GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BC_1F_9 POPULATION OF *Brassica napus* L

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CERTIFICATE

*This is to certify that the thesis entitled, "**GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BC_1F_9 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 HREEDITA AFRIN BORNO, Registration No. 15-06376 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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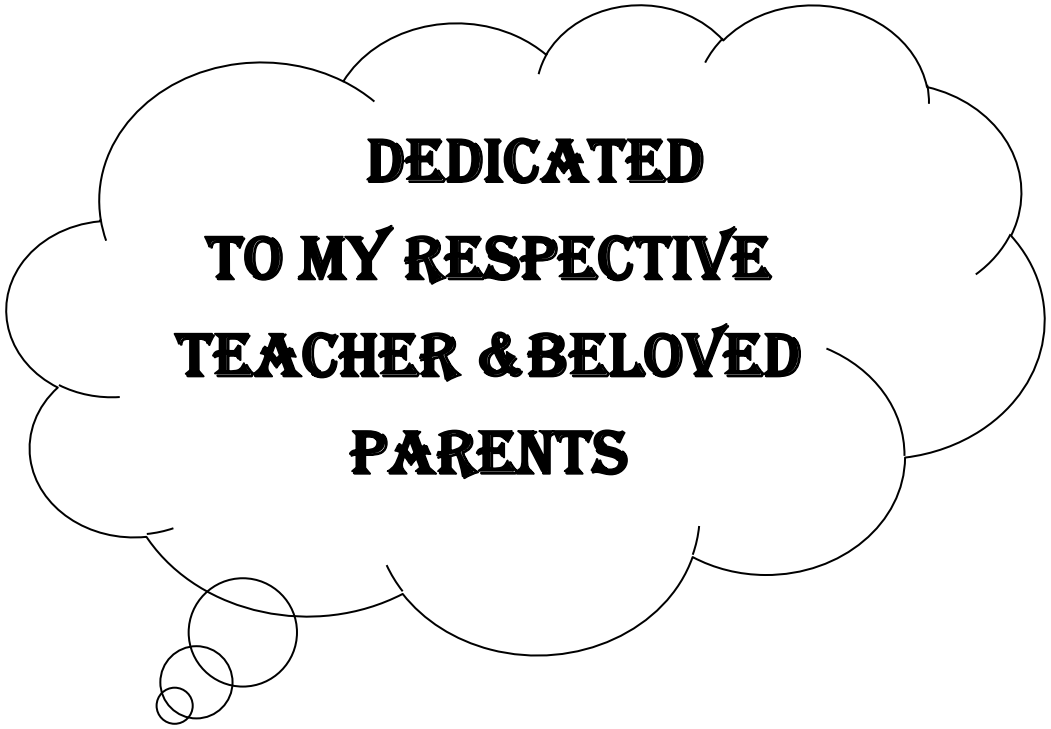
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JUNE, 2022 *The Author SAU,*
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GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BC_1F_9 POPULATION OF *Brassica napus* L

By

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ABSTRACT

Thirty genotypes of *Brassica napus* L. were evaluated based on a randomized complete block design with three replications at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, to study the variability, correlation, and path analysis during the November 2019 to March 2020 growing seasons. The genotypes were found significantly variable for all the characters. Comparatively phenotypic variance was higher than the genotypic variance for all the characters studied. The high genotypic coefficient of variation and phenotypic coefficient of variation value were observed for yield per plant (g). The maximum difference between the phenotypic and genotypic coefficient of variation was 30.31 and 13.82. Days to 50% flowering, days to maturity, thousand seed weight (g), and yield per plant (g) all showed high heritability along with genetic advance in percentage of mean, indicating additive gene expression on this trait. The significant positive correlation with yield per plant was found in seeds per siliquae, thousand seed weight (g), and yield per plant in both genotypic and phenotypic levels indicating the importance of these traits in selection for increasing yield and were identified as yield attributing characters. Thus, selection can rely upon these characteristics for the genetic improvement of the yield of *B. napus*. According to path analysis, the number of secondary branches per plant had the lowest positive direct effect and thousand seed weight (0.684) had the highest positive direct effect (0.151). Days to 50% flowering (0.194), plant height (0.204), number of secondary branches per plant (0.151), siliqua length (0.247), seeds per siliqua (0.268), and thousand seed weight (0.684) all had a positive direct impact on yield per plant (g), suggesting that direct selection based on these traits may be useful in the development of high yielding *B. napus* varieties. Considering genotypic variance and agronomic performance genotypes and based on objectives G8, G9, G18, G1, G28, and G14 might be suggested for future breeding programs.

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SOME COMMONLY USED ABBREVIATIONS

FULLWORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Agricultural	Agril.
And others	et al.
Accessions	ACC
Agronomy Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Biological	Biol
Centimeter	cm
Co-efficient of variation	CV
Ecology	etc.
Etcetera	Ecol.
Environmental variance	δ 2 e
Figure	Fig.
Food and Agricultural Organization	FAO
Genotype	G
Genetic advance	GA
Genotypic coefficient of variation	GCV
Genotypic variance	δ 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 coefficient of variation	PCV
Phenotypic variance	δ 2 p
Randomized Complete Block Design	RCBD
Replication	R
Research	Res.
Science	Sci.
Sher-e-Bangla Agricultural University	SAU
Triple super phosphate	TSP

CHAPTER I

INTRODUCTION

The Brassicaceae family includes 338 genera and 3709 species (Khaleque, 1985). In the family Brassicaceae, the genus *Brassica* is the one with the highest economic value. Major vegetables and oilseed crops are among the diverse group of species that make up this genus. There are numerous species in the Brassica family, including turnips, cauliflower, broccoli, Brussels sprouts, cabbage, and various mustards. These species are significant because they are used to make food, feed, edible oil, and other products.

The genus is notable for having more significant horticultural crops than any other genus. Although some are tiny shrubs, the majority are annuals or biennials. Brassica plants are important to agriculture, so they have acquired a lot of scientific investigation (Bilal *et al*., 2015). This genus has six economic importance with a great deal of genetic and physical diversity that is grown all over the world. Three of these species; *Brassica oleracea*, 2n = 18, *Brassica rapa*, 2n = 20, and *Brassica nigra*, 2n = 16; are diploid, while three; *Brassica napus*, 2n = 38, *Brassica juncea*, 2n = 36, and *Brassica carinata*, 2n = 34; are amphidiploid. As per the Triangle of U theory, rapeseed mustard (*Brassica napus, Brassica campestris, and Brassica juncea*) is cultivated all over the world as a vital source of edible oil (Abideen *et al*., 2013).

The best plant for generating oil is *Brassica napus* L., generally known as rapeseed, oilseed rape, and canola. Either Northern Europe or the Mediterranean region is where rapeseed was first domesticated. Oilseed rape (*Brassica napus* L.), after soybean, is the second-most significant oilseed crop on the global oilseed market (Sharafi *et al*., 2015).

Modern cultivars often have 40% to 45% oil in their seeds. Even though it contains oil, it also contains 18 to 22 percent proteins, which are made up of diverse protein building blocks like cysteine, methionine, and lysine. Because there is a dearth of these amino acids in cereal, *Brassica napus* L. serves as a substitute source of cereal (Khan, 2014).

In Bangladesh, there are seven different oilseed crops planted, although mustard alone takes up nearly 70% of the oilseed land. In Bangladesh, there are 814000 acres under cultivation, and 397000 mT are produced (BBS, 2021). The principal mustard-growing regions in Bangladesh include Cumilla, Tangail, Jashore, Faridpur, Pabna, Rajshahi,

Dinajpur, Kushtia, Kishoregonj, Rangpur, and Dhaka (BBS, 2021). About 90% of Bangladesh's annual requirement for edible oil is imported from The Daily Star (2023, August 14). There is a lot of uproar around the recent and unusual increase in soybean oil prices. However, we can make Bangladesh an independent producer of edible oil. Even in the 1970s, mustard oil was the primary cooking oil in this country back in the day. The refined mustard seeds have an oil content of about 39% to 44%. Therefore, the main breeding goals for mustard are to increase yield and oil content. It contains linoleic acid, which is preferred for nutritional reasons, as well as oleic acid, which is great for cooking oil due to its thermostability.

Although it has many advantages and is a rich source of vegetable oil, it is only used in very small doses since it contains significant levels of erucic acid and glucosinolates, which damage the heart muscle and render animal feed weak and nutrient-poor. Important breeding tactics include understanding and utilizing the genetic, physiological, and morphological foundation of yield-related features in various environmental situations. These strategies are necessary to increase the seed yield and adaptability of rapeseed and other Brassica species.

Importantly, it gives the body important fatty acids, such as linolenic and linoleic acids, which are lacking in most dietary oils. However, in Bangladesh, there is only a small room for acreage expansion due to the competition of the other three crops during the Rabi season, and due to the increasing cost and lengthy growing season, farmers are not interested in producing mustard seed. Therefore, the most crucial challenges with top priority are the development of enhanced *Brassica napus* types with short durational, better quality, and higher yield. This study used several populations, which are created by mating the parents of mustard types that would be anticipated to be short-duration and high-yielding, to replace the long-duration, low-yielding variety of *Brassica napus*. It would be possible to choose one of them based on the comparison to reduce the demand for edible oil in the future. In order Tore emphasize the factors that have the biggest impact on seed yield, it is vital to study the contributions of all the different factors that can have a positive or negative impact on this complicated feature known as seed yield.

The success of any crop improvement depends upon the presence of a substantial amount of genetic variability, heritability, as well as genetic gain in selection. The

potential of a crop to favorably respond to breeding/selection and bioengineering programs depends upon the nature and magnitude of genetic variability (Shaukat *et al.*, 2015).

In general, correlation coefficients display correlations between independent features and the strength of their linear relationships.

To decide on the appropriate selection criteria for a breeding program, plant breeders must 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, higher genetic diversity and a link between yield and yield components are vital criteria.

As a result, many scholars have turned to path coefficient analysis to make a more thorough assessment of the effects of the independent variables on the four dependent variables. Numerous researchers utilize the path coefficient analysis extensively in their breeding work with diverse crop species because it aids breeders in explaining both direct and indirect impacts (Ali *et al.*, 2013).

Therefore, this study was undertaken with the following objectives.

Objectives:

1. To select the promising lines with early maturity
2. To characterize various populations based on their yield and contributing parameters
3. To find out the relationship among the different traits and their contribution to the yield and
4. To select promising genotypes considering high yielding population.

CHAPTER II

REVIEW OF LITERATURE

Brassica napus is economically and genetically significant due to its high nutritional value and market demand. Due to this, the Brassica species has drawn considerable attention in several fields that are concerned with its production and utilization. For several nations around the world, including Bangladesh, it ranks among the most important oil crops. As a result, different rapeseed cultivars and types are subjected to varied tactics to yield better outcomes. Furthermore, a lot of research has been done on Brassica breeding in several countries to enhance quality, yield, and its contributing traits. There are now a large number of studies on the variability, correlation, and path analysis of the yield and yield-contributing features of Brassica that were conducted in various contexts. Here, environments have been developed to list the findings from the research that are relevant to the ongoing experiment. For the sake of this study, the full review section has been divided into the following sections:

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 s*p. has piqued the interest of scientists because of its agricultural and economic importance. The greatest agriculturally significant six species of Brassica are known as "crop Brassicas." *B. rapa* (AA, n=10*)*, *B. nigra* (black mustard) (BB, n=8), and *B. oleracea* (CC, n=9) were the three original diploid species that were present at first. Following them, three amphidiploid species; *B. napus* (AACC, n=19), *B. carinata* (BBCC, n=17), and *B. juncea* (AABB, n=18); emerged by spontaneous hybridization and chromosome doubling, as explained by the Triangle of U-theory.

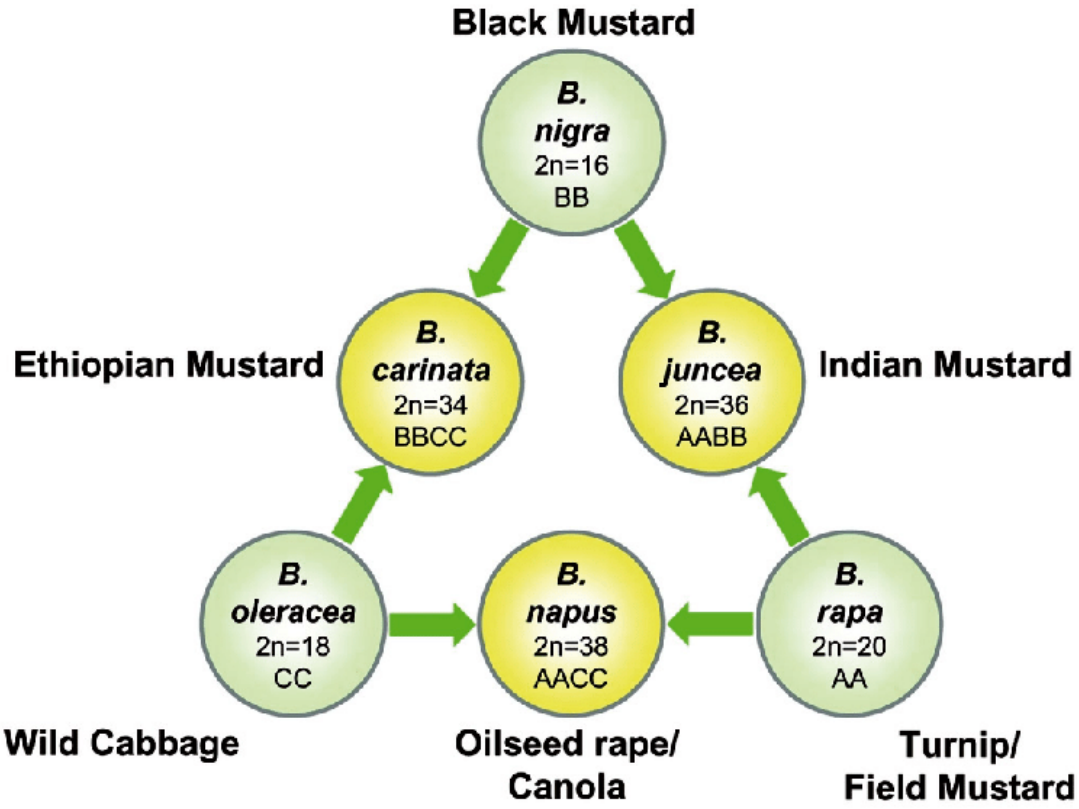

Plate 1. The "triangle of the "U" diagram, represents the genetic relationships between the six species of the genus *Brassica.*

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 are produced as weeds, especially in North America, South America, and Australia. Reviewing the information and knowledge the on performance of different genotypes, variation for genetic diversity, the relationship among yield with other yield contributing characters, genotype-environmental relations, heritability, selection on index and molecular marker-based analysis in mustard for yield and yield contributing characters is important for future breeding programs for developing short duration high yielding genotypes. *Brassica napus* L. is considered the second most important protein food resource throughout the globe after cereals. *Brassica* spp. is grown as a single or in association with other crops like wheat, chickpea, maize, etc. in both irrigated and non-irrigated regions taking us to take better steps for production and quality improvement of our local cultivars. In this aspect, many strategies and programs are conducted for the betterment of the quality and yield of

different varieties and cultivars to gain improved quality production. Due to the application of different techniques in the breeding process, remarkable improvement has been brought in the productivity and quality of edible 8 oil for using it in the 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.

