ANALYSIS OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD AND IT'S CONTRIBUTING CHARACTERS OF F_7 POPULATION IN *Brassica napus* L.

SAYMA SAYED NISHU

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

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SAYMA SAYED NISHU

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Approved by:

(Professor Dr. Firoz Mahmud)
Supervisor

(Prof. Dr. Mohammad Saiful Islam)
Co-supervisor

(Prof. Dr. Md. Abdur Rahim)
Chairman
Examination Committee

Dr. Firoz Mahmud
Associate Professor
Department Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mobile: +8801552432589
E-mail: fmahmud08@gmail.com

CERTIFICATE

This is to certify that the thesis entitled, ***"ANALYSIS OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD AND IT'S CONTRIBUTING CHARACTERS OF*** F_7 ***POPULATION IN*** **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* ***SAYMA SAYED NISHU****, Registration No.* ***18-09237*** *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: December, 2020 ***Dr. Firoz Mahmud***
Place: Dhaka, Bangladesh Supervisor

DEDICATED
TO MY
RESPECTIVE
TEACHER
&BELOVED
PARENTS

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BY

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ABSTRACT

The experiment was conducted with the aim of assessment of the genetic variability,heritability,character association, path analysis of F_7 population of *Brassica napus L.* from November 2019 to February 2020.In this experiment, forty-three genotypes of *Brassica napus* L. were evaluated based on randomized complete block design with three replications at the experimental field of Sher-e-Bangla Agricultural University, Dhaka.The genotypes were found significantly variable for all the eleven characters and From the values of mean. range and CV (%) of seed yield and yield contributing characters it was confirmed that there were considerable variation present among all the genotypes used in the experiment.The values of GCV and PCV indicated that there was least variation present among most of the characters.Comparatively, phenotypic variances were higher than the genotypic variances for all the characters studied. The high GCV and PCV value were observed for number of seed yield per plant (38.06 and 4.57 respectively). Seed yield per plant (99.47) exhibited the highest value of heritability followed by number of siliquae per plant (97.08). The significant positive correlation for seed yield per plant was found with days to maturity (0.186) and thousand seed weight (0.659). Path co-efficient analysis revealed that days to 50% flowering, number of primary branch, siliquae length, number of siliqua per plant, number of seed per siliquae and thousand seed weight had the positive direct effect on yield per plant.. Considering genetic analysis and other agronomic performance genotypes G6 (P1), G14 (P2), G18 (P2) and G9 (P3) might be suggested as promising high yielding lines with early maturity as fulfillment of farmer's demand.

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SOME COMMONLY USED ABREVIATIONS

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 Co-efficient 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 Co-efficient 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
Tripol super phosphate	TSP

CHAPTER I

INTRODUCTION

Mustard, from *Brassica* is one of the most important sources of edible vegetable oils in the world. It is commonly known as oilseed, rapeseed (the term "rape" derives from the Latin word for *turnip*, *Rapa* or *rapum*, cognate with the Greek word *rhapys),* or canola. It contributes a lion's share to the total edible oil production in the rain-fed agriculture of Bangladesh and it has an economic and commercial value that plays a vital role in fulfilling the consumers' nutritional demand.

The primary center of origin for *Brassica napus* is near the Himalayan region while the secondary center of origin is the Mediterranean region and Asia (Downy and Robelen, 1989). Although some varieties of mustard plants were well-established crops in Hellenistic and Roman times. Wild forms of mustard and its relatives, the radish and turnip, can be found over west Asia and Europe. Encyclopedia Britannica states that mustard was grown by the Indus Civilization of 2500–1700 BC.

Rapeseed cultivars are classified as winter or spring types according to their vernalization requirement to induce flowering. Oilseed rape is cultivated predominantly as winter or semi-winter forms in Europe and Asia, respectively, whereas spring-sown canola types are more suited to the climatic conditions in Canada, northern Europe, and Australia (Friedt *et al.*, 2007).

It comprises economically important crops, *Brassica napus* L. grow to 100 cm in height having a taproot system, with a succulent, straight, and cylindrical stem. The stalked lower leaves are hairless, fleshy, pinnatifid, and glaucous whereas the upper leaves contain no petioles. The inflorescence is racemose type. The rapeseed pods are siliquae-type fruit. They are green and elongated but during development that eventually ripens to brown. Two compartments are separated by an inner central wall within each pod, in which a row of seeds is developed. At maturity level, they turn into black and become hard.

The mustard plant is any one of several plant species in the genera *Brassica* and *Sinapis* in the family Brassicaceae (the mustard family) and the genus Brassica is an important member of the Cruciferae family, that florid with high diverse morphology consisting of over 3200 species. Rapeseed with th*e* autonym *B. napus* L.is one of the subspecies of Cruciferae which encompasses winter and spring oilseed, vegetable, and fodder rape.

The genus *Brassica* has generally been divided into three groups namely- rapeseed, mustard and cole crops. The rapeseed group includes the diploid *Brassica napus* L. while the mustard groups include species like *Brassica juncea*, *Brassica nigra*, and *Brassica carinata*. Rapeseed (*Brassica napus* L, genome AACC, 2n = 38) is a relatively young species that originated in a limited geographic region through spontaneous hybridizations between turnip rape (*B. rapa* L, AA, 2n = 20) and cabbage (*B. oleracea* L, CC, 2n = 18) genotypes resulting in an amphidiploid genome.

Today oilseed rape (*B. napus* L.) is one of the most important sources of vegetable oil in the world. It is not only a high-energy food but also a carrier for fat-soluble vitamins (A. D, E, and K) in the body. Lipids- fatty acid-total unsaturated 6.61 mg, fatty acid total mono saturated 62.6 g, fatty acid total poly saturated 25.3 g, among the phytosterols, betasitrol and campesterol contain more value that are 368 mg and 260 mg respectively.

In our country, mustard is the main oil trimming other than edible oil as well as mustard oil additionally fills in as a vital crude material for mechanical utilize, for example, in cleansers, paints, varnishes, hair oils, pharmaceuticals, and so on. This oil is likewise utilized by the villagers for hairdressing and body rub before the shower (Agarwal *et al.*, 2000). Dry mustard straw is also used as fuel. According to Friedt *et al.* (2007), it is used as raw material for many other products, which is ranging from rapeseed methyl ester (biodiesel) to industrial lubricants and hydraulic oils the nutritional value of rapeseed meals is compromised by the presence of glucosinolates, it is a group of, tensides for detergent and soap production and biodegradable plastics, after oil extraction the residual meal, which contains 38 to 44% of high-quality protein is used in livestock feed mixtures. However, secondary compounds typical for crucifer plant species. These leaf glucosinolates play an important role in interactions with insect pests and pathogens.

In Bangladesh mustard occupying 763855 in 2019-2020 acres of land and the total production was 358249 metric tons. (Yearbook of Agricultural Statistics-2020). In Bangladesh, the major mustard growing districts are Comilla, Tangail, Jessore, Faridpur, Pabna, Rajshahi, Dinajpur, Kushtia, Kishoreginj, Rangpur, and Dhaka. For the last several decades Bangladesh has been facing an acute shortage of edible oil. Bangladesh Agricultural Research Institute (BARI), Bangladesh Institute of Nuclear Agriculture (BINA), and Sher-e-Bangla Agricultural University (SAU) released some HYVs of mustard and the ranges of yields of these cultivars are between 1.4 to 2.1 t/ha (AIS, 2015).

