first flowering (-0.269), plant height (cm) (-0.064) and number of primary branches per plant (-0.0003) and thousand seeds weight (g) (-0.866). The trait had significant positive genotypic association with yield per plant **(0.386)** (Table 7)**.**

4.4.9 Seeds per siliqua

Number of seeds per siliqua showed positive direct effect **(2.256)** on yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 50% flowering (0.035), days to maturity (0.080), number of siliqua per plant (0.048) and siliqua length (cm) (0.152). The trait showed negative indirect effect on seed yield per plant via days to first flowering (-0.019), plant height (cm) (-0.153), number of primary branches per plant (-0.001) and number of secondary branches per plant (-0.087) and thousand seeds weight (g) (-1.619). The trait had significant positive genotypic association with seed yield per plant **(0.691)** (Table 7).

4.4.10 Thousand seeds weight (g)

Thousand seed weight had negative direct effect **(-1.859)** on yield per plant. The trait showed positive indirect effect on seed yield per plant via days to first flowering (0.027), days to 50% flowering (0.022), days to maturity (0.121), number of secondary branches per plant (0.218), number of siliqua per plant (0.065), siliqua length (cm) (0.221) and seeds per siliquae (1.965). The trait showed negative indirect effect on seed yield per plant via plant height (cm) (-0.108) and number of primary branches per plant (-0.00002). The trait had significant positive genotypic association with seed yield per plant **(0.671)** (Table 7)**.**

4.3.11 Residual effect

The residual effect (R) of path co-efficient analysis was 0.06 which reported that the traits under study contributed 94% of the yield per plant. It was said that there were some other factors those contributed 6% to the yield per plant that were not included in the present study could had significant effect on seed yield per plant. Naznin *et al.* (2015) found residual effect 0.45 in case of yield per plant.

CHAPTER V
SUMMARY AND CONCLUSION

At the farm of Sher-e Bangla Agricultural University in Dhaka, an experiment using 38 genotypes of *B. napus* was conducted to ascertain the genetic variability, correlation, and path coefficient for yield and its contributing attributes from November 2019 to March 2020. It was found that all of the genotypes used for the majority of the analyzed traits exhibit significant variation. According to the mean performance, the highest duration for days to first flowering was recorded in G22 (31.33 days) where G8 required 24.33 days to take first flowering, the lowest among the genotypes. The minimum duration to days to 50% flowering was found in G9 with 30.67 DAS where G22 took the maximum period for 50 % flowering with 43.33 days. For days to maturity, 97.00 days were required for G14 which was the highest duration for days however, the lowest days to siliqua maturity was observed in G18 (81.33 days). The highest plant height was observed in G21 (161.70 cm) and the lowest plant height was found in G7 (99.33 cm). The maximum number of primary branches per plant was noticed in G14 (8.33) and the minimum number of primary branches per plant were found in G19 (2.33). The maximum number of secondary branches were found in G5 (7.53) and the minimum number of secondary branches per plant were found in G19 (1.23). The highest number of siliquae was observed in G14 (297.33) whereas the lowest number of siliquae was found in G19 (82.93). The maximum number of seeds was found in G14 (30.01) while the lowest number of seeds were estimated in G19 (14.41). The maximum thousand seeds weight (g) was found in G14 (5.93 g) whereas the minimum thousands seed weight (g) was found in G19 (2.48 g). The highest value was observed in G14 (9.61 g), however, variety G19 was recorded for the lowest yield value as 3.69 g. For all the characters under study, the phenotypic variation was higher than the corresponding genotypic variance, indicating a greater influence of the environment on these characters' expression. Plant height (cm) and number of siliqua per plant showed higher phenotypic and genotypic variance indicating that higher environmental effect presence on these characters on the other hand lower environmental effect was found for these characters like days to first flowering, number of primary branches per plant, number of secondary branches per plant, siliqua length (cm), seeds per siliquae, thousand seeds weight (g) and seeds yield per plant (g). Characters like, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant and yield

per plant (g) exhibited high genotypic and phenotypic co-efficient of variation. The phenotypic co-efficient of variation was higher than the genotypic coefficient of variation for all the characters. Maximum difference between phenotypic and genotypic coefficient of variation were 17.84 and 8.01, respectively which indicated that the seeds per siliqua was mostly depended on the environmental condition. Highest phenotypic co-efficient of variation (46.93) and genotypic co-efficient of variation (42.39) was found in number of secondary branches per plant. High heritability coupled with high genetic advance and genetic advance in percentage of mean was found in number of siliqua per plant which indicated that additive gene expression on this character. Investigation on character association indicating that yield per plant had highest significant positive correlation with number of seeds per siliqua, siliqua length (cm), seeds per siliqua and thousand seeds weight (cm) in both genotypic and phenotypic level indicating the importance of these trait in selection for increasing yield and were identified as yield attributing characters. Path analysis revealed that highest positive direct effect was individual seeds per siliqua (2.256) and the lowest positive direct effect was number of siliqua per plant (0.113). Days to 50% flowering, days to maturity, plant height (cm), number of secondary branches per plant, siliqua length (cm) and seeds per siliquae showed positive direct effect on yield per plant (kg) indicating that direct selection based on these traits may be helpful in evolving high yielding varieties of *B. napus*.