Knowledge of genetic diversity gives the breeder a dependable instrument for crop improvement. Breeders must first satisfy two key conditions to boost Brassica production and quality: greater genetic variability and a connection between yield and yield components. Genetic variability is the degree to which distinct genotypes of the same trait tend to differ from one another. In contrast to genetic diversity, variability describes the degree of variation within a particular group. The variety among Brassica spp. is covered in a number several articles.

2.2 Genetic variability, heritability, and genetic advance

It is essential to understand the genetic diversity, heritability, and anticipated genetic development of different traits in a collection of mustard populations because it has been hypothesized that these genetic factors are influenced by the growing environment. Many researchers found varying sizes of genetic variation, heritability, and genetic progress for the same character. The recent research on mustard analyzed these genetic traits, and the findings will be helpful for breeding projects.

Aytac and Kinaci (2009) experimented with 10 winter rapeseed genotypes for variation, genotypic and phenotypic correlations, and broad, sense 10 heritability for seed yield, yield quality and yield contributing characters for two years. They observed maximum broad sense heritability get genetic advance seed yield followed.

Mekonnen *et al.* (2014); evaluated thirty-six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were 7 observed for several siliqua per plant, primary and secondary branches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in 11 primary branches per plant. Higher GCV and PCV for seed yield, number of siliqua per plant, and primary and secondary branches ted that, it might provide a 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 siliqua per plant, secondary branches per plant, plant height, seed yield/plot and hectare and lowest one was in primary branches per plant.

Walle *et al.* (2014); carried out a study with thirty-six genotypes of Ethiopian mustard (*Brassica carinata*) and the result revealed that there were significant differences in days to 50% flowering, plant height and primary branches per plant. GCV was lower than the PCV for 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.

Alam (2010) conducted a study to assess the differences present in several variables for their heritability, genetic advancement, etc. using 26 F_4 populations of specific interparietal crosses of *Brassica rapa*. Those characters differed significantly from one another. Little variation in phenotypes and genotypes was found when looking at plant size, siliqua length, and the number of days to 50% flowering on siliqua per plant. Plant height, the number of primary, secondary, and siliqua branches per plant, as well as how many of these branches there were on each plant, all showed high heritabilities in conjunction with significant genetic progress and extremely significant genetic progress in the percentage of the mean. The siliqua's length, however, showed little heredity.

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*.

The heritability and genetic development of plant height, the number of siliquae per raceme, the length of the main raceme, the seed output per plant, the weight of 1000 seeds, and the oil content were all examined by Mahak *et al*. in 2004. Days to blossoming, 1000-seed weight, days to maturity, and weight were the traits with the highest 12 heritability and genetic advancement as a proportion of the mean. Thakral (2004) reported significant variation in his study on variation for yield and yield contributing characters in rapeseed for eight Indian rapeseed parental lines and their 28

F_1 hybrids. Strong PCV and GCV were found for the traits of plant height and seed production.

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 (GCV and PCV, respectively) were high in magnitude. Except for plant height, all the examined features had small discrepancies between the PCV and GCV and good heritabilities, 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 and suggests that phenotypic.

Malik *et al.* (2000) reported very high broad sense heritability (h2 b>90%) while dealing with multiple *B. napus* strains for the number of primary branches per plant, days to 50% flowering, and oil content 16. In addition, they reported low heritability (h2 1, 50%) for seed production, plant height, and siliqua number per plant. Lodhi *et al.* (1979) examined 55 genotypes of *B. napus, B. rapa,* and *B. juncea* and found high heritability for each of these traits.

Heritability was investigated in an experiment with *Brassica napus* by Afrin *et al.* (2011). The highest broad sense heritability was found in the plant height, while moderate broad sense heritability was found in the number of primary and secondary branches, siliqua length, number of seeds per siliqua, number of siliquae per plant, thousand seed weight, and seed yield per plant. The heritability was lowest in the days to 80% maturity.

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

Thirty-six genotypes of Ethiopian mustard (*Brassica carinata*) were used in a study by Walle *et al*. (2014), and the results revealed that there were significant variations in the days to 50% flowering, plant height, and primary branches per plant. GCV was lower than PCV for every yield-related characteristic that was looked at. Plant height,

secondary branch count, and days to 80% maturation all demonstrated high heritability and high genetic advancement.

2.3 Interrelationship of characters

Analyzing the relationship between various attributes in a breeding program is essential. Numerous works have been written about the connections between the characteristics of Brassica spp. A review of a few of these texts is given:

Correlation coefficient analysis can be used to determine the type and degree of any relationship between any two quantifiable variables. It reduces intricate connections between events to a simple kind of association. The degree to which one variable depends on another, however, is not taken into consideration by the 15-correlation measure. In pure correlation studies, the direct contribution of each component to the yield, and the indirect effects each component has as a result of its association with other components cannot be distinguished from one another. Path coefficient analysis works well in this case. 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.

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

Brassica rapa was utilized in an experiment by Uddin *et al*. (2013) to explore the correlation between various yield components. The experiment included seven parents and twenty-one F_2 progenies. The findings revealed a strong significant positive correlation between the yield per plant and the number of primary branches per plant, secondary branches per plant, and siliqua per plant at both phenotypical and genotypic levels, as well as a significant positive correlation between days to flowering and days to maturity at the genotypic level.

Rameeh (2012) sought to ascertain the impact of planting date on variables related to yield as well as the changes in correlations between the traits in different genotypes of rapeseed planted at various times. Phonological characteristics, yield components, seed yield, and oil % all showed significant genotype and planting date effects. Significant differences in planting date genotypes were also found for these traits. The association

between flowering time and the number of siliquas per plant varied less than the correlation between flowering time and other variables at various planting dates.

In an experiment with 100 genotypes of *Brassica juncea*, Maurya *et al*. (2012) found a strong positive link between the length of the siliqua, seed yield, thousand-grain weight, and days to 50% blooming.

In an experiment using summer rapeseed, Aytac *et al.* (2008) found a positive and substantial link between seed yield and plant height, the number of siliquas per main stem, the number of seeds per siliqua, and the total number of seeds produced per plant.

Research by Ali *et al*. (2003) revealed a strong and positive association between seed weight and flowering time. The production of seeds has been directly positively impacted by seed weight and siliqua/plant. A good selection criterion for improving the seed quality and yield of winter-type rapeseeds may be the direct positive effect of seed weight coupled with a significant and direct positive correlation with seed yield.

Kumar *et al*. (2009) studied 12 yield-related trials in 15 genotypes of *B. napus* and *B. campestris*. For most characters studied, the genotypic correlation coefficient was higher in magnitude than the corresponding phenotypic correlation coefficient. Seed yield was positively correlated with plant height and 1000 seed weight.

In a study, Mahmud *et al.* (2008) discovered a highly substantial positive correlation between the number of primary branches, secondary branches, and siliqua on a plant and its seed output.

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

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

In the Department of Plant Breeding and Genetics at the University of Agriculture, Faisalabad, research on correlation for various quantitative variables related to yield and quality was done by Khan *et al.* (2006) in the years 2002–2003. *Brassica napus* L. eleven accessions and DGL as a reference cultivar were investigated. All the studied parameters, except 1000-grain weight, showed a large range of genetic variation. Seed yield per plant was positively and significantly correlated with the number of primary branches (0.4015), the number of siliquae per plant (0.505), the number of seeds per siliqua (0.79648), the length of the siliqua (0.37037), and the seed yield per plot. At the genotypic level, it was negatively and insignificantly correlated with the quantity of the secondary branches (-0.36663) and the protein content (-0.1372). They also found that indirect selection for the number of seeds per siliqua would be effective in improving the seed yield per plant in present the reading material.

According to a study by Ghosh and Gulati (2001), the number of siliquae on the main shoot, plant height, the number of secondary 32 branches, and oil content were significantly correlated positively with seed yield. These components had a very strong, favorable correlation with one another. The most crucial selection criteria for increasing seed yield in Indian mustard appeared to be there, and the findings imply that choosing one of these traits may result in an automatic accumulation of the others.

2.4 Path co-efficient analysis

The path analysis assists in determining the direct and indirect contributions of the features to yield. There is no way to differentiate between pure correlation studies, each component's direct contribution to yield, and the indirect effects each component has due to its interactions with other components. The goals of this study are achieved using path coefficient analysis. Wright (1921) invented it and gave it its original definition as a tool for genetic analysis that distinguishes between features' direct influences on yield through other components and their indirect effects on yield. Here, several researchers who have investigated the impact of a variable's direct and indirect interactions with the dependent variable on several features in rapeseed and mustard are reviewed.

In their investigation of 14 mustard genotypes, Afroz *et al*. (2004) discovered that plant height was most directly influenced by the quantity of siliqua per plant, seed yield per plant, primary branch count, 1000-seed weight, and siliqua shattering per plant.

According to Zahan (2006), silica/plant had a favorable direct effect on yield/plant. Days to 50% flowering also had a detrimental direct impact on yield and plan.

To evaluate the nature and degree of variability of 11 yield-related features of five mustard genotypes, Tusar *et al*. (2006) conducted a study. According to phenotypic correlation analyses, plant height, total dry matter production, and husk weight were all positively and significantly correlated with seed yield per hectare. Additionally, positively correlated with seed yield were the number of siliqua per plant, the weight of 1,000 seeds, the rate of crop growth 60 to 75 days after sowing, and the number of branches per plant. According to a path coefficient analysis, the number of siliqua per plant, followed by the number of seeds per siliqua and the weight of 1,000 seeds, had the greatest direct impact on seed yield. The number of siliqua per plant and the weight of 1,000 seeds also had an indirect impact. 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 a very high positive direct effect on yield, but its correlation with yield was insignificant and negative.

To estimate path analysis, Rashid (2007) conducted experimented of *oleiferous Brassica* species. He found that the yield per plant had the highest direct effect on days to maturity, the number of seeds per siliqua, the number of siliquae per plant, and the number of primary and secondary branches per plant.

In an experiment with an F_2 population of *Brassica rapa* to study path analysis, Parveen (2007) found that the number of seeds per siliqua had the greatest direct impact on plant yield.

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

Brassica napus was used in a study by Afrin *et al.* (2011) to determine the path co-efficient between the characteristics. The number of siliqua per plant, siliqua length, and plant height were found to have the highest positive and direct effects on seed yield per plant, respectively.

In an experiment with seven parental and twenty-one F_2 offspring of *Brassica rapa*, Uddin *et al*. (2013) studied the path coefficient and found that days to 50% flowering, the number of primary branches per plant, the number of 19 secondary branches per plant, the number of siliqua per plant, the length of the siliquae, the number of seeds per siliqua, and the weight of a thousand seeds per plant all directly correlated positively with the number of seeds produced per plant, while the plant

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

To explore the path analysis, Siddikee (2006) experimented on oleiferous *Brassica campestris* L., and the results showed that thousand seed weights had the strongest direct positive impact on seed yield per plant.

Twenty-eight winter rape seed cultivars were examined by Sharafi *et al.* (2015), and the results revealed that the number of plants, seeds, and 1000 seed weight had a favorable direct impact on seed yield.

CHAPTER III

MATERIALS AND METHOD

This chapter discusses the information regarding the materials and methods that were used in experiments, it includes a concise explanation of the locations of the experimental site, soil characteristics, climate, materials used in the experiment, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural practices, harvesting, data recording procedure, statistical analysis, etc. Below are the details of the supplies and procedures utilized in this experiment, organized under the following headings:

3.1 Experimental site

This research was conducted in the experimental fields of Sher-e-Bangla Agricultural University, Dhaka–1207 from November 2019 to March 2020 which was located at 23˚ 74′N latitude and 90˚ 35′ E longitudes with an elevation of 8.6 meters from the sea level (Appendix-1).

3.2 Soil and climate:

The experimental site was carried out in the subtropical zone. The soil of the experimental site belongs to the Agro-ecologicalical legion of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture olive-gray with medium distinct dark yellowish-brown mottles. The pH was 5.47 to 5.63 in the organic carbon content was 0.82% (Appendix II). The temperature, humidity, and rainfall during the period of the experiment were collected from the Bangladesh Meteorological Department, Agargaon, Dhaka.

3.3 Experimental materials

Thirty healthy seeds of *B. napus* L. were collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in the experiment are shown in Table 1.

Table 1. Materials used for the experiment

SL NO	Genotypes	Accession Code	Seed Source
1	G1	Nap-(205×0130) ×Nap-0130	SAU
2	G 2	Nap-(108×0130) ×Nap-108	SAU
3	G 3	Nap-(108×2066) ×Nap-2066	SAU
4	G 4	Nap-(9905×9901) ×Nap-9905	SAU
5	G5	Nap-(9908×2066) ×Nap-9908	SAU
6	G6	Nap-(9908×2066) ×Nap-9908	SAU
7	G7	Nap-(108×9908) ×Nap-108	SAU
8	G8	Nap-(9905×9908) ×Nap-9908	SAU
9	G9	Nap-(2066×0130) ×Nap-2066	SAU
10	G10	Nap-(9905×9908) ×Nap-9908	SAU
11	G11	Nap-(9906×205) ×Nap-205	SAU
12	G12	Nap-(9905×0130) ×Nap-9905	SAU
13	G13	Nap-(2066×205) ×Nap-205	SAU
14	G14	Nap-(9905×0130) ×Nap-9905	SAU
15	G15	Nap-(2066×205) ×Nap-205	SAU
16	G16	Nap-(205×0130) ×Nap-205	SAU
17	G17	Nap-(9906×9901) ×Nap-9906	SAU
18	G18	Nap-(9905×108) ×Nap-9905	SAU
19	G19	Nap-(108×2066) ×Nap-108	SAU
20	G20	Nap-(9905×2066) ×Nap-9905	SAU
21	G21	Nap-(108×205) ×Nap-108	SAU
22	G22	Nap-(9901×203) ×Nap-9901	SAU
23	G23	Nap-(2066×0130) ×Nap-0130	SAU
24	G24	Nap-(9908×0130) ×Nap-9908	SAU
25	G25	Nap-(2066×205) ×Nap-2066	SAU
26	G26	Nap-(108×0130) ×Nap-108	SAU
27	G27	Nap-(9908×0130) ×Nap-0130	SAU
28	G28	Nap-(9905×0130) ×Nap-9905	SAU
29	G29	Nap-(108×0130) ×Nap-108	SAU
30	G30	Nap-(9905×9901) ×Nap-9905	SAU

3.4 Methods

The following methods have been accomplished to experiment:

3.4.1 Land preparation

The experimental plot was prepared by several plowing and cross plowing and also by laddering and harrowing with a tractor and power tiller to bring good tilth condition. Weeds and other stubbles were removed from the experimental plot.

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of cow dung, fertilizers like urea, triple super phosphate, muriate of potash, gypsum, and zinc sulfate were applied in quantities of 270, 170, 100, 150 and 5 kg/ha, respectively, along with 10 ton/ha of cow dung. The half amount of urea, the total amount of cow dung, TSP, MP, Gypsum, Zinc Oxide, and Boron were applied during the final land preparation. The rest amount of the urea was applied as a top dressing after 25 days (about 3 and a half weeks) of sowing. The manure and fertilizer, doses, and application methods are represented in Table 2.