There is a limited scope to increase the acreage of mustard production because of high production cost, long duration, and the pressure of others crops in the rabi season. This study was to work on F_7 materials which contain 43 genotypes of mustard variety of *Brassica napus* L. which would be fitted well between Aman-mustard-boro cropping patterns by replacing the long durational, low-yielding variety.It is mandatory to separate the overall variability into heritable and non-heritable components because it enables the breeders to adopt a suitable breeding procedure. Information of genetic variability and character association is a prerequisite for initiating a successful breeding program aiming to develop high-yielding varieties. On the other hand, analysis of the correlation coefficient among the characters has importance for selecting breeding materials. To obtain more specific information on the direct and indirect influence of each of the component characters upon seed yield, path co-efficient analysis has to be done.

Objectives:

- To analyze the genetic variability and heritability of the F_7 populations *of Brassica napus* genotypes.
- To study the interrelationships of yield and yield contributing characters and find out their direct and indirect effects via path analysis
- To select promising high yielding populations with early maturity.

CHAPTER II

REVIEW OF LITERATURE

The high nutritious value and the demand of the consumers are concerned, *Brassica napus* re important for both economically and genetically. Thereby, the species of *Brassica* has been received much attention in many aspects of its production and utilization. It is one of the most important oil crops of Bangladesh as well as for many countries of the world. With that view, several techniques a several are applied on different rapeseed varieties and cultivars to obtain for better result, extensive researches on Brassica breeding which have been performed in many countries for the enrichment of quality, yield and it is contributing characters.

There are many available researchers on variability, correlation, and path analysis of yield and yield contributing characters of *Brassica* which was performed under different environments. Environments have been made here to summarize the findings of this study which are relevant to the present experiment. For the sake of this investigation, the whole review section has been divided into the following sections, namely –

2.1 Origin and Geographical distribution
2.2 Genetic variability, Heritability, and Genetic advance
2.3 Correlation among different characters
2.4 Path co-efficient analysis

2.1 Origin and geographical distribution:

Brassica sp. has been a matter of huge scientific interest because of their both agricultural importance and economical values. Six Particularly *Brassica* species that have the highest agricultural importance are recognized as ‘crop *Brassicas*’ (Gómez-Campo *et al.*,1999). Initially, three ancestral diploid species: *B. rapa* (AA, n=10), B. nigra (black mustard) (BB, n=8) and *B. oleracea* (CC, n=9) has existed. After that, through spontaneous hybridization followed by chromosome doubling, three amphidiploid species emerged, those are *B. napus* (AACC, n=19), *B. carinata* (BBCC, n=17), and *B. juncea* (AABB, n=18) as described by the Triangle of U-theory.

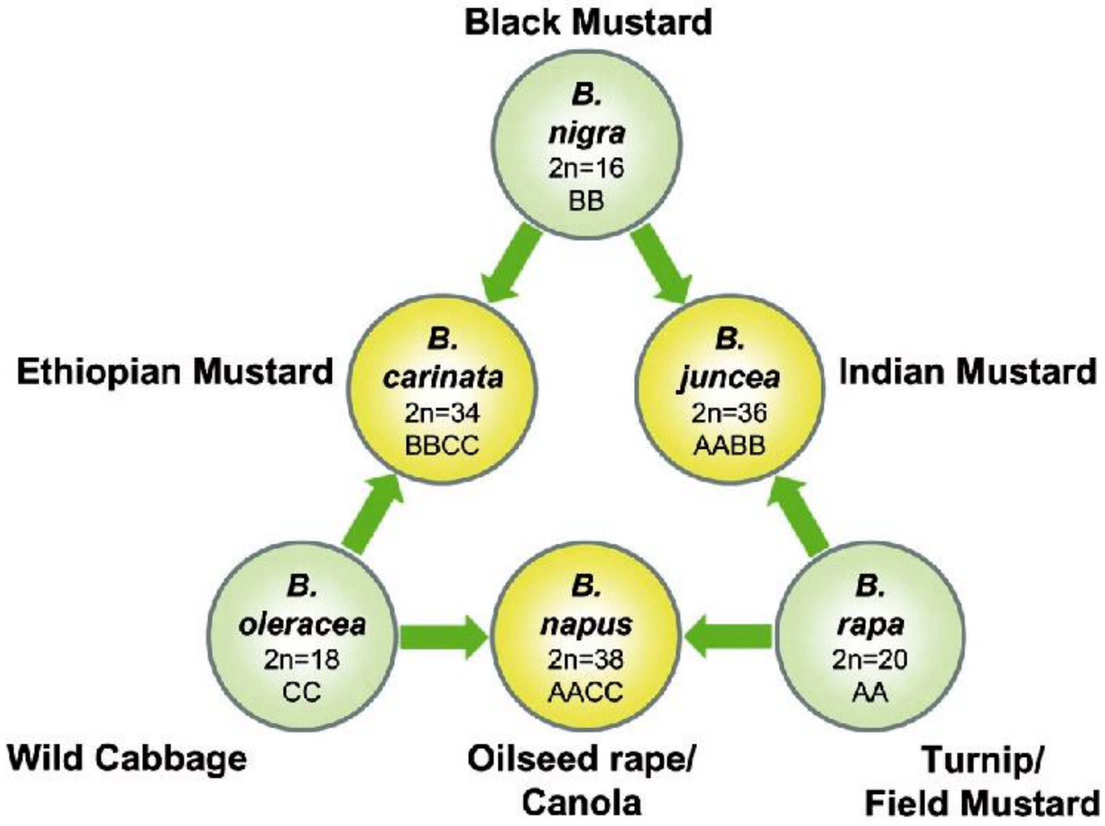


Plate 1: - The "triangle of “U" diagram, representing the genetic relationships between the six species of the genus *Brassica*.

Artificial re-synthesis of *B. napus* from *B. rapa* and *B. oleracea* showed the same result with the triangle of U (Olsson, 1960), which agreement has been confirmed by molecular analysis that was experimenter by Warwick and Black in 1991. The triangle of U shows how three of the *Brassica spp*. were derived from three lineal genomes and those are denoted by the letters AA, BB, and CC. In which reaches diploid genomes are responsible for a common *Brassica* species. The triangle of U is featured out on the triangular diagram in Plate 1.

The genus is native in Western Europe, the Mediterranean, and temperate regions of Asia as wild species. Many of the wild species are found as weeds, especially in North America, South America, and Australia. Thereby, the cultivated species, which are grown worldwide. For successful mustard plant breeding in Bangladesh, identification of suitable parental lines based on genetic parameters, nature and magnitude of genetic variability and the correlation of different yield attributing characters are important. Yield in mustard is accumulated with many yields contributing characters like plant height, days to maturity, primary and secondary branches, main raceme length, etc. Rauf in 2016 also narrated that variation for genetic diversity, the relationship among yield with other yield contributing characters, genotype-environmental relations, heritability, selection index, and molecular marker-based analysis in mustard for yield and yield contributing characters is important for future breeding programs for developing short duration high yielding genotypes.

B. napus L. is considered the important protein food resource. *Brassica spp*. is grown in both irrigated and non-irrigated regions of the country as a single or in association with other crops like wheat, chickpea, maize, etc. We must take better steps for the production and quality improvement of our local cultivars. In that respect, for gaining improved quality production, many strategies and programs are conducted for the betterment of the quality and yield of different varieties and cultivars. Due to the application of different techniques in the breeding process, remarkable improvement has been brought in the productivity and quality of this edible oil which is using in the human diet. Under a particular environment, a substantial number of literary materials are available on variability, genetic diversity, correlation, and path analysis of yield and yield contributing characters of *Brassica* are grown.

A dependable tool to the breeder for the improvement in crops is the information about genetic variability. To the breeders who wish to improve the production and quality of

Brassica, the basic requirements are the knowledge of origin and distribution for betterment of breeding program.

2.2 Genetic variability, heritability, and genetic advance

Genetic parameters are reported to be influenced by growing environmental conditions with that view the information on genetic variation, heritability, and expected genetic advance of different characters of a set of mustard populations is important. The study, these genetic parameters were estimated with 43 genotypes on F_7 Generation in *Brassica napus and* the information would be helpful for further breeding programs.