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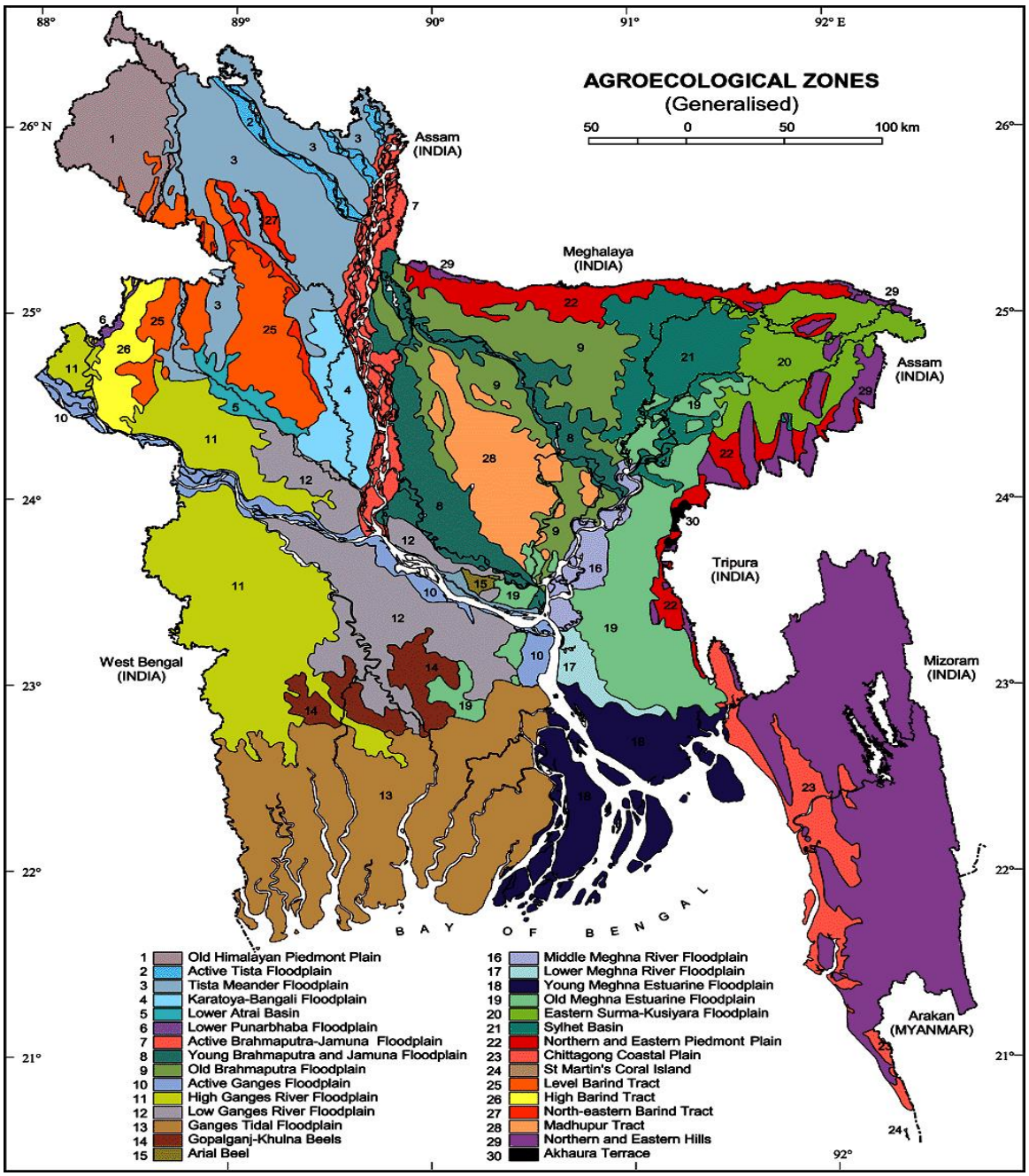
APPENDICES

Appendix I. Map showing the experimental site under the study



Legend showing the research site

Appendix II: Physical and chemical characteristics of initial soil depth of the experimental site.

A. Physical composition of the soil:

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

B. Chemical composition of the soil:

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

Appendix III: Monthly average temperature, average relative humidity and total rainfall and total sunshine of the experimental site during the period from November, 2019 to March, 2020.

Month	Air temperature (°C)		Relative humidity (%)	Total rainfall (mm)	Sunshine (hr)
	Minimum	Maximum			
November, 2019	20.5	29.2	73	34.4	7.3
December, 2019	17	26.4	73	12.8	7.4
January, 2020	15.3	26	71	7.7	7.6
February, 2020	17.4	29.8	64	28.9	7.5
March, 2020	21.3	34	62	65.8	10.1