Table 2. List of fertilizer with doses and application procedures

SL No	Fertilizer	Doses	Application procedure
01	Cow dung	10 ton/ha	As basal
02	Urea	270 kg/ha	50% basal and 50% at 25 DAS
03	TSP	170 kg/ha	As basal
04	Mop	100 kg/ha	As basal
05	Gypsum	150 kg/ha	As basal
06	Zinc oxide	5 kg/ha	As basal
07	Boron	3 kg/ha	As basal

3.4.3 Experimental design and layout

The experiment was done in a Randomized Complete Block Design (RCBD) with three replications. The total land of the experiment was 20 m × 25 m = 300 m^2. Each replication size was 6m × 5m, and the distance between replication to replication was

1 m. The spacing between lines to the line was 30 cm. Seeds were sown in lines in the experimental plots in November 2020. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. A pictorial view of the experimental field during seed sowing is represented in plate 2.

Plate 2. A pictorial view of the experimental plot during seed sowing

3.4.4 Intercultural operations

Different intercultural operations such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots as per need. Irrigation was given after the sowing of seeds to bring proper moisture condition of the soil to get uniform germination of the seeds. A good drainage system was maintained for the proper release of rainwater from the experimental plot during the growing period. After 14 days (about

2 weeks) from the time of sowing, the first weeding was completed. The first thinning was carried out simultaneously and a second one was carried out seven days later to maintain a spacing of 30 cm between plants, or 10 cm (about the length of a credit card), between plants in each row. A pictorial view of the experimental field during thinning is represented in plate 3.

After seeding, Brassica plants require a key weed-free period of 15 to 30 days (about 4 and a half weeks). After 30 days (or roughly 4.5 weeks) after the time of sowing, a second weeding was completed. During the siliquae development stage, aphid infestation occurred in 34 crops. Aphids were controlled using Malathion-57 EC @ 2ml/liter of water. In the late afternoon, the insecticide was applied.

Plate 3. A pictorial view of the experimental field during thinning

Plate 4. A pictorial view of the experimental field during supervision by supervisor

3.4.5 Crop harvesting

Depending on the ripeness, harvesting began around 90 days (around 3 months) after sowing (DAS). The crop was supervised to be mature when 80% of the plants displayed signs of maturity, such as straw-colored siliquae, leaves, stems, and ideal seed color in mature siliquae. In every replication, ten plants were randomly chosen from the F_9 progeny. The plants were uprooted and collected after being properly labeled. Data on many factors were recorded from these plants. Plate provides a visual representation of an experimental field at the harvesting stage. A pictorial view of the experimental field at the vegetative stage, vegetative stage, and flowering stage is presented in Plates 4, 5, and 6 respectively.

Plate 5. The pictorial view of the experimental field during the vegetative stage

Plate 6. The pictorial view of experimental field during the flowering stage

Plate 7. The pictorial view of the experimental field during the harvesting period

3.4.6 Data collection

Eleven characters were examined in terms of several genetic parameters and their interactions. Ten plants from each line from each replication were used for data collection, a total of 900 plants for the attributes below.

3.4.6.1 Days to 1st flowering

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

3.4.6.2 Days to 50% flowering

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

3.4.6.3 Days to Maturity

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

3.4.6.4 Plant height (cm)

This measurement was taken in centimeters (cm) from the shoot to the tip of a siliqua of ten representative plants.

3.4.6.5 Number of primary branches per plant

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

3.4.6.6 Number of secondary branches per plant

The total number of branches arising from the primary branch of a plant was counted as the number of secondary branches per plant.

3.4.6.7 Number of siliqua per plant

The total number of siliqua of each plant was counted and considered as the number of siliqua per plant.

3.4.6.8 Siliqua length (cm)

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

3.4.6.9 Number of seeds per siliqua

Well, filled seeds were counted from five siliqua which were considered as the number of seeds per siliqua.

3.4.6.10 Thousand seeds weight (g)

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

3.4.6.11 Yield per plant (g)

All the seeds produced by a representative plant were weighed in grams (g) and considered as the seed yield per plant.

3.5 Statistical analysis

To investigate the mustard genotype about yield and yield-contributing traits, the gathered data from 30 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.

3.5.1 Analysis of variance (ANOVA)

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

3.5.2 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 squares for genotypes

MSE = Mean sum of square for error, and

r = Number of replications

- **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

3.5.3 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%)

3.5.4 Estimation of heritability in the 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

3.5.5 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_g^2 σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

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

3.5.6 Estimation of genetic advance in the percentage of mean

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

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

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

3.5.7 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 to make defensible conclusions on the genetic divergence of mustard genotypes.

3.5.8 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

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

Where, r denotes the simple correlation coefficient and P denotes the path coefficient.

P's in the above equations may be conveniently solved by arranging them in a 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, the 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

CHAPTER IV

RESULTS AND DISCUSSION

In the current study, information on thirty different *Brassica napus* genotypes was acquired on eleven parameters relating to vegetative, reproductive, and yield component features, with a focus on growth and yield. The data were recorded based on 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 siliqua per plant, siliqua length (cm), seeds per siliqua, thousand seeds weight (g) and seeds yield per plant (g) of 30 genotypes of *B. napus*. The data were statistically analyzed and thus acquired results are described below under the following headings:

4.1 Varietal performance and genetic parameter

4.2 Correlation studies

4.3 Path co-efficient analysis

4.1 Varietal performance and genetic parameter

Any crop improvement program's success depends on the breeder's ability to identify and accumulate the necessary genetic variability, as well as to select for yield indirectly through highly heritable traits that are yield-related after the environmental component of phenotypic variation has been eliminated (Mather, 1949). To compute the estimate of heritability that assists the breeder in predicting the expected GA potentially by selection for a character, it is important to have previous knowledge about both PCV and GCV. The results of the analysis of variance (ANOVA), range, grand mean, coefficient of variation (CV%), mean performance, genotypic and phenotypic variance, heritability in the broad sense (h^2b), and expected genetic advance as a percentage of the mean (GA) for all eleven traits are provided in Tables 3 through Table 5. Figure 9 displays the genetic and phenotypic coefficient of variation; Figure 10 depicts heritability and genetic progress as a percentage of the mean. Plant height, the number of primary branches per plant, and the number of secondary branches per plant are regarded to be the three growth-attributing characteristics out of the eleven characteristics studied. Days to 50% flowering and days to maturity were viewed as earliness characteristics. Reproductive traits included the number of siliqua per plant,

their length, the number of seeds they contained, and their weight in terms of one thousand seeds. An economic characteristic that is the yield per plant studied below is an explanation of the variability's specifics, split down each character. The genotypes of eleven traits were examined.

4.1.1 Days to first flowering

Highly significant variation was found among the genotypes in the case of days to first flowering with the mean sum of square 13.07** (Table 3). It varied from 24.00 DAS to 32.00 DAS with a mean value of 27.99 (Table 4). The highest duration for days to first flowering was recorded in G29 (32.00 DAS) followed by G16 and G22 (31.00 DAS) where G8 required 24.00 DAS to take first flowering, the lowest among the genotypes (Table 4). The phenotypic variance was (5.90) slightly higher than the genotypic variance (3.58) and the genotypic and phenotypic coefficient of variations were 6.76 and 8.68, respectively. This minor difference between the phenotypic and genotypic coefficient of variation explored that the present variation was mainly contributed by the genotypes as the environmental influences were negligible. The value of GCV and PCV indicated lower variation was present among the genotypes for the trait. Days to first flowering showed the highest heritability (60.71%) with medium genetic advance as a percentage of the mean (10.86%) indicated, inheritance of days to first flowering might be controlled by the additive gene effects (Table 5). It was supported by Shekhawat *et al.* (2014) finding in which high heritability (62.05%) with moderate genetic advance (15.36%) was estimated, suggesting that high to moderate heritability with high to moderate genetic advance was due to additive gene action and simple selection may be effective.

4.1.2 Days to 50% flowering

Significant variations were observed in days to 50% flowering among the 38 advanced populations of *B. napus* (47.07**) (Table 3). The minimum duration of days to 50% flowering was found in G9 with 30.33 DAS indicating that 50% flowers appeared earlier in G9 than other genotypes after sowing. The earliness of 50% flowering of the population indicated that the plants matured early. The genotype G22 took the maximum period for 50 % flowering with 43.00 DAS followed by G3(42.33) and G16(42.00) (Table 4) The mean value was recorded as 35.22. Ali *et al.* (2002) found days to 50% flowering for parents which ranged from 39 to 46 days. The phenotypic

variance (17.97) was higher than the genotypic variance (14.55) and the variation between them was moderate indicating that the environment had a moderate influence on the expression of the character (Table 5). The GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) were moderate with values of 10.86 and 12.07 per percent respectively (Table 5) (Figure 9). High heritability of 80.98% with low genetic advance (7.07%) was noted for the character and the value of genetic advance in percent of mean was high (20.13%) (Table 5) (Figure 9). High heritability having low genetic advance but high genetic advance in percent of mean suggested the prevalence of additive and non-additive gene action and so, improvement through selection might be effective. Akter (2010) reported high heritability (88.86%) and low genetic advance (2.06) for days to 50% flowering which was similar to the findings.

4.1.3 Days to Maturity

The mean sum of squares for days to siliqua maturity was 54.95** with a high amount of variation (Table 3). The average days required to be matured of the siliqua was 86.51 ranging from 76.33 DAS to 92.33 DAS (Table 4). For days to maturity, 92.33 DAS was required for G20 which was the highest duration for days to maturity followed by G10 (90.67 DAS), however, the lowest days to maturity was observed in G18 (76.33 DAS) (Table 4). The mean performance of days to maturity in 30 genotypes of *B. napus* is shown in Figure 1 through a line graph. Days to siliqua maturity exhibited moderate genotypic variance (15.95) and higher phenotypic variance (23.06) along with lower phenotypic coefficient of variation (5.54) and genotypic coefficient of variation (4.61). The difference between phenotypic variance and genotypic variance indicates environmental factors slightly influencing the expression of this trait. (Table 5). A high heritability (69.15%) was observed for the trait including, a lower value of genetic advance (6.84%) and genetic advance as a percentage of the mean (7.89%) indicating 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 the low genotypic advance in percent of the mean for days to siliqua maturity, therefore, Selena action for this trait might rewarding. It was Alando supported by Tewachew and Mohammed (2018), who estimated heritability for days to siliqua maturity was moderate.

4.1.4 Plant height (cm)

Considerable variation among the genotypes was observed in plant height. ANOVA revealed the mean sum squares for plant height was 166.23** (Table 3) where the maximum plant height was 134.00 cm and the lowest was 96.67 cm (Table 4) with a mean value of 115.27. The highest plant height was observed in G1 (134.00 cm) followed by G29 (132.63 cm). The lowest plant height was found in G17 (96.67 cm) (Table 4). The Mean performance of plant height (cm) in 30 genotypes of *B. napus* is shown in Figure 2 through a line graph. For plant height, the genotypic and phenotypic variance was recorded as 32.72 and 100.79 respectively (Table 5) with higher environmental variance (68.08). Differences between these two variances indicate environmental factors influence the expression of this trait. The highest genotypic, phenotypic, and environmental variances were observed in plant height as reported by Khan *et al.*, (2013). Phenotypic and genotypic coefficient of variation for the trait was lower 8.71 and 4.96 respectively, (Table 5). On the contrary, moderate genotypic and phenotypic coefficient of variations (14.22 and 15.89 respectively) was found by Nagoo *et al.,* (2021). Low heritability (32.46%) with a low value of genetic advance (6.71%) and low genetic advance as a percentage of the mean (5.82%) were observed for plant height. It was found Patel *et al.* (2019) findings, revealed plant height expressed high heritability (89.72%) with moderate genetic advance as a percent of the mean (14.62%). Mekonnen *et al.* (2014), Bibi *et al.* (2016) and, Gupta *et al.* (2019) reported high heritability with high genetic advance as a percentage of the mean for plant height. Moderate heritability with low genetic advance as a percent of mean revealed that expression of plant height was controlled by non-additive genetic action, hence, selection for this trait may not be effective to get shorter plants.

4.1.5 Number of primary branches per plant

The number of primary branches per plant showed highly significant variations among the tested advanced populations (0.79**) (Table 3). The Maximum number of primary branches per plant was noticed in G28 (5.33) and the minimum number of primary branches per plant was found in G4 (3.00) (Table 4). The mean value was 3.74 (Table 4). G28 showed the maximum number of primary branches per plant (5.33) indicating more siliquae than the other populations which ultimately increased yield per plant. The Mean performance of the number of primary branches per plant in 30 genotypes of *B. napus* is presented in Figure 3 through a line graph. The genotypic and phenotypic variance was recorded as 0.15 and 0.49 percent, respectively which suggested that there was less influence of environment on this character (Table 5). Naznin *et al*. (2015) showed the least differences between the phenotypic variance (1.27) and genotypic variance (0.86) in the case of the number of primary branches per plant which indicated that there was less influence of environment on this character. The Findings of Hosen *et al.* (2008) also agreed with this result. The values of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) were high, 10.44 and 18.84 percent (Figure 9), respectively. Moderate heritability 30.68% along with low genetic advance (0.44%) (Table 5) (Figure 10) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded as moderate (11.91%) (Table 5) (Figure 10).

Table 3. Analysis of variance for eleven characters of 30 genotypes of *Brassica napus*

Characters	Mean sum of square			CV (%)
	Replication (r-1) = 2	Genotype (g-1) = 29	Error (r-1) (g-1) = 58	
DFF	0.74	13.07**	2.32	5.44
DFPF	1.21	47.07**	3.42	5.26
DM	22.01	54.95**	7.11	3.08
PH	280.89	166.23**	68.08	7.16
NPBP	3.24	0.79**	0.34	15.69
NSBP	6.84	1.25*	0.70	26.97
NSPP	387.58	950.89**	326.62	14.07
SL	2.52	0.80*	0.48	8.47
SPS	47.48	21.61**	8.96	11.22
TSW	0.95	2.70**	0.24	10.1
SYPP	0.39	8.39**	0.21	7.83

*, 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=r of siliqua per plat, SL= Siliqua length (cm), SPS= Seeds per siliquae, TSW= Thousand seeds weight (g), SYPP= Seeds yield per plant (g)

Table 4. Mean analysis of yield contributing parameters

Genotypes	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	SYPP
G1	25.00gh	32.33hij	85.00cde	134.00a	3.00d	1.33f	107.33i	6.87d	20.50g	3.30h	3.73m
G2	25.00gh	32.33hij	83.33e	112.00 de	3.67 bcd	3.67abcd	152.93abc	8.70ab	25.40bcdef	3.90efgh	3.92lm
G3	28.00cdef	42.33a	77.67f	112.67cde	4.00bc	4.00ab	148.67abcde	8.46abc	22.73efg	5.81a	6.06cdef
G4	30.00abc	31.33ij	90.33ab	115.00cde	3.00d	3.00abcde	158.00ab	8.43abc	24.87bcdefg	3.71h	4.10jklm
G5	27.33defg	32.00hij	89.00abc	110.67de	3.00d	3.47 abcde	139.33abcdefg	8.23abc	25.00bcdefg	5.67ab	7.74b
G6	27.33defg	32.00hij	89.00abc	122.00 abcd	3.67bcd	3.00abcde	110.33ghi	6.93d	26.67abcde	3.77gh	3.77m
G7	25.00gh	31.33ij	88.00abcd	102.67 ef	3.67 bcd	3.83abc	122.00defghi	8.00abcd	28.33abc	5.88a	6.20cdef
G8	24.00h	30.67ij	83.67de	112.20 de	3.67 bcd	3.00abcde	146.40abcde	8.33abc	28.67abc	5.813a	6.47cde
G9	25.00gh	30.33j	88.00abcd	120.50 bcd	3.67bcd	3.83abc	150.60abcd	8.73ab	25.00bcdefg	3.77gh	4.03klm
G10	29.00bcd	32.00hij	90.67ab	112.33 cde	3.83bcd	4.00ab	109.33hi	8.36abc	30.53a	3.76gh	5.92defg
G11	28.00cdef	32.00hij	89.33abc	120.43bcd	4.00bc	2.33def	120.30efghi	7.52cd	29.00ab	4.68de	4.84hij
G12	28.67bcde	32.00hij	78.00f	117.00 cd	3.67bcd	3.33abcde	143.50abcdef	8.73ab	30.47a	6.2967a	9.69a
G13	30.00abc	31.67ij	90.00ab	114.67 cde	3.00d	2.67bcdef	138.00abcdefgh	8.40abc	27.00abcde	5.53abc	7.51b
G14	28.67bcde	40.33abcd	89.33abc	109.67def	4.33b	3.00abcde	149.00abcde	8.12abc	23.33defg	3.85fgh	4.14jklm
G15	29.00bcd	41.00abc	88.33abc	115.67 cde	4.33b	3.00abcde	107.33i	8.60abc	25.33bcdefg	5.69ab	7.95b
G16	31.00ab	42.00ab	87.67bcde	114.67cde	4.33b	3.00abcde	135.67abcdefghi	8.10abc	27.40abcde	4.78cd	5.76efg
G17	29.67abcd	39.00bcde	86.67bcde	96.67f	3.83bcd	3.00abcde	108.33i	8.67ab	26.47abcde	5.62ab	6.61cd
G18	27.67cdef	35.00fgh	76.33f	111.33de	3.00d	3.00abcde	115.33fghi	7.50cd	25.00bcdefg	3.72gh	5.60fg
G19	28.67bcde	36.00efg	77.00f	110.33 de	3.67bcd	3.83abc	114.90fghi	7.77bcd	23.93cdefg	3.77gh	4.07klm
G20	27.33defg	36.00efg	92.33a	109.33def	3.33cd	2.17ef	163.52a	9.10a	31.33a	6.30a	10.09a
G21	30.67ab	40.00abcd	85.00cde	115.00 cde	3.67bcd	3.33abcde	110.67ghi	8.43abc	29.00ab	3.79gh	5.55fgh

Table 4. (Cont'd.)