Bhuiyan (2018) worked with Thirty-two genotypes of *Brassica napus*. The research was conducted in the experimental fields of Sher-e-Bangla Agricultural University, Dhaka–1207 during the Rabi season (Mid November 2017 to February 2018) to estimate the pattern of inheritance and heritability for important traits. The genotypes were crossed in a diallel manner and in the following season (2017-2018) all the F5 hybrids along with parents were evaluated under field condition in a randomized complete block design. Graphical analysis showed over dominance for all parameters. Recorded data showed a high significance of variations (9.042) between the accessions at a 1% level of probability. In her study, the yield per plant was remarked the maximum in G4 (Nap 2037 × Nap 2057) (10.66 g) and the minimum for G19 (Nap 2037 × Nap 206) (3.15g). The values of GCV were 29.20% and PCV was 29.44%. That is slightly higher than GCV denoting that the genotype had moderate variation.

Poul (2017); experimented with seventy genotypes of F_4 generation, it was observed that thousand seed weight is a vital character of rapeseed and mustard, where the highest consideration is on the seed yield. This character has been found to vary widely from genotypes to genotypes and from the environment to environment. In this finding, the environment has a significant role in the expression of this trait with medium heritability of 69.37 % coupled with high genetic advance over the percentage of mean 53.53 % were noticed.

Rauf (2016); studied 35 genotypes of *Brassica* and in that finding, among the genotypes, most of them showed significant variation indicating the wide scope of selection for these characters besides 50% flowering date, days of maturity, plant height, siliqua length, number of seed per siliqua, seed yield per plant were insignificant. In that study, observed high heritability 99.474% with low genetic advance (3.695) and high genetic advance in the percentage of mean 58.094% for seed yield per plant indicated this trait was controlled by additive gene and this character he considered as for future breeding program.

Hira (2015); explored an experiment with 50 genotypes of F_6 generation of *Brassica napus and* observed the analysis of variance revealed highly significant differences among the genotypes concerning plant height (cm), Primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length (cm), seeds per siliqua, thousand seed weight (g) and seed yield per plant (g). GCV was lower than the PCV for all yield-related characters studied. High heritability with high genetic advance was observed in thousand seed weights and seeds yield per plant.

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

Rameeh (2013) evaluated twenty-four rapeseed genotypes including two cultivars and 22 advanced lines where the layout was based on randomized complete block design with three replications. Phenological traits exhibited significant genotypes effects on plant height, yield components, and seed yield. Thereby, this is indicating significant genetic differences among the genotypes and high broad-sense heritability was estimated for phonological traits, pods oil, main axis, and seed yield, signifying selection gain for improving these traits. In addition to the high value of the genetic coefficient of variation were observed on the duration of flowering and pods on the main axis.

The quantitative trait locus mapping of yield and yield components of *B. napus* L. was worked by Heiliger (2012). Near Fort Collins, Colorado: population SE in 2010 (n=183) and population DHYB (n=150) in 2011, two DH canola mapping populations were grown side-by-side both in irrigated and rainfed treatments. Where the Days to flowering, yield, and yield-related traits were studied tend the heritability and relationships among these traits under different water regimes. studied for better understanding. For that point of view, QTL mapping was conducted separately for each in which the genotype with treatment and the treatment on genotype interaction effects could be treatment. R-QTL software is used in each population to detect additive and epistatic effects. Analysis of variance revealed an influence of genotype ($p<0.0001$) on all traits in both populations. The Result of the SE1 population was, treatment effects on seed yield, siliques per the main inflorescence, and seeds per silique were significant ($p<0.05$), and genotype by treatment interactions were significant ($p<0.01$) for all traits. On the other hand, in the DHYB population, the treatment effects on seed yield, siliques per the main inflorescence, thousand seed weight, and Date to flowering were significant ($p<0.05$) and for seed yield and TSW ($p<0.05$) in the DHYB population.

Zebarjadi *et al.* (2011); experimented to study some traits to estimate genetic parameters in 16 rapeseed genotypes. There were two conditions (irrigation and non-irrigation), the statistical analysis showed significant differences among the genotypes. This study is based on the data for 13 different characters including plant height, oil percent, oil yield, etc. After analysis, it observed in stress condition heritability was the maximum oil percentage, whereas low genetic advance was observed for thousand kernel weights.

Afrin *et al.* (2011); conducted an experiment in *B. napus* L. for an experiment about heritability. In this study, the plant height represented the highest value of broad-sense heritability. On another side, the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliquae, number of siliquae per plant, thousand seed weight, and seed yield per plant studied the moderate broad sense heritability. In that case, Days to 80% maturity showed the lowest heritability.

Alam (2010), conducted an experiment in which there were twenty-six F_4 populations of *B. rapa* L. to study the variation among them. In that study, it was revealed that higher phenotypic variation was present than the genotypic variation. There was also observed high heritability with the high genetic advance in plant height, number of primary branches per plant, number of secondary branches per plant, and number of siliquae per plant.

Aytac and Kinaci (2009) experimented with 10 winter rapeseed genotypes. That experiment was carried out studied of variation, genetic and phenotypic correlations, and broad-sense heritability. They analyzed seed yield, yield, and quality as characters for 2 years. After that, they observed that the maximum broad sense heritability gets genetic advance in respect of seed yield performance.

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

Jahan (2008) a field experiment was conducted, here was studied on inter-genotypic variability and genetic diversity in F_4 lines which were obtained through inter-varietal crosses along with 8 released varieties of *B. rapa* L. For all the characters, there was significant variation observed among all genotypes. Considering genetic parameters there observed high genotypic coefficient of variation (GCV) for the number of secondary branches/plants, siliqua/plant, yield/plant whereas days to maturity revealed extremely lonely low GCV. High heritability with the low genetic advance in percent of mean was observed for days to maturity. That founding indicated that non-additive gene effects were responsible for the expression of this character thereby selection for such trait might not be rewarding. For plant height and days to 50% flowering, high heritability with a moderate genetic advance in percent of mean was observed which was indicating that this trait was under additive gene control thereby selection for genetic improvement for this trait would be effective.

Parveen (2007); studied variability in F_2 progenies. There were 17 *Brassica rapa* genotypes of the inter-varietal crosses. The significant 10 variations among the different genotypes were used in the experiment. The study revealed that the number of primary branches per plant and secondary branches per plant showed high heritability coupled with high genetic advance and exceedingly highly high genetic advance in percentage.

Baradaran *et al.* (2007); reported results of the field studies in Iran to determine the variation in 15 rape cultivars and the results of the analysis of variance studied significant differences between yield and number of siliquae, per plant, harvest index, oil percent which expressed the most important trials for high PCV and GCV for the number of siliqua per plant and weight of thousand seeds.

Khan *et al.* (2006); studied the variation for yield and yield contributing characters is rapeseed and the reported significant variation for eleven accessions of *Brassica napus* L. Indicated that a wide range of genetic variation with high PCV and GCV for seed yield, siliqua per plant, seeds per siliquae, siliquae length was observed.

Goswami *et al.* (2005); experimented on variability studies on several traits like the number of secondary branches, siliqua on the main raceme, seeds per siliqua, 1000-seed weight, and seed yield per plant. As a result, it represented that the coefficient of variation of siliqua per plant was significant over the other characters and there was considerable variability for the above character studied.

Kardam and Singh (2005); studied the nature and magnitude of associations for 10 characters in progenies of Indian rapeseed which was obtained from six crosses during rabi 2002-03 in Rajasthan, India. For most of the characters, the PCV was higher in magnitude compared to GCV. Seed yield per plant was a positively significant variable with plant height, number of seeds per siliqua, and 1000- seed weight.