Genotypes	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	SYPP
G22	31.00ab	43.00a	90.33ab	121.00abcd	3.50bcd	3.67abcd	111.00ghi	8.47abc	27.00abcde	5.79a	7.75b
G23	28.00cdef	36.67efg	87.33bcde	125.77abc	4.33b	2.17ef	115.33 fight	8.09 abc	29.33ab	5.78a	6.51cde
G24	28.67bcde	38.33cde	85.33cde	111.00 de	3.67bcd	2.50cdef	123.33defghi	7.64bcd	27.33abcde	3.85fgh	4.48jklm
G25	28.67bcde	37.67def	88.67abc	118.00 cd	3.33cd	3.33abcde	109.67hi	8.50abc	29.00ab	4.93bcd	5.27ghi
G26	26.00fgh	33.67ghi	89.33abc	112.00 de	4.00bc	2.67bcdef	107.33i	7.83bcd	20.80fg	5.85a	6.14cdef
G27	25.00gh	32.67hij	90.00ab	116.00 cde	3.39bcd	3.00abcde	138.00abcdefgh	8.37abc	27.00abcde	4.71d	5.26ghi
G28	26.33efgh	31.33ij	87.33bcde	117.00cd	5.33a	4.33a	142.00abcdef	8.00abcd	28.00abcd	4.63def	4.74ijk
G29	32.00a	35.00fgh	88.67abc	132.63ab	4.00bc	2.83bcde	125.33cdefghi	8.51abc	28.07abcd	4.51defg	4.53ijkl
G30	29.00bcd	33.67ghi	88.00abcd	115.67 cde	3.40bcd	2.83bcde	129.67bcdefghi	7.87bcd	27.67abcd	4.81cd	6.72c
Min	24.00	30.33	76.33	96.67	3.00	1.33	107.33	6.87	20.50	3.30	3.73
Max	32.00	43.00	92.33	134.00	5.33	4.33	163.52	9.10	31.33	6.30	10.09
Mean	27.99	35.22	86.51	115.27	3.74	3.09	128.87	8.16	26.62	4.81	5.91
SE	1.24	1.51	2.18	6.74	0.48	0.68	14.76	0.57	2.44	0.40	0.37
LSD	2.49	3.02	4.36	13.49	0.95	1.37	29.54	1.13	4.89	0.79	0.75

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 siliqua per plant, SL= Siliqua length (cm), SPS= Seeds per siliquae, TSW= Thousand seeds weight (g), SYPP= Seeds yield per plant (g)

Table 5. Estimation of genetic parameters in eleven characters of 30 genotypes of *Brassica napus*

Parameters	Mean	σ^2p	σ^2g	σ^2 e	PCV	GCV	ECV	Heritability (%)	Genetic Advance (5%)	Genetic Advance (% of mean)
DFF	27.99	5.90	3.58	2.32	8.68	6.76	1.92	60.71	3.04	10.86
DFPF	35.12	17.97	14.55	3.42	12.07	10.86	1.21	80.9and n8	7.07	20.13
DM	86.66	23.06	15.95	7.11	5.54	4.61	0.93	69.15	6.84	7.89
PH	115.26	100.79	32.72	68.08	8.71	4.96	3.75	32.46	6.71	5.82
NPBP	3.71	0.49	0.15	0.34	18.84	10.44	8.41	30.68	0.44	11.91
NSBP	3.10	0.89	0.18	0.70	30.31	13.82	16.49	20.78	0.40	12.97
NSPP	128.44	534.71	208.09	326.62	18.00	11.23	6.77	38.92	18.54	14.43
SL	8.18	0.59	0.11	0.48	9.36	3.99	5.37	18.15	0.29	3.50
SPS	26.67	13.18	4.22	8.96	13.61	7.70	5.91	32.02	2.39	8.98
TSW	4.81	1.06	0.82	0.24	21.40	18.86	2.53	77.72	1.65	34.26
YPP	5.84	2.94	2.73	0.21	29.34	28.28	1.06	92.87	3.28	56.14

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

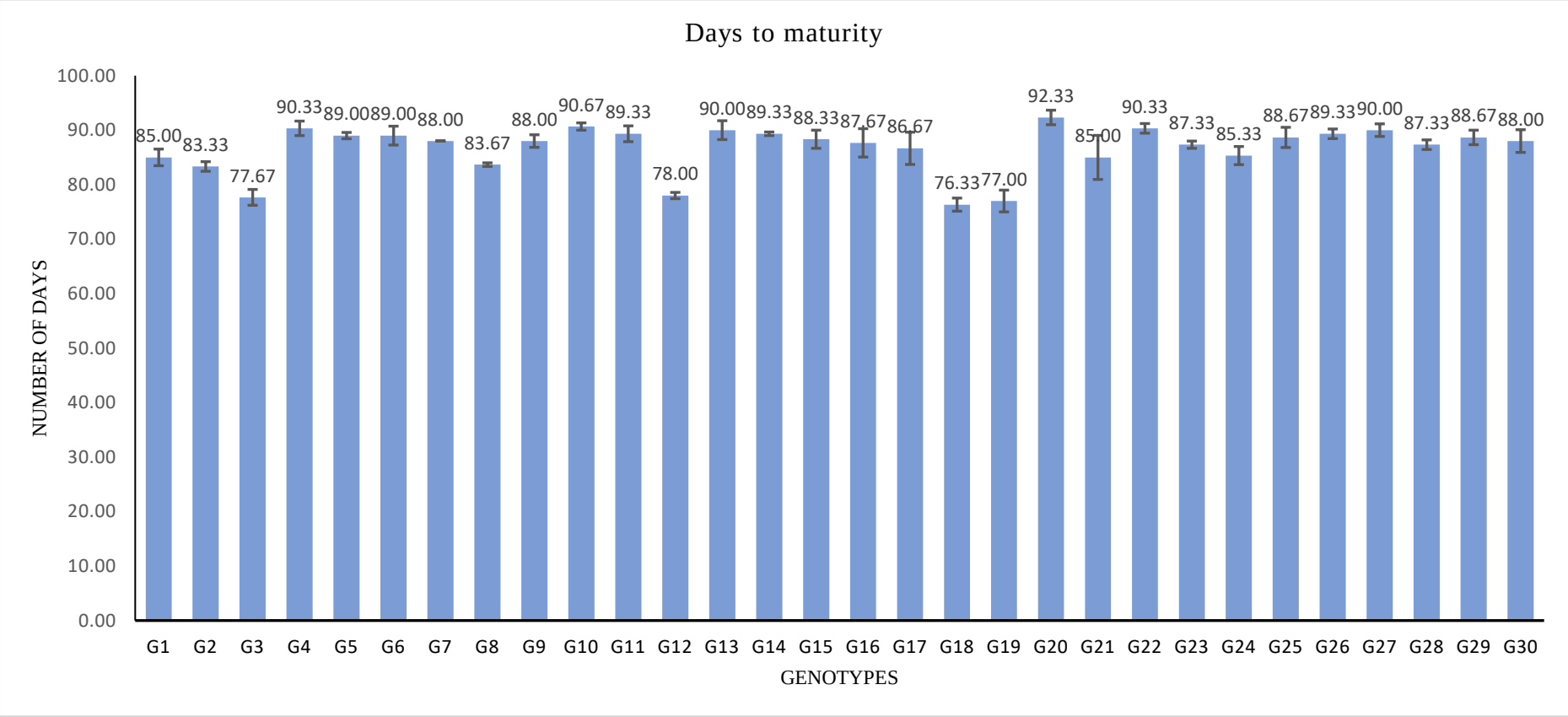

Figure 1. Mean performance of days to maturity in 30 genotypes of *B. napus*

4.1.6 Number of secondary branches per plant

Significant variations were observed for the number of secondary branches per plant (1.25*) suggesting that large variations are present among the tested genotypes (Table 3). The maximum number of secondary branches was found in G28 (4.33) with a greater number of siliquae per plant (142.00) which was a good sign for increasing yield and ultimately highest seed yield per plant was found in G20 (10.09). The minimum number of secondary branches per plant was found in G1 (1.33). The mean value was 3.09 (Table 4). The Mean performance of the number of secondary branches per plant in 30 genotypes of *B. napus* is presented in Figure 4 through a line graph. The genotypic and phenotypic variance were recorded as 0.18 and 0.89 respectively and the phenotypic variance was slightly higher than the genotypic variance. Less environmental influence was found due to little difference between genotypic and phenotypic variance. The values of moderate GCV (Genotypic Coefficient of Variation) and high PCV (Phenotypic Coefficient of Variation) were 13.82 and 30.31 percent, respectively (Table 5) (Figure 9). Sikarwar *et al.* (2017) reported a high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for the number of secondary branches per plant. Naznin *et al.* (2015) showed the same findings. Low heritability 20.78% along with low genetic advance (0.40%) (Table 5) (Figure 10) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded as moderate (12.97%) (Table 5) (Figure 10).

4.1.7 Number of siliqua per plant

The mean sum of squares for the number of siliquae per plant was 950.89**revealed that highly significant variation was present among the selected genotypes (Table 3). The maximum siliqua production was recorded as 163.52 while the lowest value was 107.33 with a mean value of 128.87 siliqua per plant. The highest number of siliquae was observed in G20 (163.52) which was statistically similar to G9 (150.60) whereas the lowest number of siliquae was found in G26 (107.33) (Table 4). The Mean performance of the number of siliqua per plant in 30 genotypes of *B. napus* is presented in Figure 5 through a line graph. In the case of Brassica species siliqua, the number ranged from 215.66 to 350.66, as estimated by Patel *et al.*, (2021). The phenotypic variance (534.71) and

genotypic variance (208.09) was higher with a large environmental variance (326.62) found for the selected trait. However, the moderate genotypic coefficient of variance (11.23) and phenotypic coefficient of variance (18.00) were recorded (Table 5). For the number of siliqua per plant, the lower GCV (7.49) and moderate PCV (11.38) were supported by Yadava *et al.,* (2011). The larger difference between phenotypic variance and genotypic variance indicates higher environmental influences on the expression of the trait. Similar results were observed by Khan *et al.,* (2013).

The heritability estimated for this trait was moderate (38.92%) along with moderate genetic advance (18.54%) and a moderate genetic advance as a percentage of the mean (14.43%), (Table 5). Mandal *et al*. (2022) similarly observed high heritability (80.61%) with moderate genetic advance (14.36%). So, this trait could be exploited for further improvement by the selection procedure. Mekonnem *et al.* (2014) and Alam (2010) estimated that siliquas per plant had moderately high GCV and genetic advance and high heritability.

4.1.8 Siliqua length (cm)

The mean siliqua length was 8.16 and ranged from 6.87 to 9.10 cm (Table 4). The genotypes of G20 (9.10 cm) had long siliqua which was followed by G9 and G12 (8.73 cm) and G2 (8.70 cm). The siliqua was shorter in G1 (6.87 cm) and it was followed by G6 (6.93 cm) (Table 4). The mean sum of squares was significant (0.80*) which indicated a considerable amount of variation for this trait in the varieties (Table 3). The genotypic and phenotypic variance for siliqua length was seen as a value of 0.11 and 0.59, respectively. Siliqua length exhibited low GCV (3.99%) and PCV (9.36%) values (Table 5). A Similar result was seen by Khan *et al.* (2013). As PCV is higher than GCV thus we can conclude that the trait is controlled by its genotype as well as the influence of the environment. A low heritability estimates of 18.15%, low genetic advance of 0.29% and a low genetic advance as the percent of mean 3.50% were observed (Table 5). Low heritability with a combination of low genetic advance as a percent of mean suggested that this character was predominantly controlled by the 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.

4.1.9 Seeds per siliqua

The number of seeds per siliqua ranged from 20.50 to 31.33 with an average of 26.62 among the different varieties (Table 4). The maximum number of seeds was found in G20 (31.33) which was statistically like G10 (30.53) and G12 (30.47) while the lowest number of seeds was estimated in G1 (20.50) followed by G26 (20.80). The Mean performance of seeds per siliqua in 30 genotypes of *B. napus* is presented in Figure 6 through a line graph. The mean sum square for the trait was recorded as 21.61** (Table 3). According to Patel *et al.* (2021) seeds per siliqua varied from 11.80 to 16.46. The genotypic and phenotypic variance for the trait was 4.22 and 13.18, respectively with an environmental variance of 8.96 (Table 5). Lower case of genotypic coefficient of variance (7.70) and moderate phenotypic coefficient of variance (13.61were observed for the trait. Yadava *et al.* (2011) obtained a similar genotypic and phenotypic coefficient of variance (1.11 and 2.03, respectively). Moderate phenotypic variance with considerable environmental variance indicated that the expression of the character was moderately associated with the environmental interaction. A moderate heritability (32.02%) besides lower genetic advance (2.39%) and genetic advance as a percentage of the mean (8.98%) indicates, that the character is governed by both non-additive gene actions. Improvement of the character required further selection procedures for the extended generations. High heritability (86.00%) and moderate genetic advance (10.81werewas narrated by Hussain *et al.* (2014) and Czern (2020).

4.1.10 Thousand seeds weight (g)

Thousand seed weights (g) showed significant variations (2.70**) among the tested genotypes (Table 3). Maximum thousand seeds weight (g) was found in G20 (6.30 g) which increased the possibility of higher yield and ultimately highest yield was found from G20 (10.09 g) followed by G26 (5.85 g), G22 (5.79 g) and G23 (5.78 g) whereas minimum thousands of seeds weight (g) was found in G1 (3.30 g) (Table 4) with an average mean value of 4.81 g (Table 4). The mean performance of thousand seed weights in 30 genotypes of *Brassica napus* L. is embellished in Figure 7 through a bar graph. The values of phenotypic variance and genotypic variance were 1.06 and 0.82, respectively. The little difference between them indicates the less influence of the environment on this trait. The values of GCV (Genotypic Coefficient of Variation) and

PCV (Phenotypic Coefficient of Variation) were moderate, 18.86 and 21.40 percent, respectively (Table 5) (Figure 9).

High heritability 77.72% along with low genetic advance (1.65%) (Table 5) (Figure 10) indicates the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded as high (34.26%) (Table 5). 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.

4.1.11 Yield per plant (g)

Significant variation was observed among the genotypes and the mean sum of squares for yield per plant was 8.39** (Table 3). The estimated result revealed that yield per plant varied from 3.73 g to 10.09 g with an average of 5.91 g (Table 4). The highest value was observed in G20 (10.09 g) which was statistically similar with G12 (9.69 g), G5 (7.74 g) and G13 (7.51 g). However, Genotype G1 was recorded for the lowest yield value at 3.73 g (Figure 8). Yield per plant exhibited the lowest value for genotypic (2.73) and phenotypic variance (2.94) whereas the environmental variance was negligible. The estimated phenotypic coefficient of variance (29.34) and genotypic coefficient of variance (28.28) were high (Table 5), indicating high variations were exhibited by yield per plant that could be beneficial for selecting the segregating lines next. The highest heritability (92.87%) was recorded for this character along with low genetic advance (3.28%) and high genetic advance as a percentage of the mean (56.14%). Therefore, selection might be effective as the expression was controlled by the additive genetic effects. Yadava *et al.* (2011) recorded the maximum GCV and PCV for seed yield per plant (51.46 and 55.64) followed by biological yield per plant (48.98 and 52.27), harvest index (24.20 and 36.70), test weight (25.64 and 26.17) and siliqua the on the main primary branches. While Patel *et al.* (2019) found the moderate phenotypic coefficient of variation in seed yield per plant (16.42) and total number of branches per plant (11.58). Afrin *et al.* (2017), Rout *et al.* (2019) and Aktar *et al.* (2019) observed high heritability coupled with high genetic advance as percentage of the mean for seed yield of *Brassica juncea*.

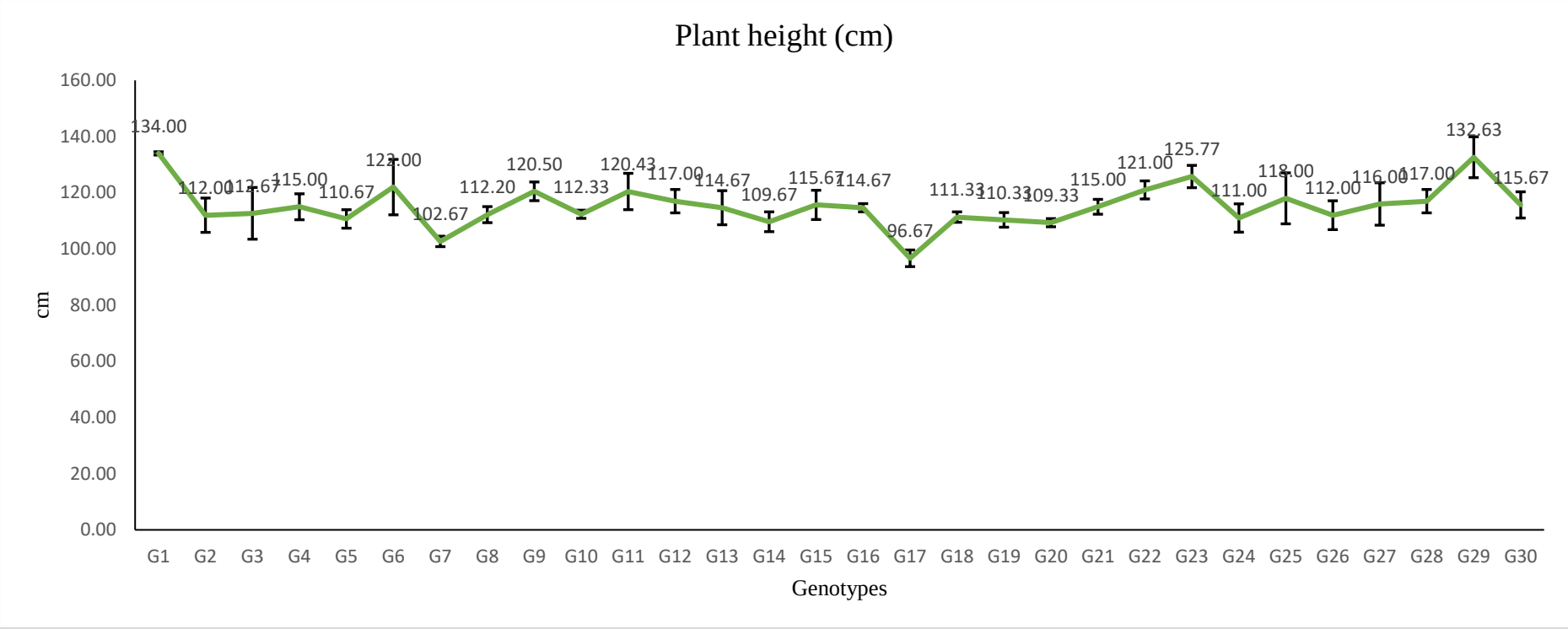

Figure 2. Mean performance of plant height (cm) in 30 genotypes of *B. napus*

A

B

C

Plate 8. Pictures showing (A) Highest siliqua length of genotype G20, (B) lowest siliqua length of genotype G1, (C) variation among 1000 seeds of *Brassica napus*

4.2 Correlation studies

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. When selecting two opposing desired characters has an impact on the main characters, the phenotypic and genotypic correlation displays the degree of association between various characters, which aids in basing the selection process on the necessary balance. 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.Given its complexity, yield is controlled by several different genes. To determine 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 coefficient for 11 traits across the genotypes of *Brassica napus* that were examined.

4.2.1 Days to first flowering

Days to first flowering exhibited highly significant and positive correlation with days to 50% flowering (r_g = 0.593**, r_p = 0.539**), siliqua length (cm) (r_g = 0.356**) and seeds per siliqua (r_p = 0.260*), pointing out a possible increase in days to 50% flowering, siliqua length (cm) and seeds per siliqua by increasing days to first flowering. It exhibited a highly significant and negative correlation with the number of siliqua per plant (r_g = -0.366**) which indicated a possible increase in the number of siliqua per plant by decreasing days to first flowering. It also showed insignificant and positive correlation with days to maturity ($r_g = 0.169^{ns}$, $r_p = 0.027^{ns}$), plant height (cm) ($r_g = 0.158^{ns}$, $r_p = 0.011^{ns}$), number of primary branches per plant ($r_g = 0.010^{ns}$, $r_p = 0.084^{ns}$), number of secondary branches per plant ($r_p = 0.063^{ns}$), siliqua length (cm) ($r_p = 0.099^{ns}$), seeds per siliqua ($r_g = 0.199^{ns}$) and yield per plant (g) ($r_g = 0.184^{ns}$, $r_p = 0.143^{ns}$). It also showed an insignificant and negative correlation with the number of secondary branches.

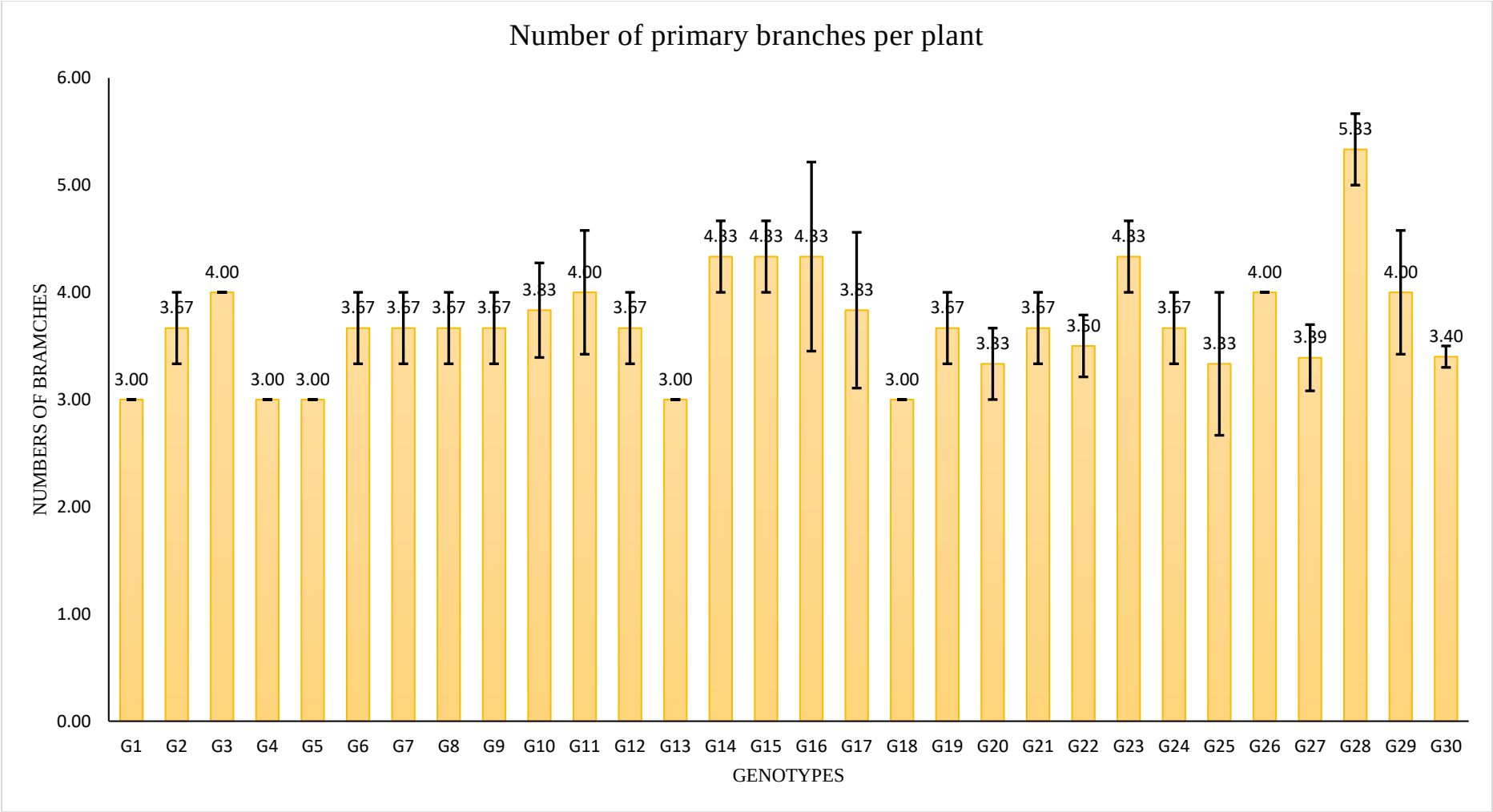

Figure 3. Mean performance of number of primary branches per plant in 30 genotypes of *B. napus*

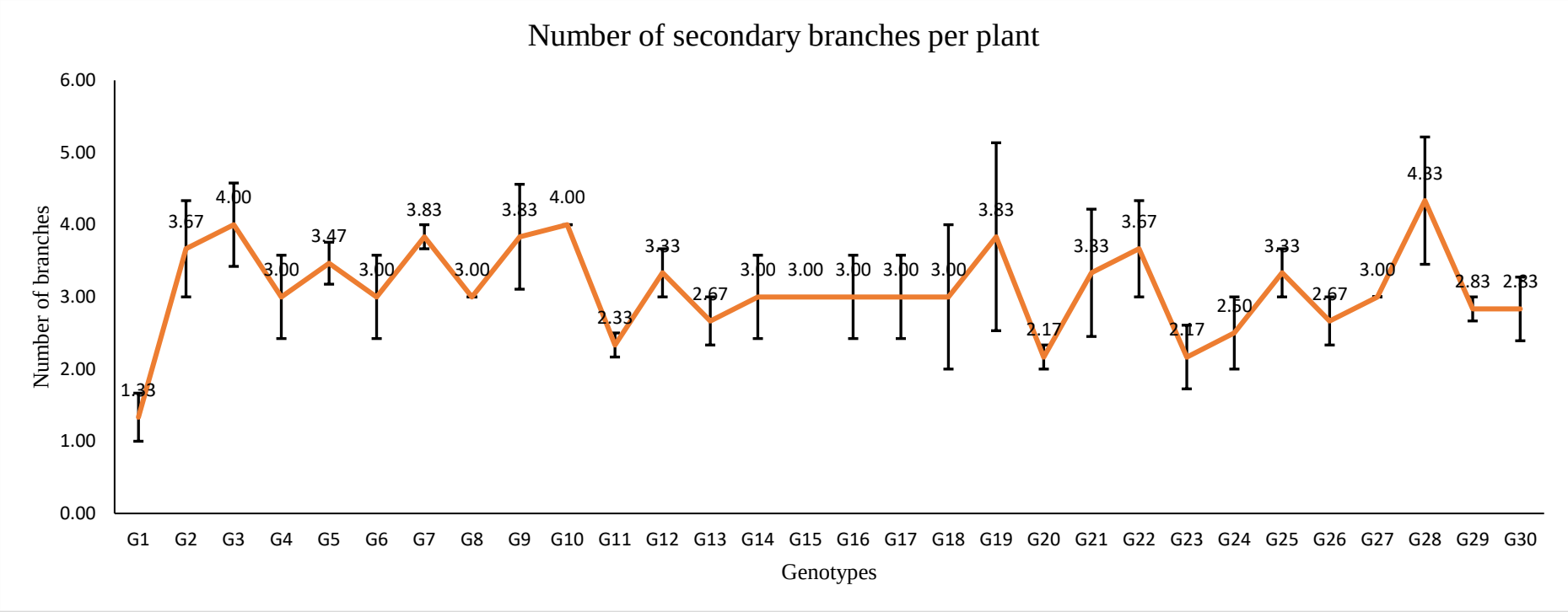

Figure 4. Mean performance of number of secondary branches per plant in 30 genotypes of *B. napus*

plant (r_g = -0.102^{ns}), number of siliqua per plant (r_p = -0.083^{ns}) and thousand seeds weight (g) (r_g = -0.004^{ns}, r_p = -0.008^{ns}). An insignificant association of these traits revealed that the combination of these traits was largely influenced by environmental factors (Table 6).