Uddin *et al.* (2005); analyzed the variation for yield and yield contributing characters in rapeseed and reported significant variation from (*B. napus* L.) genotypes, for yield and yield components. The considerable high genotypic and phenotypic coefficients of variation occurred for 1000 seed weight, seed yield per plant, and siliqua per plant.

Yadava *et al.* (2004); estimated heritability in the broad sense and genetic advance for plant height, maturity, and siliqua number on the main raceme in 29 varieties of Indian rapeseed. The result represented that the heritability and genetic advance were high for yield per plant, plant height, and day s to first flowering.

Thakral (2004); worked on variation for yield and yield contributing characters in rapeseed and reported the significant variation for 8 Indian rapeseed parental lines and their 28 F_1 hybrids. They noticed that plant height and seed yield characters estimated a high value of PCV and GCV.

During rabi season in India, Choudhary *et al.* (2003); studied variability in Indian mustard on 10 characters. There was observed a wide range of variability for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua, and thousand seed weight. For secondary branches per plant, seed yield per plant, and the number of siliquae per plant the genotypic and phenotypic coefficient of variability was recorded highly heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant which was indicating a preponderance of additive gene action.

Gupta *et al.* (2002); studied yield and seven yield components in 18 strains of *Brassica napus* L.for morphological and phenological yield characters and he reported high expected genetic advance and high heritability for plant height, 1000-seed weight, and yield per plant, indicating additive gene effects for this character. A high heritability estimate with low expected genetic advance indicating non-additive gene effects were shown by the number of siliquae per plant.

Tyagi *et al.* (2001); evaluated forty-five hybrids of Indian mustard for seed yield and yield components which were obtained from crossing 10 cultivars. The result explored the variation was the highest for plant height of parents and their hybrids and the seed yield per plant exhibited the highest coefficient of variation (41.1%).

An experiment was conducted for studies of genetic variability by Pant and Singh (2001) where used 25 genotypes. Analysis of variance revealed highly significant genotypic differences for all characters except for days to flowering, number of primary branches, and oil content. Seed yield per plant had the highest coefficient both for genotypic and phenotypic variability. All traits showed high heritability with the highest value estimated for seed yield per plant whereas the estimates of genetic advance were comparatively low for oil content and days to flowering. This study recommended that the genotypic coefficient of variation and heritability estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

Ghosh and Gulati (2001); studied genetic variability and association of yield components in Indian mustard with thirty six genotypes. The genotypic and phenotypic coefficients of variability (GCV and PCV, respectively) were high in magnitude for all the characters except plant height was estimated by that study. The differences between the PCV and GCV were narrow for all the characters studied, coupled with high heritability except plant height. High heritability, coupled with high genetic advance was observed for several primary branches, several siliquae on the main shoot, main shoot length, and some seeds per siliqua. This result suggests by the phenotypic selection, the importance of additive gene action for their inheritance and improvement could be brought.

Singh *et al.* (2001); studied different morpho-physiological characters of 29 genotypes of *B. napus* grown under normal and stress conditions of production and they found for days to 50% flowering, the existence of significant genetic variability.

An experiment was conducted by Shalini *et al.* (2000); to study variability in *Brassica juncea* L. in which different genetic parameters were estimated to assess the magnitude of genetic variation in 81 diverse Indian mustard genotypes. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all 10 characters which were under-studied. Genotypic coefficient of variation, estimates of variability, heritability values, and genetic gain were moderate to high for thousand seed weight, several siliquae per plant, and several secondary branches per plant. This result indicating that the response to selection would be remarkably high for these yield components. The other characters presented a low coefficient of variation, medium to low heritability and low genetic gain was observed.

Malik *et al*, (2000); observed high broad-sense heritability ($h^2b>90\%$) for many primary branches per plant and oil content while working with different strains of *B. napus*. They also observed low heritability for plant height, number of siliquae per plant, number of seeds per siliqua, and seed yield.

Thousand seed weight is an especially important character of rapeseed and mustard, where the highest consideration is on the seed yield. This character varied from genotypes to genotypes and from environment to environment a respectable number of works of literature are available on the variability of this trait. High heritability coupled with high genetic advance for seed yield per plant, number of secondary branches per plant, siliqua per plant, 1000 seed weight (g), and number of primary branches per plant which was observed by Sheikh *et al.* (1999) while working with 24 genotypes.

An experiment was conducted by Khulbe and Pan (1999); to estimate the variability, heritability, and genetic advance for yield and its components in Indian mustard. The study revealed maximum variability for seed yield and all the characters except oil content exhibited high heritability with high or moderate genetic advance. Which is suggesting the role of additive gene action in conditioning the traits. Non-additive gene action influenced of days to maturity, while environment had a major influence on oil content and the use of pedigree selection or biparental mating in advanced generations was advocated to achieve substantial gains.

2.3 Correlation among different characters

For estimated interrelationship among the character, the analysis of correlation among different traits is important in a breeding program. Quite several researchers were quite interested in those topics thereby we get a respectable number of pieces of literature on the correlation among characters of *Brassica sp.* From these, some of literatures are reviewed here.

Zajac *et al.* (1993); carried an experiment to study the phenotypic correlation between yield and its component. The study reported that there was a strong positive correlation occurred between seeds per siliqua and actual yield whereas a positive but weaker correlation was observed between seed yield and siliquae per plant. Summarized the number of seeds per siliqua had the greatest influence and the siliquae number per plant had the smallest effect on yield.

Tang *et al.* (1997); conducted a breeding program of yellow-seeded rapeseed. Based on variance analysis and path analysis, there used 16 yellow-seeded lines of *B. napus* L. which were derived from eight genetic sources. The study were evaluated for their genetic variation of the seed coat ratio, cellulose content, oil content of the seed coat, and the embryo. Correlation Analysis is studied between yellow and brown-seeded plants of the same observable line among those traits. As a result, the correlation analysis revealed a highly significant positive correlation of seed coat thickness with the cellulose content of the seed coat whereas a highly significant negative correlation with seed coat oils content and the 1000-seed weight.

Kumar *et al.* (1999) carried out a field experiment where there were 33 genotypes of *Brassica spp* in respect of magnitude with their corresponding phenotypic co-efficient, it was observed that the genotypic correlation coefficients were high. The seed yield had a positive correlation with plant height, siliqua number, number of siliquae per plant, and 1000 seed weight. It suggested that the improvement of those characters could improve the seed yield.

Malik *et al.* (2000) estimated no further significant correlation of days to maturity with seed yield for both phenotypic and genotypic levels of variances. There was showed negative correlation significantly with the number of seeds/siliqua and 1000 seed weight by the number of branches/plant and amount of siliquae/plant. Suggesting that genotypes having a high number of branches with a high number of siliquae reduced the number of seeds/siliqua and seed size.

A study was conducted by Ghosh and Gulati (2001). In that study, it was estimated seed yield displayed a significant positive combination with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliquae on the main shoot, and oil content. In the study, these components presented a significant positive correlation with each other. The findings indicate that for improving seed yield in Indian mustard, selection for one of these characters might automatically accumulate the other variables and this was a significant selection parameter

Pankaj *et al.* (2002) studied for correlation between yield and yield component traits with four parental cultivars and the 174 progenies of resultant crosses. This study observed the genetic correlation was higher than the phenotypic correlation for most of the factors. The number of siliquae per plant had shown a strong positive and significant correlation with yield per plant at both levels. The number of seeds per siliquae was positively associated with siliqua length and yield per plant at both levels.