4.2.2 Days to 50% flowering

Days to 50% flowering exhibited a highly significant and positive correlation with number of primary branches per plant (r_g = 0.328**, r_p = 0.201^{ns}) and siliqua length (cm) (r_g = 0.354**, r_p = 0.077^{ns}). It exhibited a highly significant and negative correlation with the number of siliqua per plant (r_g = -0.322**) which indicated a possible increase in the number of siliqua per plant by decreasing days to 50% flowering. It also showed insignificant and negative correlation with number of primary branches per plant (r_p = 0.201^{ns}), number of secondary branches per plant (r_g = 0.030^{ns}, r_p = 0.001^{ns}), siliqua length (cm) (r_p = 0.077^{ns}), thousand seeds weight (g) (r_g = 0.166^{ns}, r_p = 0.120^{ns}) and yield per plant (g) (r_g = 0.166^{ns}, r_p = 0.146^{ns}). It also showed insignificant and negative correlation with days to maturity (r_g = -0.107^{ns}, r_p = -0.087^{ns}), plant height (cm) (r_g = -0.173^{ns}, r_p = -0.082^{ns}), number of siliqua per plant (r_p = -0.154^{ns}), and seeds per siliquae (r_g = -0.129^{ns}, r_p = -0.050^{ns}). Insignificant association of these traits suggested that the interrelationship between these traits was largely influenced by environmental factors (Table 6).

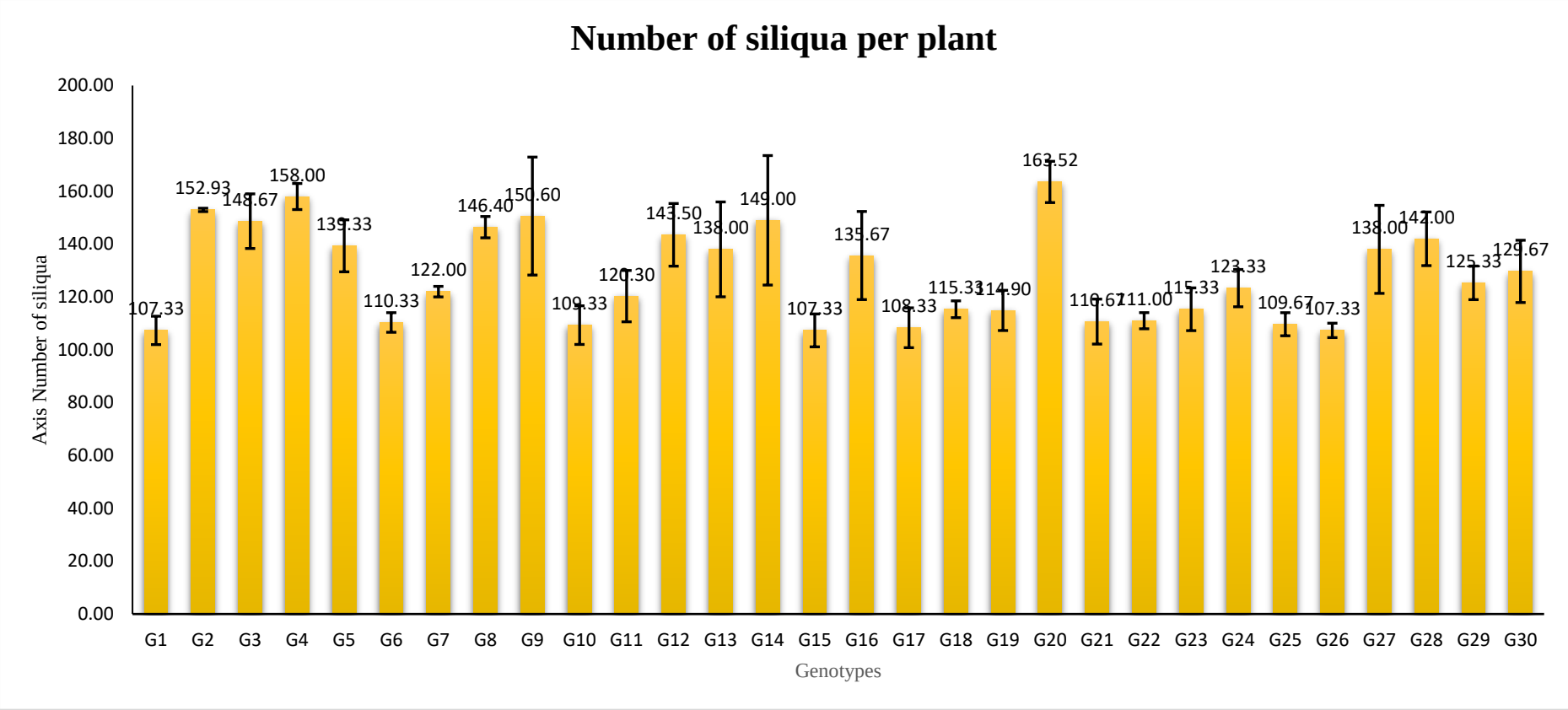

Figure 5. Mean performance of the number of siliqua per plant in 30 genotypes of *B. napus*

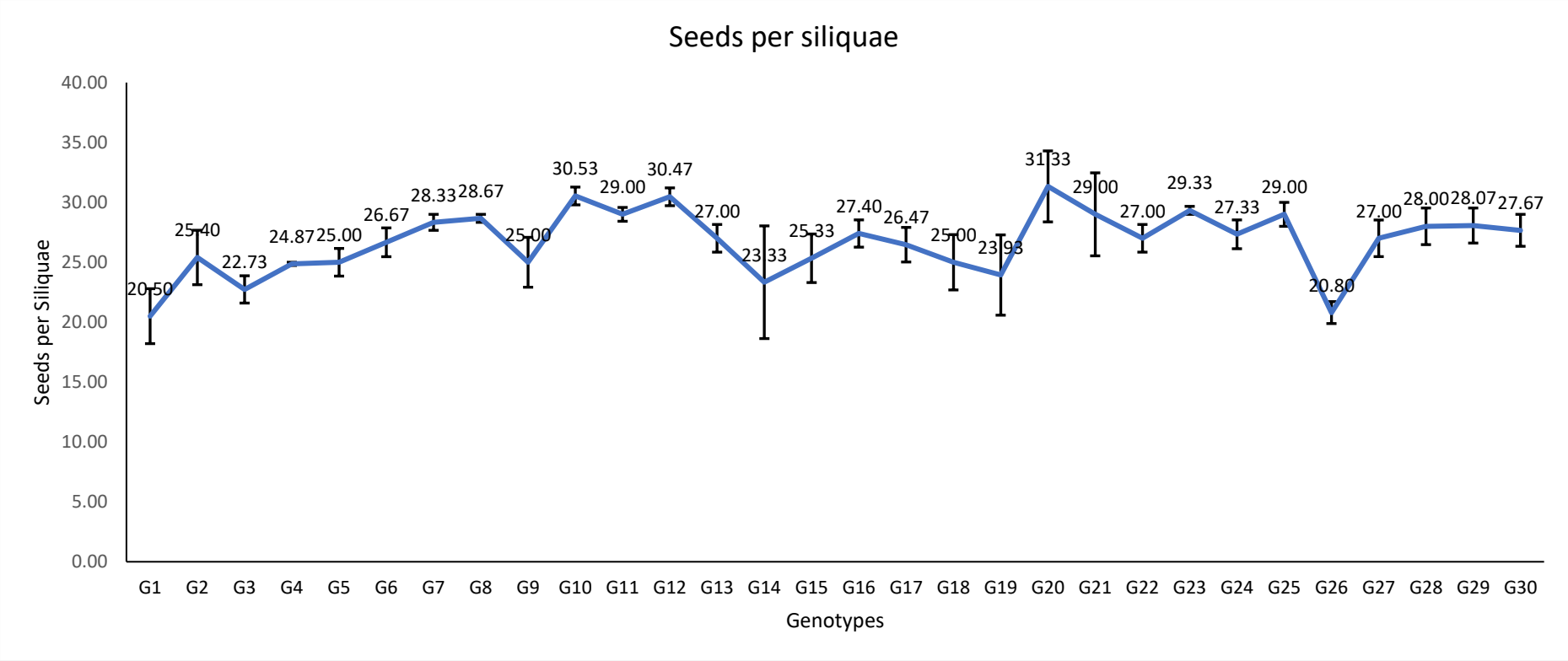

Figure 6. Mean performance of seeds per siliquae in 30 genotypes of *B. napus*

4.2.3 Days to Maturity

Days to 80% maturity exhibited a highly significant and positive correlation with siliqua length (cm) (r_g = 0.385**) and seeds per siliqua (r_g = 0.410**, r_p = 0.068^{ns}) which indicated a possible increase of days to maturity increases the siliqua length (cm) and seeds per siliquae. It also exhibited a highly significant and negative correlation with the number of secondary branches per plant (r_g = -0.357**) which indicates a possible increased number of secondary branches per plant by decreasing days to days to maturity. It also showed an insignificant and positive correlation with plant height (cm) (r_g = 0.114^{ns}, r_p = 0.109^{ns}), number of primary branches per plant (r_g = 0.009^{ns}, r_p = 0.071^{ns}), the number of siliqua per plant (r_g = 0.074^{ns}), seeds per siliquae (r_g = 0.410**, r_p = 0.068^{ns}), thousand seeds weight (g) (r_g = 0.104^{ns}, r_p = 0.097^{ns}) and yield per plant (g) (r_g = 0.089^{ns}, r_p = 0.047^{ns}) and negative correlation with the number of secondary branches per
plant (r_p = -0.131^{ns}), number of siliqua per plant (r_p = -0.048^{ns}) and siliqua length (cm) (r_p = -0.007^{ns}) (Table 6).

4.2.4 Plant height (cm)

Plant height (cm) exhibited highly significant and negative correlation with number of secondary branches per plant (r_g = -0.702**), siliqua length (cm) (r_g = -0.366**, r_p = -0.267*), thousand seeds weight (g) (r_g = -0.322**, r_p = -0.209*) and yield per plant (g) (r_g = -0.349**) pointing out a possible increase in plant height by decreasing number of secondary branches per plant, siliqua length (cm), thousand seeds weight and yield per plant (g). It exhibited an insignificant and positive correlation with the number of primary branches per plant (r_g = 0.174^{ns}, r_p = -0.087^{ns}) which indicated that this trait had a very little contribution toward the increase in the number of primary branches per plant. It also showed insignificant and negative correlation with number of secondary branches per plant (r_p = -0.189^{ns}), number of siliqua per plant (r_g = -0.120^{ns}, r_p = -0.178^{ns}), seeds per siliqua (r_g = -0.032^{ns}, r_p = -0.061^{ns}) and yield per plant (g) (r_p = -0.185^{ns}) indicated that environmental factors largely influenced on the association between these traits (Table 6)

4.2.5 Number of primary branches per plant

The number of primary branches per plant exhibited a highly significant and positive correlation with the number of secondary branches per plant (r_g = 0.648**) which indicated a possible increase in the number of primary branches per plant increases the number of secondary branches per plant. It also showed an insignificant and positive correlation with the number of secondary branches per plant ($r_p = 0.108^{ns}$), number of siliqua per plant ($r_g = 0.030^{ns}$), siliqua length (cm) ($r_g = 0.013^{ns}$, $r_p = 0.062^{ns}$), seeds per siliquae ($r_g = 0.149^{ns}$, $r_p = 0.091^{ns}$) and thousand seeds weight (g) ($r_g = 0.120^{ns}$, $r_p = 0.099^{ns}$) indicating that it had a very little contribution toward the increase in the number of secondary branches per plant, the number of siliqua per plant, siliqua length (cm), seeds per siliquae and thousand seeds weight (g). It also showed an insignificant and negative correlation with the number of siliqua per plant ($r_p = -0.074^{ns}$) and yield per plant (g) ($r_g = -0.145^{ns}$, $r_p = -0.096^{ns}$) (Table 6).

4.2.6 Number of secondary branches per plant

The number of secondary branches per plant exhibited a highly significant and positive correlation with the number of siliqua per plant (r_g = 0.376**), siliqua length (cm) (r_g = 0.366**, r_p = 0.344**) and seeds per siliquae (r_g = 0.215*) which indicated a possible increase in the number of secondary branches per plant increases the number of siliqua per plant, siliqua length (cm) and seeds per siliqua . Naznin *et al.* (2015) reported that seed yield/plant had a significant and positive correlation for the number of siliqua per plant ($r_p = 0.036^{ns}$), seeds per siliquae ($r_p = 0.027^{ns}$), thousand seeds weight (g) ($r_g = 0.007^{ns}$) and yield per plant (g) ($r_p = 0.005^{ns}$). It also showed an insignificant and negative correlation with thousand seeds weight (g) ($r_p = -0.005^{ns}$) and yield per plant (g) ($r_g = -0.136^{ns}$) (Table 6).

4.2.7 Number of siliqua per plant

The number of siliquae per plant showed a highly significant and positive correlation with siliqua length (cm) (r_g = 0.841**, r_p = 0.285**) which indicates a possible increase in seed yield per plant.

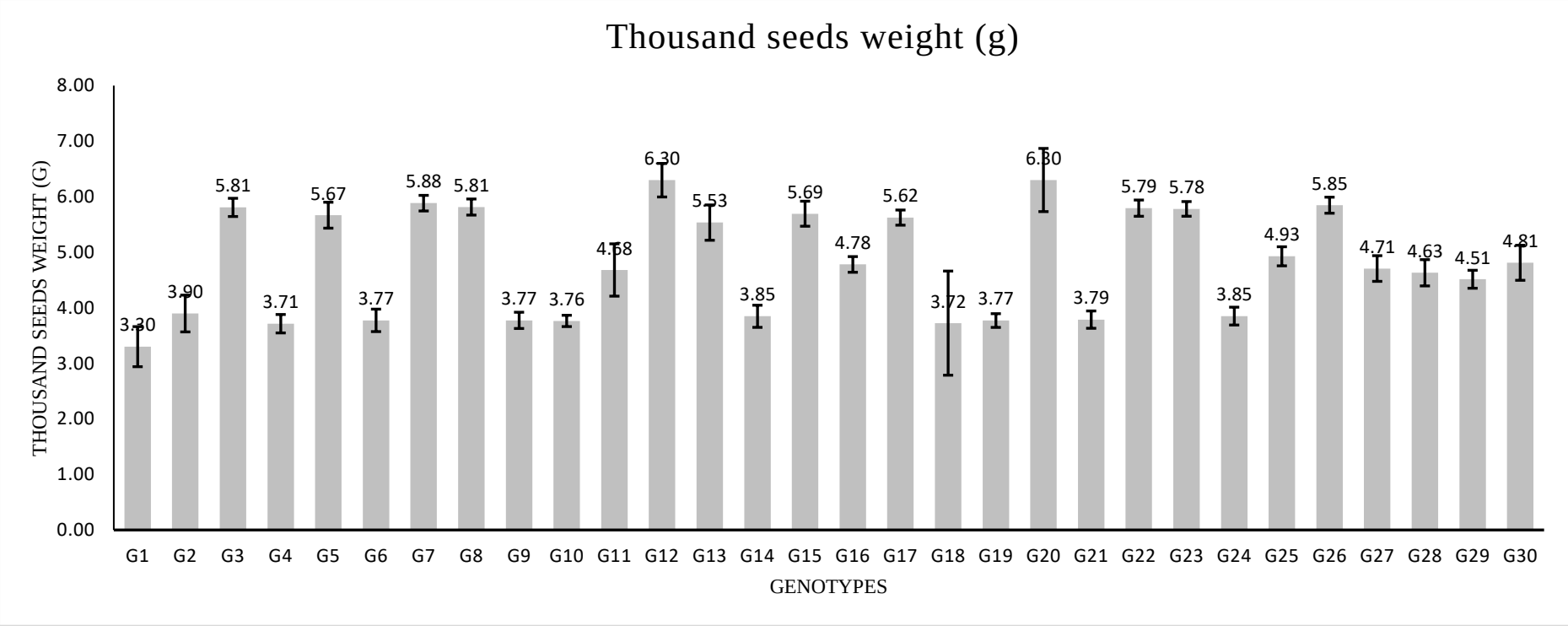

Figure 7. Mean performance of thousand seed weight in 30 genotypes of *Brassica napus*