A field experiment was conducted to determine the genetic potential of *Brassica spp*. In that experiment, eight accessions were sown in randomized complete block design in four replications. Plant height the number of primary branches, the number of secondary branches, the number of pods per plant, and the seed index were estimated as positively correlated with seed yield. The emphasis should be given during experimentation for improvement of those characters for improvement in seed yield per plant, suggested by Khan and Khan (2003).

Mahak *et al.* (2004) experimented and studied correlation for eight genotypes of Indian mustard seed. It was recorded seed yield per plant studied the positive correlation with the number of primary branches, length of the main raceme 1000-seed weight, and oil content. The recommendation was that the selection should be applied to these traits to improve seed yield in Indian mustard.

Khan *et al.* (2006) researched correlation for some quantitative traits to research yield and quality in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2002-2003. It was used eleven accessions of *Brassica napus* L. along with DGL as a standard variety was studied. Understudy a wide range of genetic variation existed among all the characters except 1000-grain weight were found out by this study. Correlation analysis estimated seed yield per plant was positively and significantly correlated with number of primary branches (0.401), siliqua per plant (0.505), seeds per siliqua (0.796), siliqua length (0.370) and seed yield per plot (0.409) whereas it was negatively and non-significantly associated with number of secondary branches (-0.367) and protein contents (-0.137) at genotypic level. Indicated the indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

An examination was completed by Tuncturk and Ciftci (2007) in Van, where Turkey amid 2000, 2001 and 2002 also researched to find out the connections among yield and some yield segments of 16 genotypes of mustard cultivars (*Brassica napus* L.) by utilizing relationship and path coefficient examination.

The outcomes factually uncovered the positive connection between seed yield with the quantity of branch (r=0.219), number of pods per plant (r=0.424), the quantity of seeds per case (r= 0.247), and 1000-seed weight (r= 0.161). Number of pods per plant, 1000-seed weight, and number of seeds per pods have demonstrated an impressive direct constructive outcome on seed yield. There the positive direct effect of number of pods per plant, number of seeds per pod and number of branches per plant was associated with significant and positive correlation with seed yield. From this study these yield segments proposed vast selection criteria to enhance seed yield for rapeseed breeding.

Jeromel *et al.* (2008) conducted a field experiment using 30 rapeseed genotypes of 30 genotypes estimated the highest seed yield per plant for four cultivars. There was an integrated correlation between plant height and height of the first lateral branch as well as between plant height and seed yield per plant and another was between plant height and seed oil content. The strongest direct effect on seed yield per plant was estimated for plant height, followed by the effect of number of pods per plant. This kind of experiment helped rapeseed breeders to optimize their breeding programs more successful.

Kumar *et al.* (2009) studied with 12 yield related trails in 15 genotypes of *B. napus* and *B. campestris*. It estimated the seed yield was positively correlated with plant height and 1000 seed weight.

Singh *et al.* (2010) studied sixty-two F_1 and twenty-four parental lines of *Brassica juncea* and observed the positive correlation was present in plant height, primary branches per plant, secondary branches per plant, seed per siliqua, thousand grain weights with seed yield.

Afrin *et al.* (2011) studied on *Brassica napus* and observed the positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliquae per plant. The highest significant positive correlation was studied between days to 50% flowering and plant height.

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

Uddin *et al.* (2013) conducted an experiment with seven parental and twenty-one F_2 progenies of *Brassica rapa* to study correlation among different yield component, in which he found high significant positive correlation with number of primary branches per plant, number of secondary branches per plant and siliquae per plant at both phenotypically and genotypically yield per plant. In addition, yield also had high and significant positive correlation at genotypically in days to flowering and days to maturity.

Ejaz-Ul-Hasan *et al.* (2014) studied correlation between different traits of *Brassica napus* and observed, between plant height and seeds per plant high and positively significant phenotypic correlation.

Mokonnen *et al.* (2014) studied *Brassica carinata* and found that at both genotypic and phenotypic level, seed yield per plant was positively correlated with plant height, days to maturity, secondary branches per plant and thousand seed weight. There were also found that plant height was strongly and positively correlated with number of pods per plant indicating for improving number of pods, plant height should be taken under progress.

Hira (2015)., in her experiment with *Brassica napus*, she stated that more emphasis should be given for plant height, secondary branches per plant, siliqua per plant and thousand seeds weight as they showed exceedingly highly high to fair degree of positive association with seed yield at both genotypic and phenotypic level in her founding.

Rauf (2016). Emphasized that comparing correlation coefficient values of eleven variables on seed yield, both significant and insignificant differences were observed. He got as genetic correlation coefficient was higher than phenotypic correlation coefficient, it implied that the apparent association of two characters was due to phenotypic value was decreased by the significant interaction of environmental factors.

Paul (2017). carried out an experiment and observed that, seed yield per plant was significant positive correlation with siliquae per plant (0.746 and 0.643) at both genotypic and phenotypic levels and with days to 50% flowering (0.366) at genotypic level which suggesting that genotypes 64 with high partitioning efficiency gave increase in seed yield per plant.

Khatun (2018). Carried out an experiment for analysis of the genetic diversity and character association. After observation it was found seed yield as a complex product being influenced by several quantitative traits. Some of these traits which was used for the experiment were highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield was very much essential to establish selection criteria thereby breeders always look for genetic variation among traits to select desirable type.

2.4 Path co-efficient analysis

It becomes difficult when more characters are involved in correlation study to ascertain the traits which really contribute towards the yield. The path analysis under such situation helps to determine the direct and indirect contribution of these traits towards the yield whereas correlation coefficient analysis helps to explore the nature and degree of relationship between any two measurable characters.

The measure of correlation does not consider dependence of one variable over the other. Direct contribution of each component to the yield and the indirect effects which effect reflect through its association with other components cannot be differentiated from mere correlation studies. For that’s why path analysis resolves these complex relations between the events and turns into simple form of association.

Path co efficient analysis was first developed and described by Wright in 1921, as a tool in genetic analysis by which partition direct and indirect effects of the association on yield and the characters on yield through other components were identified. The association between the various characters in a rapeseed and mustard had been studied for investigating the direct and indirect effects of a variable over the dependent variable and as through we get an enormous number of reviewed here.

Genotypic path was worked out in the study done by Afrin (2017) considering yield per plant as dependent character and its attributes as independent characters viz., days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, length of siliqua (cm), no. of seeds per siliqua and 1000 seed weight (g). Each component has two path actions viz., direct effect on yield and indirect effect through components which are not revealed by correlation studies whereas plant height, primary branches of plant, secondary branches of plant, siliqua per plant, seeds per plant.

Rauf (2016). In that study the direct and indirect effects of yield contributing characters on seed yield were done by using path analysis and reported that seed yield as the ultimate product of several yield contributing characters. Where it was considered seed yield per plant as effect (dependent variable) and days to 50% flowering, days to 80% maturity, plant height, siliqua length, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, number of siliqua per plant, and 1000-seed weight were treated as causes or independent variables.

Hira (2015). Conducted both correlation and path co-efficient studies and revealed that for siliquae per plant, siliqua length, and thousand seeds weight and plant height were the most important components for getting higher yield. Suggested that that siliqua per plant, and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher grain yield in *Brassica napus*.

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

Mekonnen *et al.* (2014); conducted an experiment to study path co-efficient in *Brassica carinata*. This study revealed days to maturity and secondary Braches per plant had positive and direct genotypic correlation with seed yield.

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

To determine the most important traits which was affecting grain yield in Canola and identified the quantity of direct and indirect effects on grain yield, an experiment was conducted with 10 Canola varieties in a RCBD design with three replications by Khayat *et al.* (2012). Stepwise regression and path analysis revealed the number of pods per plant had the highest direct effect on grain yield as well as the dry matter, thousand grain weight and days to maturity also had a high direct effect on grain yield.

Afrin (2011); studied with *B. napus* to analysis the path co-efficient among the characters. The plant height found as the highest positive and direct effect on seed yield per plant followed by number of siliquae per plant and siliqua length.

Alam (2010); studied path co-efficient analysis that revealed plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliquae and siliqua length had the direct positive effect on yield per plant. On contrary, days to 50% flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plant.

The path co-efficient analysis by Hosen (2008) was worked with five parental genotypes of *B. rapa* and their ten F_3 progenies including reciprocals that exhibited result as thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua.

An experiment was conducted by Parveen (2007); with F_2 population of *Brassica rapa* to study the path analysis where observation showed the highest direct effect on yield per plant was number of seeds per siliqua.

Rashid (2007); carried out an experiment with 40 *Brassica* species to estimate path analysis where the highest direct effect of yield was observed on days to maturity, number of seeds per siliqua, number of siliquae per plant and number of primary and secondary branches per plant.

By path analysis, Zahan (2006); it was reported siliquae per plant had positive direct effect on yield per plant whereas the days to 50% flowering had negative direct effect on yield per plant.

Khan *et al.* (2006); carried out a study on correlation for some quantitative traits relating to yield and quality. The results indicated a wide range of genetic variation among all the characters under study except 1000-grain weight. In correlation analysis, seed yield per was plant positively and significantly correlated with number of primary branches (0.401), siliqua per plant (0.505), seeds per siliqua (0.796), siliqua length (0.370) and seed yield per plot (0.409). However, seed yield gave opposite result that was negatively and non-significantly associated with number of secondary branches (-0.367) and protein contents (-0.137) at genotypic level. That founding indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

Goswami *et al.* (2005); conducted experiment on variability studies for number of secondary branches, siliquae on main shoot, seeds per siliqua, 1000-seed weight, and seed-yield per plant where the results showed that the coefficient of variation of pods per plant, filled grains per pod and 1000-grain weight on yield per plant were significant and there was considerable variability for the above character studied.

Afroz *et al.* (2004); studied path coefficient analysis and found maximum direct positive effects by plant height, number of siliquae per plant, number of primary branches per plant, 1000-seed weight and number of siliquae shattering per plant on seed yield per plant.

An experiment was conducted by Poonam and Singh (2004) in 40 Indian mustard germplasms to determine the correlation and path coefficient values between yield and yield attributing character. Path coefficient analysis of seed yield per plot with different correlated characters was partitioned into direct and indirect effects. Plant height had the highest positive direct effect (0.836) followed by number of seeds per siliqua (0.791). The number of primary branches per plant, siliqua per plant and days to maturity had low but negative direct effects on seed yield.

Sudan *et al.* (2004); studied path analysis with Indian mustard. From this study path analysis number of primary branches was the most important character with the highest direct effect on seed yield. Other characters i.e., days to flowering, 1000 seed weight and number of seeds per siliqua had high positive effect on yield via other character. This study suggested that the scope of their simultaneous improvement through selection.

Choudhary *et al.* (2003); studied correlation and path coefficient analysis in 28 genotypes of Indian mustard which was including three controls. The observations were analyzed for seed yield per plant and 11 quantitative characters viz., days to 1st flowering, days to maturity, length of main axis, primary branches per plant, secondary branches per plant, number of siliquae per plant, siliqua length, number of seeds per siliqua, 1000- seed weight. The reaction of this study was to Alternaria black spot-on leaf and on siliquae. The highly significant and positive correlation with seed yield per plant was observed for all 28 the characters had, except for reaction to Alternaria black spot on both leaf and siliqua and days to 1st flowering.

Gupta *et al.* (2002); studied on significant correlation ship between plant height, number of siliquae on the main raceme and number of seed per siliqua, while plant height was significantly correlated with number of siliquae on the main raceme of 18 lines rapeseed. In general, genotypic correlations were greater than phenotypic or environmental correlations and seed yield were positively correlated with number of siliquae on the main raceme and 1000-seed weight.

Srivastava and Singh (2002); reported that number of primary branches per plant, number of secondary branches per plant and 1000 seed weight had strong direct effect on seed yield while working with Indian mustard (*B. juncea* L.) and suggested that number of primary branches and 1000 seed weight were vital selection criteria for improvement in productivity of Indian mustard.

Shalini *et al.* (2000); studied path analysis of Indian mustard germplasm, the result revealed the observation that number of siliquae per plant had the highest direct effect on seed yield followed by 1000 seed weight, number of primary branches per plant and plant height and most of the characters had an indirect effect on seed yield.

Sheikh *et al.* (1999); worked with 24 diverse genotypes of mustard for assess the direct and indirect effect of seven quantitative and developmental traits on seed yield. Thousand seed weight and siliqua per plant had highly positive direct effect on seed yield was experimented.

The number of siliquae per plant had the highest positive direct effect on seed yield was estimated by Yadava *et al.* (1996); while studied path co-efficient analysis of 6 yield components of 25 diverse varieties of Indian mustard.

Uddin *et al.* (1995); studied path analysis with 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and 1000 seed weight had high positive direct effect on seed yield per plant.

Yadava *et al.* (1993); when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed number of siliquae per plant had the highest positive direct effect on seed yield.

Dhillor *et al.* (1990); recorded the plant height as the highest positive direct effect on seed yield per plant in *B. juncea*, but Singh *et al.* (1997); found negative direct effect of the trait on seed yield. Han (1990); studied *B. napus* and estimated negative direct effect of number of siliquae per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield.

CHAPTER III

MATERIALS AND METHODS

The purpose of this study was for analysis of genetic parameter and character association of yield and its' contributing characters of F_7 of *B. napus* L.This chapter consists of a concise explanation of 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 and statistical analysis etc. since this chapter deals with the information about materials and methods that were used in conducting the experiment. The details of the materials and methods that used or followed in this experiment has been presented below under the following headings:

3.1 Experimental site

This research study was carried out in the experimental fields of Sher-e-Bangla Agricultural University, Dhaka–1207 during November 2018 to February 2019 which was located at 23°74″N latitude and 90°35″ E longitudes with an elevation of 8.6 meter from the sea level (Appendix-1). Photograph showed experimental sites (Plate 2).

3.2 Soil and climate:

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

3.3 Experimental materials

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

Plate 2. Pictorial view of experimental field during supervision by supervisor Prof. Dr. Firoz Mahmud.

Table 1. Materials used for the experiment

SL NO	**Genotypes**	**F_7 Populations**
1	G1	(Nap 2001×Nap179)
2	G2	(Nap94006×BS-13)
3	G3	(Nap2057×BS-13)
4	G4	(Nap2001×Nap2022)
5	G5	(Nap2057×Nap248)
6	G6	(Nap2012×Nap2013)
7	G7	(Nap2057×Nap2022)
8	G8	(Nap 200×Nap 2022)
9	G9	(Nap 94006×Nap2001)
10	G10	(Nap 9908×Nap2001)
11	G11	(BS-7×Nap206)
12	G12	(Nap 2057×Nap2012)
13	G13	(Nap 248×Nap159)
14	G14	(Nap 2037×Nap2022)
15	G15	(Nap 2037×Nap 2013)
16	G16	(Nap 94006×Nap 2013)
17	G17	(Nap 9908×Nap 94006)
18	G18	(BS-7×Nap 94006)
19	G19	(Nap 179×Nap 2012)
20	G20	(Nap 94006×Nap 2012)
21	G21	(BS-13×Nap 2013)
22	G22	(Nap9406×Nap 2013)
23	G23	(Nap9406×Nap2057)

Table 1. Materials used for the experiment (Contd.)