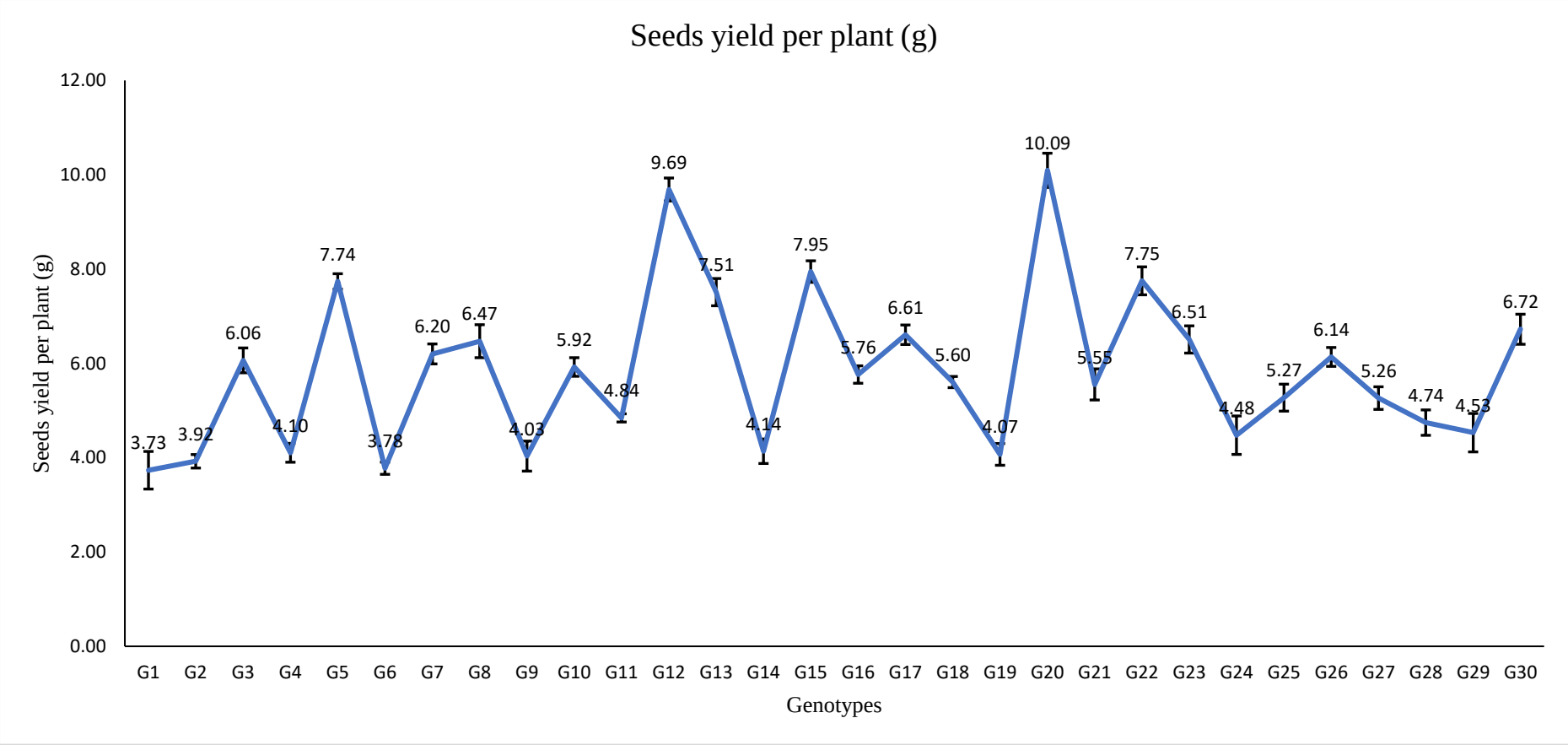

Figure 8. Mean performance of seed yields per plant in 30 genotypes of *Brassica napus* L.

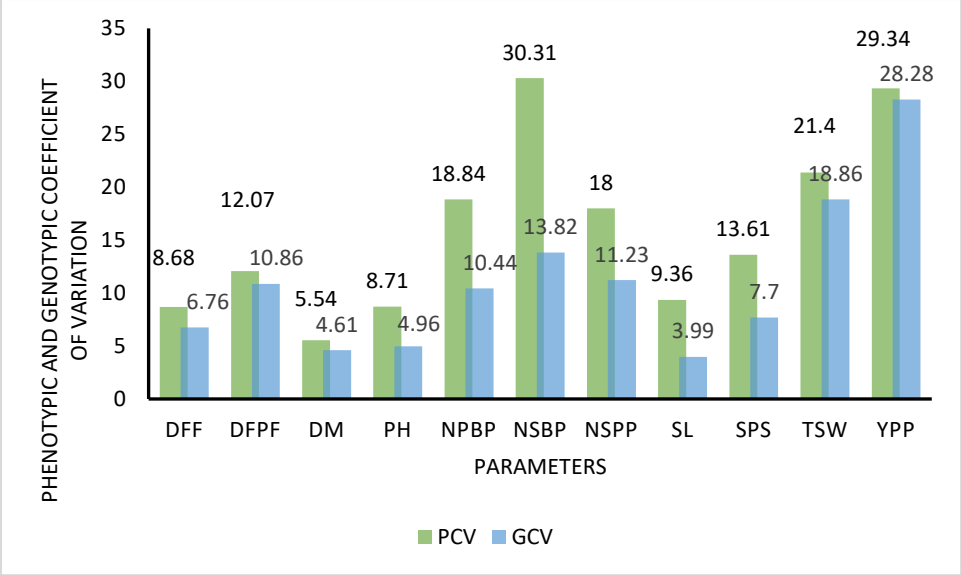

Figure 9. Phenotypic and genotypic coefficient of variation of 11 characters of 30 genotypes of *B. napus*

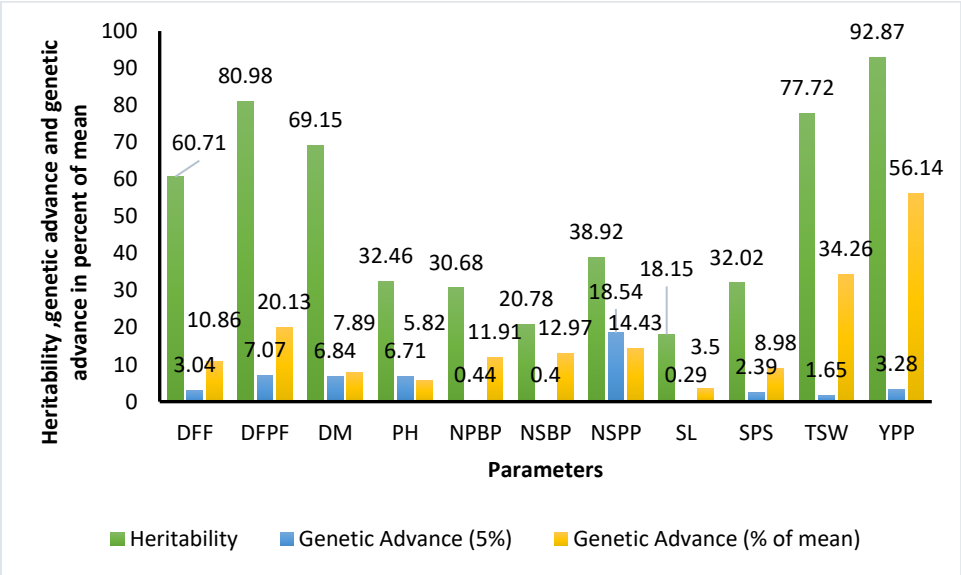

Figure 10. Heritability, genetic advance, and genetic advance in percentage of mean of 11 characters of 30 genotypes of *B. napus*

The number of siliqua per plant increases the length of siliqua (cm). Naznin *et al.* (2015) also showed a highly significant positive association between the amount of siliqua per plant with seed yield per plant. It also showed an insignificant and positive correlation with seeds per siliquae ($r_g = 0.002^{ns}$, $r_p = 0.132^{ns}$), thousand seeds weight (g) ($r_g = 0.128^{ns}$, $r_p = 0.102^{ns}$), and yield per plant (g) ($r_g = 0.146^{ns}$, $r_p = 0.080^{ns}$) stated that it had a very little association with seeds per siliqua, thousand seeds weight (g) and yield per plant (g) (Table 6).

4.2.8 Siliqua length (cm)

Highly significant and positive correlation of length of siliqua (cm) was observed in seeds per siliqua ($r_g = 0.494^{**}$, $r_p = 0.324^{**}$), thousand seeds weight (g) ($r_g = 0.801^{**}$, $r_p = 0.256^{*}$) and yield per plant (g) ($r_g = 0.772^{**}$, $r_p = 0.367^{**}$) which indicated a possible increase in length of siliqua (cm) increases the seeds per siliquae, thousand seeds weight (g) and yield per plant (g) (Table 6).

4.2.9 Seeds per siliquae

The Number of seeds per siliqua showed a significant and positive correlation with thousand seeds weight (g) ($r_g = 0.442^{**}$) and yield per plant (g) ($r_g = 0.560^{**}$, $r_p = 0.312^{**}$) indicating a possible increase in the number of seeds per siliqua increases thousand seeds weight (g) and yield per plant (g). It also showed an insignificant and positive correlation with thousand seed weight (g) ($r_p = 0.141^{ns}$) stating that it had a very little association with thousand seed weight (Table 6).

4.2.10 Thousand seeds weight (g)

Thousand seed weights exhibited a highly significant and positive correlation with yield per plant (g) ($r_g = 0.885^{**}$, $r_p = 0.741^{**}$) at both genotypic and phenotypic levels indicating that an increase in thousand seed weights tends to increase seed yield per plant. A similar result was also reported by Parveen *et al.* (2015) (Table 6).

4.3 Path coefficient analysis

The complex relations between the numerous qualities associated with the dependent variable are not considered by simple correlation. The linear relationship between the independent variables is displayed by the correlation coefficients.

Table 6. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of *Brassica napus*

Character		DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW
DFPF	r_g	0.593**									
	r_p	0.539**									
DM	r_g	0.169^{ns}	-0.107^{ns}								
	r_p	0.027^{ns}	-0.087^{ns}								
PH	r_g	0.158^{ns}	-0.173^{ns}	0.114^{ns}							
	r_p	0.011^{ns}	-0.082^{ns}	0.109^{ns}							
NPBP	r_g	0.010^{ns}	0.328**	0.009^{ns}	0.174^{ns}						
	r_p	0.084^{ns}	0.201^{ns}	0.071^{ns}	-0.087^{ns}						
NSBP	r_g	-0.102^{ns}	0.030^{ns}	-0.357**	-0.702**	0.648**					
	r_p	0.063^{ns}	0.001^{ns}	-0.131^{ns}	-0.189^{ns}	0.108^{ns}					
NSPP	r_g	-0.366**	-0.322**	0.074^{ns}	-0.120^{ns}	0.030^{ns}	0.376**				
	r_p	-0.083^{ns}	-0.154^{ns}	-0.048^{ns}	-0.178^{ns}	-0.074^{ns}	0.036^{ns}				
SL	r_g	0.356**	0.354**	0.385**	-0.366**	0.013^{ns}	0.366**	0.841**			
	r_p	0.099^{ns}	0.077^{ns}	-0.007^{ns}	-0.267*	0.062^{ns}	0.344**	0.285**			
SPS	r_g	$0.199n^{s}$	-0.129^{ns}	0.410**	-0.032^{ns}	0.149^{ns}	0.215*	0.002^{ns}	0.494**		
	r_p	0.260*	-0.050^{ns}	0.068^{ns}	-0.061^{ns}	0.091^{ns}	0.027^{ns}	0.132^{ns}	0.324**		
TSW	r_g	-0.004^{ns}	0.166^{ns}	0.104^{ns}	-0.322**	0.120^{ns}	0.007^{ns}	0.128^{ns}	0.801**	0.442**	
	r_p	-0.008^{ns}	0.120^{ns}	0.097^{ns}	-0.209*	0.099^{ns}	-0.005^{ns}	0.102^{ns}	0.256*	0.141^{ns}	
SYPP	r_g	0.184^{ns}	0.166^{ns}	0.089^{ns}	-0.349**	-0.145^{ns}	-0.136^{ns}	0.146^{ns}	0.772**	0.560**	0.885**
	r_p	0.143^{ns}	0.146^{ns}	0.047^{ns}	-0.185^{ns}	-0.096^{ns}	0.005^{ns}	0.080^{ns}	0.367**	0.312**	0.741**

*, 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 siliqua per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seeds yield per plant (g)

However, when a causal relationship between variables is required, describing these associations alone is insufficient. It has been proposed that yield factors may influence seed yield directly, indirectly, or both. Therefore, it was vital to ascertain how yield components affected seed yield. Consequently, the most popular statistical technique applied for this purpose is path coefficient analysis. As a result, the impacts of yield components on seed yield can be calculated both directly and indirectly using the other components. 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 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 siliqua per plant, siliqua length (cm), seeds per siliqua and thousand seeds 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.

4.3.1 Days to first flowering

Path coefficient analysis revealed that days to first flowering had a negative direct effect **(-0.116)** on seed yield per plant. The trait showed a positive indirect effect on seed yield per plant via days to 50% flowering (0.115), plant height (cm) (0.032), number of siliqua per plant (0.052), siliqua length (cm) (0.088) and seeds per siliqua (0.053) followed by a negative indirect effect via days to maturity (-0.017), number of primary branches per plant (-0.005), number of secondary branches per plant (-0.015) and thousand seeds weight (g) (-0.003) Finally, the trait showed positive genotypic correlation with seed yield per plant **(0.184)** which was significant (Table 7).

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

Trait	DFF	DFPF	DM	PH	NPBP	NSBP	NSPP	SL	SPS	TSW	SYPP
DFF	**-0.116**	0.115	-0.017	0.032	-0.005	-0.015	0.052	0.088	0.053	-0.003	0.184^{ns}
DFPF	-0.069	**0.194**	0.011	-0.035	-0.151	0.005	0.046	0.088	-0.035	0.114	0.166^{ns}
DM	-0.020	-0.021	**-0.102**	0.023	-0.004	-0.054	-0.010	0.095	0.110	0.071	0.089^{ns}
PH	-0.018	-0.034	-0.012	**0.204**	-0.080	-0.106	0.017	-0.091	-0.008	-0.220	-0.349**
NPBP	-0.001	0.064	-0.001	0.035	**-0.461**	0.098	-0.004	0.003	0.040	0.082	-0.145^{ns}
NSBP	0.012	0.006	0.036	-0.143	-0.299	**0.151**	-0.053	0.091	0.058	0.005	-0.136^{ns}
NSPP	0.042	-0.062	-0.008	-0.025	-0.014	0.057	**-0.141**	0.208	0.0005	0.088	0.146^{ns}
SL	-0.041	0.069	-0.039	-0.075	-0.006	0.055	-0.119	**0.247**	0.132	0.548	0.772**
SPS	-0.023	-0.025	-0.042	-0.006	-0.069	0.033	-0.0003	0.122	**0.268**	0.302	0.560**
TSW	0.0005	0.032	-0.011	-0.066	-0.056	0.001	-0.018	0.198	0.119	**0.684**	0.885**
Residual effect 0.09											

*, 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 siliqua per plant, SL= Siliqua length (cm), SPS= Seeds per siliqua, TSW= Thousand seeds weight (g), SYPP= Seeds yield per plant (g)

4.3.2 Days to 50% flowering

Days to 50% flowering showed a positive direct effect (**0.194**) on seed yield per plant. Islam *et al*. (2016) showed that days to 50% flowering had a positive direct effect on seed yield per plant which was similar to the result. Zahan (2006) also reported a similar finding. The trait showed positive a indirect effect on seed yield per plant via days to maturity (0.011), number of secondary branches per plant (0.005), number of siliqua per plant (0.046), siliqua length (cm) (0.088) and thousand seeds weight (g) (0.114). The trait showed negative a indirect effect on seed yield per plant via days to first flowering (-0.069), plant height (cm) (-0.035), number of primary branches per plant (-0.151), and seeds per siliquae (-0.035). Finally, the trait showed a positive genotypic correlation with yield per plant **(0.166)** which was nonsignificant (Table 7).

4.3.3 Days to Maturity

Days to 80% maturity showed a negative direct effect **(-0.102)** towards yield per plant. Naznin *et al*. (2015) reported a negative direct effect of days to maturity toward yield per plant that was similar to the present finding. Rashid et al. (2013) showed a similar result. The trait showed a positive indirect effect on seed yield per plant via siliqua length (cm) (0.095), plant height (cm) (0.023), seeds per siliqua (0.110), and thousand seeds weight (g) (0.114). The trait showed a negative indirect effect on seed yield per plant via days to first flowering (-0.020), days to 50% flowering (-0.021), number of primary branches per plant (-0.004), number of secondary branches per plant (-0.054) and number of siliqua per plant (-0.010). The trait had a non-significant and negative genotypic association with yield per plant **(0.089)** (Table 7)**.**

4.3.4 Plant height (cm)

Plant height exhibited a positive direct effect **(0.204)** on yield per plant. Uddin *et al.* (2013) demonstrated that plant height had a positive direct effect on yield per plant which supported the result. The trait showed a positive indirect effect on seed yield per plant via the number of siliqua per plant (0.017). The trait showed a negative indirect effect on seed yield per plant via days to first flowering (-0.018), days to 50% flowering (-0.034), days to maturity (-0.012), number of primary branches per plant (-0.080), number of secondary branches per plant (-0.106), siliqua length (cm) (-0.091), seeds per siliqua (-0.008) and thousand seeds weight (g) (-0.220). The trait had an insignificant positive genotypic association with seed yield per plant (0.340). Direct

effect **(0.204)** is positive and higher than the genotypic correlation coefficient **(-0.349)** which exhibited a true relationship between them and direct selection for this trait will be rewarding for yield improvement (Table 7).

4.3.5 Number of primary branches per plant

The number of primary branches per plant showed a negative direct effect **(-0.461)** on yield per plant. The trait showed a positive indirect effect on seed yield per plant via days to 50% flowering (0.064), plant height (cm) (0.035), number of secondary branches per plant (0.098), siliqua length (cm) (0.003), seeds per siliqua (0.040) and thousand seeds weight (g) (0.082). The trait showed a negative indirect effect on seed yield per plant via days to first flowering (-0.001), days to maturity (-0.001), and number of siliqua per plant (-0.004). The trait had a non-significant negative genotypic association with yield per plant **(-0.145)** (Table 7).

4.3.6 Number of secondary branches per plant

The number of primary branches per plant showed a positive direct effect **(0.151)** on yield per plant. Naznin *et al.* (2015) revealed that the number of secondary branches per plant had a high positive direct effect on yield per plant which supported the present finding. Khan (2010) also agreed to the finding. The trait showed a positive indirect effect on seed yield per plant via days to first flowering (0.012), days to 50% flowering (0.006), days to maturity (0.036), siliqua length (cm) (0.091), seeds per siliqua (0.058) and thousand seeds weight (g) (0.005). The trait showed a negative indirect effect on seed yield per plant via plant height (cm) (-0.143), number of primary branches per plant (-0.299), and number of siliqua per plant (-0.053). The trait had a non-significant negative genotypic association with seed yield per plant **(-0.136)** (Table 7)**.**

4.3.7 Number of siliqua per plant

The number of siliquae per plant exhibited a negative direct effect **(-0.141)** on yield per plant. The trait showed a positive indirect effect on seed yield per plant via days to first flowering (0.042), number of secondary branches per plant (0.057), siliqua length (cm) (0.208), seeds per siliqua (0.0005) and thousand seeds weight (g) (0.088). The trait showed a negative indirect effect on seed yield per plant via days to 50% flowering (-0.062), days to maturity (-0.008), plant height (cm) (-0.025), and number of primary branches per plant (-0.014). The trait had a non-significant positive genotypic

association with yield per plant (0.146). Direct effect **(-0.141)** is negative and lower than the genotypic correlation coefficient **(0.146)** which exhibited a true relationship between them and direct selection for this trait will be not effective for yield improvement (Table 7).

4.3.8 Siliqua length (cm)

The length of siliqua showed a positive direct effect **(0.247)** on yield per plant. The trait showed a positive indirect effect on seed yield per plant via days to 50% flowering (0.069), number of secondary branches per plant (0.055), seeds per siliqua (0.132) and thousand seeds weight (g) (0.548). The trait showed a negative indirect effect on seed yield per plant via days to first flowering (-0.041), days to maturity (-0.039), plant height (cm) (-0.075), number of primary branches per plant (-0.006) and number of siliqua per plant (-0.119). The trait had significant positive genotypic association with yield per plant **(0.772)** (Table 7).

4.3.9 Seeds per siliquae

Seeds per siliqua showed a positive direct effect **(0.268)** on yield per plant. The trait showed a positive indirect effect on seed yield per plant via the number of secondary branches per plant (0.033), siliqua length (cm) (0.122) and thousand seeds weight (g) (0.302). The trait showed a negative indirect effect on seed yield per plant via days to first flowering (-0.023), days to 50% flowering (-0.025), days to maturity (-0.042), plant height (cm) (-0.006), number of primary branches per plant (-0.069) and number of siliqua per plant (-0.0003). The trait had a significant positive genotypic association with yield per plant **(0.560)** (Table 7).

4.3.10 Thousand seeds weight (g)

Thousand seed weights had a positive direct effect **(0.684)** on yield per plant. The trait showed a positive and indirect effect on seed yield per plant via days to first flowering (0.0005), days to 50% flowering (0.032), number of secondary branches per plant (0.001), siliqua length (cm) (0.198) and seeds per siliqua (0.119). The trait showed a negative indirect effect on seed yield per plant via days to maturity (-0.011), plant height (cm) (-0.066), number of primary branches per plant (-0.056) and number of siliqua per plant (-0.018). The trait had a significant positive genotypic association with yield per plant **(0.885)** (Table 7).

4.3.11 Residual effect

The residual effect (R) of path co-efficient analysis was 0.09 which reported that the traits under study contributed 91% of the yield per plant. It was said that some other factors that contributed 9% to the yield per plant that were not included in the present study could have a significant effect on yield per plant. Naznin *et al.* (2015) found a residual effect of 0.45 in the case of yield per plant. Islam *et al.* (2016) found 0.43 in case of yield per plant (Table 7).

CHAPTER V

SUMMARY AND CONCLUSION

At the farm of Sher-e Bangla Agricultural University in Dhaka, an experiment using 30 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. Three replications of the Randomized Complete Block Design (RCBD) were used to draw up the field experiment in the main field. 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 G29 (32.00 DAS) where G8 required 24.00 DAS to take first flowering, the lowest among the genotypes. The minimum duration of days to 50% flowering was found in G9 with 30.33 DAS and G22 took the maximum period for 50 % flowering with 43.00 DAS. For days to maturity, 92.33 DAS were required for G20 which was the highest duration for days to maturity however, the lowest days to maturity was observed in G18 (76.33 DAS). The maximum plant height was 134.00 cm and the lowest was 96.67 cm. The Maximum number of the primary branches per plant was noticed in G28 (5.33) and a minimum number of the primary branches per plant was found in G4 (3.00). The maximum number of secondary branches was found in G28 (4.33) and the minimum number of the secondary branches per plant was found in G1 (1.33). The highest number of siliqua was observed in G20 (163.52) whereas the lowest number of siliqua was found in G26 (107.33). The genotypes of G20 (9.10 cm) had long siliqua and the siliqua was shorter in G1 (6.87 cm). The maximum number of seeds was found in G20 (31.33) while the lowest number of seeds were estimated in G1 (20.50). The Maximum thousand seed weight (g) was found in G20 (6.30 g) which increased the possibility of higher yield and ultimately the highest yield was found from G20 (10.09 g) whereas the minimum thousands seed weight (g) was found in G1 (3.30 g). The highest value was observed in G20 (10.09 g) however, Genotype G1 was recorded for the lowest yield value at 3.73 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 a higher phenotypic and genotypic variance indicating that higher environmental effect was present in the characters On the other hand lower environmental effect was found for the characters like days to first

flowering, number of primary branches per plant, number of secondary branches per plant, siliqua length (cm), seeds per siliqua, thousand seeds weight (g) and yield per plant (g). Characters like, yield per plant (g) exhibited high genotypic and phenotypic co-efficient of variation. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters. The Maximum difference between the phenotypic and genotypic coefficient of variation was 30.31 and 13.82, respectively which indicated that the number of secondary branches per plant mostly depended on the environmental condition. The Highest phenotypic co-efficient of variation (30.31) for several secondary branches per plant and genotypic co-efficient of variation (28.28) was found in yield per plant. High heritability coupled with the genetic advance in the percentage of mean was found in days to 50% flowering, days to maturity, thousand seeds weight (g), and yield per plant (g) which indicated that additive gene expression on this character. Plant height (cm) showed moderate heritability with moderate genetic advance and moderate genetic advance in the percentage of mean that might be the presence of additive and non-additive gene expression. Moderate heritability and low genetic advance were found in plant height (cm), number of primary branches per plant, and seeds per siliqua**.** Investigation on character association indicated that yield per plant had the highest significant positive correlation with seeds per siliqua, thousand seeds weight (g) and yield per plant (g) in both genotypic and phenotypic levels indicating the importance of the trait in selection for increasing yield and were identified as yield attributing characters. Thus, selection can be relied upon by the characters for the genetic improvement of the yield of *B. napus*. Path analysis revealed that the highest positive direct effect was thousand seeds weight (g) (0.684) and the lowest positive direct effect was the number of secondary branches per plant (0.151). Days to 50% flowering, plant height (cm), number of secondary branches per plant, siliqua length (cm), seeds per siliqua, and thousand seeds weight (g) showed a positive direct effect on yield per plant (g) indicating that direct selection based on these traits help evolving high yielding varieties of *B. napus*. On the other hand, a negative direct effect was found by Days to first flowering, days to maturity, number of primary branches per plant, number of siliqua per plant and yield per plant (g). Based on genotypes' yield and yield-contributing traits, the selection was done among them. The genotypes G8 for days to first flowering, G9 for days to 50% flowering, G18 for days to maturity, G1 for plant height (cm), G28 for number of

primary branches per plant and number of secondary branches per plant, G20 for number of siliqua per plant, siliqua length (cm), seeds per siliqua, thousand seeds weight (g), and yield per plant (g) were selected based on the objectives. In light of this, it might be chosen to use the genotypes G8, G9, G18, G1, G28 and G14 in further breeding programs.

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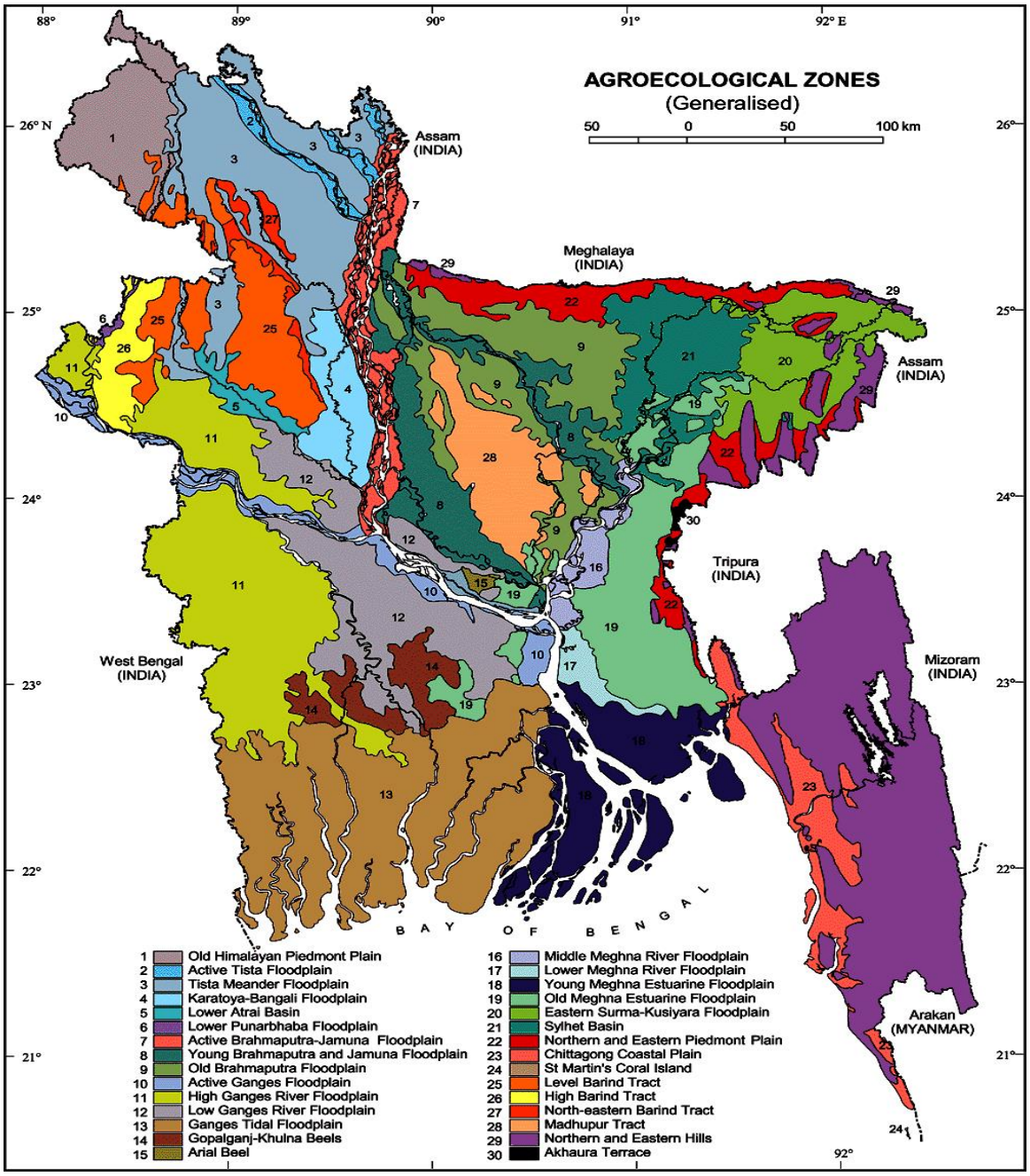
APPENDICES

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, 2020	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