SL NO	**Genotypes**	**F_7 Populations**
24	G24	(Nap2012 × Nap 2022)
25	G25	(Nap2001 × BS-7)
26	G26	(Nap2001 × Nap 206)
27	G27	(Nap 179 × Nap 206)
28	G28	(Nap 179 × Nap 2012)
29	G29	(BS-13 × Nap 206)
30	G30	(Nap248 × Nap2013)
31	G31	(Nap2057 × Nap 2001)
32	G32	(Nap206 × Nap2013)
33	G33	(BS-13 × Nap 2013)
34	G34	(Nap179 × Nap 2022)
35	G35	(BS-7 × Nap 2057)
36	G36	(Nap94006 × Nap179)
37	G37	(Nap248 × Nap 206)
38	G38	(Nap179 × Nap 2057)
39	G39	(Nap206 × Nap2012)
40	G40	(Nap 9908 × Nap206)
41	G41	(Nap248 × Nap2022)
42	G42	(Nap94006 × Nap2057)
43	G43	(Nap179 × Nap 2012)

3.4 Methods

The following precise methods have been followed to carry out the experiment:

3.4.1 Land preparation

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

3.4.2 Application of manure and fertilizer

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

3.4.3 Experimental design and layout

Field lay out was done after final land preparation (Plate: 3). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 20 m × 25 m = 300m^2. Each replication size was 6m × 5m, and the distance between replication to replication was 1m. The spacing between lines to line was 30cm. Seeds were sown in lines in the experimental plots on 4 November, 2019. 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.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period.

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

Plate 3. Field lay out preparation after final land preparation

Plate 4. Intercultural operations (Thinning)

The first weeding was done after 14 days (about 2 weeks) of sowing. At the same time, 1st thinning was done (Plate: 4) and another after 7 days of 1st thinning for maintaining 10 cm (about the length of the long edge of a credit card) from plant to plant in rows of 30 cm apart. The critical weed free period for *Brassica* is 15 to 30 days (about 4 and a half weeks) after sowing. Second weeding was done after 30 days (about 4 and a half weeks) of sowing. Aphid infection was found in the 34 crops during the siliquae development stage. To control aphids Malathion-57 EC @ 2ml/liter of water was applied. The insecticide was applied in the afternoon.

3.4.5 Crop harvesting:

Harvesting was done from about 90 days (about 3 months) after sowing (DAS) depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e., straw color of siliquae, leaves, stems desirable seed color in the mature siliquae, the crop was assessed to attain maturity. Fifteen plants were selected at random F_7 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly.

Data were recorded on different parameters from these plants. A pictorial view of experimental field at harvesting stage is presented in Plate 5

3.4.6 Data collection

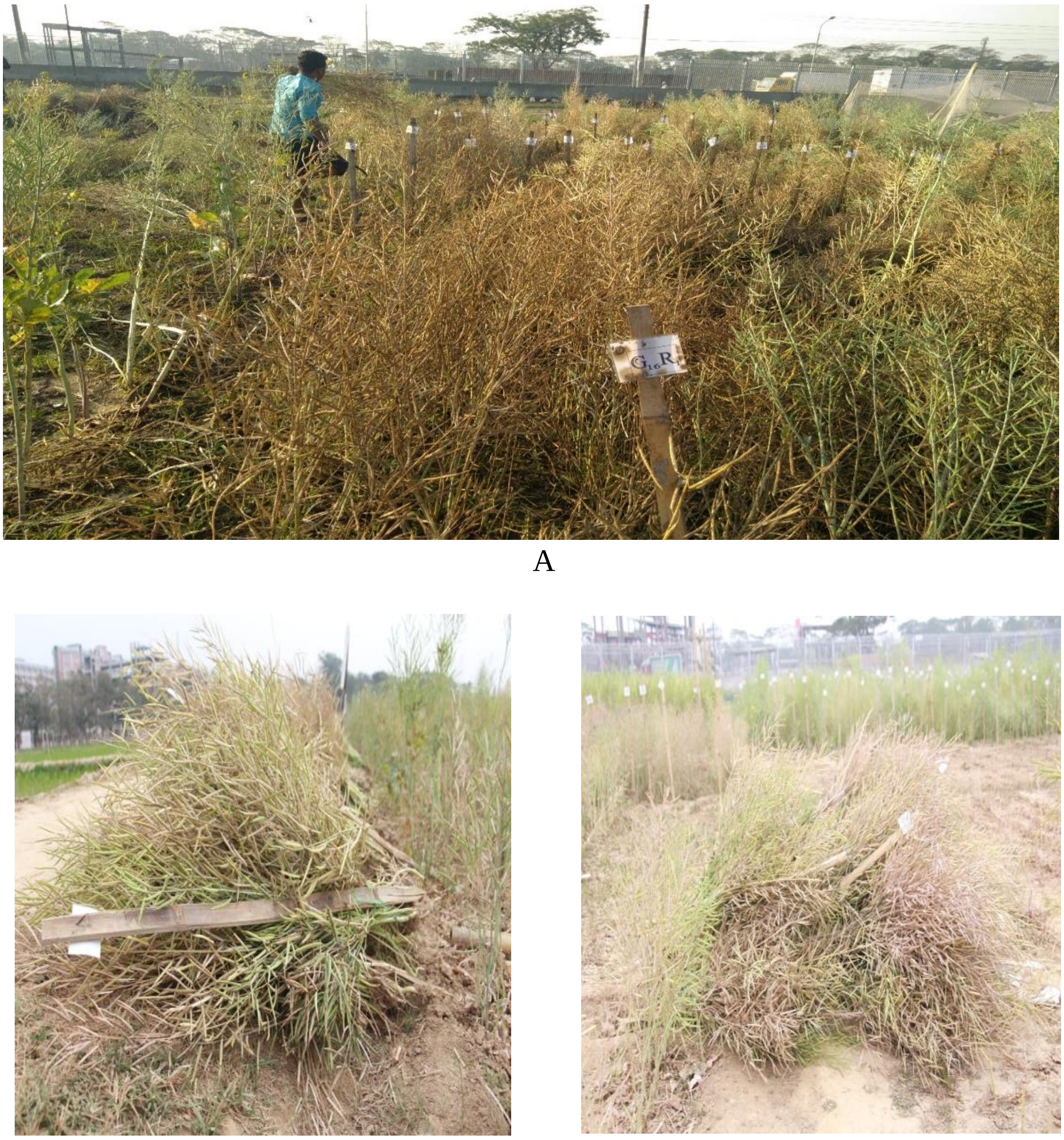
Studying different genetic parameters and inter-relationships, eleven characters were taken into consideration. The data were recorded on ten plants from each line from each replication which means 1290 plants on the following traits.

Days to 1st flowering: Days to 50% flowering were recorded from sowing date to the date of 50% flowering of every entry.

Days to 50% maturity: The data were recorded from the date of sowing to siliquae maturity of 80% plants of each entry.

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

Number of secondary branches per plant: The total number of branches arisen from the primary branch of a plant was counted as the number of secondary branches per plant**.**



A

B

C

Plate 5: Crop harvesting from experimental field. Where,

A= The plants were harvested by uprooting,

B= Fifteen plants were selected at random from each replication,

C= Plants were tagged properly.

Number of siliquae per plant: Total number of siliquae of each plant was counted and considered as the number of siliquae per plant.

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

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

1000-seed weight (g): Weight in grams of randomly counted thousand seeds of each entry was recorded.

Seed yield per plant (g): All the seeds produced by a representative plant was weighed in g and considered as the seed yield per plant

3.5 Statistical analysis

Mean data of the characters were used to statistical analyze like analysis of variaancce (ANOVA), mean, range were calculated by using Statistix 10 software program. Genotypic and phenotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic coefficient of variation were calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956); path coefficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 and Microsoft Excel 2016 software.

3.5.1 Estimation of genotypic and phenotypic variances

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

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

Where, GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

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

Where, σ^2_g = Genotypic variance

σ^2_e = Error variance

3.5.2 Estimation of genotypic and phenotypic co-efficient of variation

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

Genotypic co-efficient of variation (GCV %) = $\sqrt{\frac{\sigma_g^2}{\bar{x}}} \times 100$

Where, σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

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

Phenotypic co-efficient variation (PCV %) = $\sqrt{\frac{\sigma_p^2}{\bar{x}}} \times 100$

Where, σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

3.5.3 Estimation of heritability

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

Heritability, $h^2{}_b$% = $\sqrt{\frac{\sigma_g^2}{\sigma_p^2}} \times 100$

Where, h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.5.4 Estimation of genetic advance

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

Genetic advance, GA = K. $h^2 . \sigma^2_p$ Or. Genetic advance, GA=K. $\frac{\sigma_g^2}{\sigma_p^2} \cdot \sigma_P$

Where, K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_P = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.5.5 Estimation of genetic advance mean’s percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance}}{\text{Population mean}} \times 100$$

3.5.6 Estimation of genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation, } r_{gxy} = \frac{PCOV_{xy}}{\sqrt{PV_x \cdot GV_y}} = \frac{\sigma_{pxy}}{\sqrt{\sigma_{px}^2 \cdot \sigma_{py}^2}}$$

Where, σ_{pxy} = Phenotypic covariance between the trait x and y

σ_{px}^2 = Phenotypic variance of the trait x

σ_{py}^2 = Phenotypic variance of the trait y

3.5.7 Estimation of path co-efficient

It was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield per hectare.In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3…. 11 on y for yield,S set of simultaneous equations is required to be formulated as shown below:

$$r_{1.y} = P_{1.y} + r_{1.2}P_{2.y} + r_{1.3}P_{3.y} + r_{1.4}P_{4.y} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{1.11}P_{11.y}$$
$$\mathrm{r}_{2\cdot\mathrm{y}} = \mathrm{r}_{1.2}\mathrm{P}_{1.\mathrm{y}} + \mathrm{P}_{2.\mathrm{y}} + \mathrm{r}_{2.3}\mathrm{P}_{3.\mathrm{y}} + \mathrm{r}_{2.4}\mathrm{P}_{4.\mathrm{y}} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + \mathrm{r}_{2.11}\mathrm{P}_{11\mathrm{y}}$$
$$r_{3.y} = r_{1.3}P_{1.y} + r_{2.3}P_{2.y} + P_{3.y} + r_{3.4}P_{4.y} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{3.11}P_{11.y}$$
$$r_{4.y} = r_{1.4}P_{1.y} + r_{2.4}P_{2\cdot y} + r_{3.4}P_{3-y} + P_{4.y} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{4.11}P_{11.y}$$
$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots.$$
$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots.$$
$$\mathrm{r}_{11.y} = \mathrm{r}_{1.11}\mathrm{P1.y} + \mathrm{r}_{2.11}\mathrm{P}_{2.\mathrm{y}} + \mathrm{r}_{3.11}\mathrm{P}_{3.\mathrm{y}} + \mathrm{r}_{4.11}\mathrm{P}_{4.\mathrm{y}} \ldots\ldots\ldots\ldots\ldots\ldots. + \mathrm{r}_{7.11}\mathrm{P}_{11.y}$$

Where,

$r_{1.y}$ = Genotypic correlation coefficients between y and I th character (y = Fruit yield)

$P_{1.y}$ = Path coefficient due to i th character (i= 1, 2, 3….11) .

1=Days to first flowering

2= Days to 50% flowering

3= Days to maturity

4=Plant height (cm)

5=Primary branches per plant

6=Secondary branches plant

7= Silique per plant

8= Silique length (cm)

9= Seeds per siliqua

10= Thousand seed weight (g)

11= Seed yield per plant (g)

Total correlation, say between 1 and y i.e., $r_{1.y}$ is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2}P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3}P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4}P_{4.y}$ = indirect effect of 1 via 4 on y

………………………………………….

………………………………………......

$r_{1.11}P_{11.y}$= indirect effect of 1 via 11 on y

Where, $P_{1.y}$, $P_{1.y}$, $P_{3.y}$. ……… $P_{11.y}$= Path coefficient of the independent variables 1, 2, 3,….,11 on the dependent variable y, respectively. $r_{1.y}$, $r_{2.y}$, $r_{3.y}$, …., $r_{11.y}$ = Correlation coefficient of 1, 2, 3,…., 11 with y, respectively.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula (Singh and Chaudhary, 1985) given below:

$$\mathrm{P}_{\mathrm{RY}}^{2} = 1 - \left(\mathrm{r}_{1.y}\mathrm{P}_{1.\mathrm{y}} + \mathrm{r}_{2.\mathrm{y}}\mathrm{P}_{2.\mathrm{y}} + \cdots \ldots \ldots \ldots \ldots .. + \mathrm{r}_{11.\mathrm{y}}\mathrm{P}_{11\mathrm{y}}\right)$$

Where $\mathrm{P}_{\mathrm{RY}}^{2}$=$\mathrm{R}^2$

Hence, residual effect, R = ($\mathrm{P}_{\mathrm{RY}}^{2}$)$^{1/2}$

$P_{1.y}$= Direct effect of the i^{th} character on yield y.

$r_{1.y}$= Correlation of the i^{th} character with yield y.

CHPTER IV
RESULTS AND DISCUSSION

In this chapter, the data was evaluated from the 43 F_7 populations of *B. napus* L. genotypes to find out the genetic variability, character association, path analysis. The studies of F_7 segregating generations of *B. napus* L. carried out during Rabi season 2019-20 in experimental field of Sher-e-Bangla Agricultural University. The data were subjected on different characters such as days to 50% flowering, no. of siliquae per plant, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of seeds per siliquae, siliquae length (cm), 1000 seed weight (g) and seed yield per plant (g). After exploring the data statistically, the result from the study is explained below under the following headings:

1. Analysis of variance study in *Brassica napus L.*
2. Genetic variability, heritability and genetic advance
3. Association analysis
4. Path coefficient analysis

4.1 Analysis of variance

The achievement in any crop improvement program depends on the capability of the breeder to define and accumulate the required genetic variability and to select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation. The information of Genotypic Variance and Phenotypic Variance both are important for a breeder to predict the expected Genetic Advance possibility by selection for a desire character can be computed.

There is a clear indication of highly significant amount of variability among the genotypes for all the characters studied viz. days of first flowering, days 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, siliquae per plant, siliquae length (cm), seeds per siliquae, thousand seed weight (g) and seed yield per plant (g) in the analysis of variance. Though the results revealed the presence of high variability for yield and its contributing characters among the genotypic studied but there is a lot of scope for selecting the majority of the traits in the genotypes. The mean sums of squares of all the characters are presented in

Table 3. This Significant differences among the genotypes was observed before, by many researchers like Khatun (2018), Paul (2017), Afrin (2017), Bhuiyan (2018), Uddin *et al.* (2005), Khan *et al.* (2006), Xu-Suqin *et al.* (2006), Parveen (2007), Zebarjadi *et al.* (2011).

4.2 Genetic variability, heritability and genetic advance

The amount of genetic variability presented in the population is highly responsible for the success of crop improvement programmed. Through selection or hybridization followed by selection the extent of genetic variability can be determined the speed and quantum of genetic improvement. Phenotypic variance measures the magnitude of variability that is arising out of differences in phenotypic values. On the other hand, the genotypic variance measures the magnitude of variation due to difference within the genotypic values.

For effective selection, the heritability estimates separate the environmental influence from the total variability and indicates the accuracy with which phenotypic performance can identify its genotypic performance by which the relative amount of heritable portion of the variation can be determined. There is a presence of narrow gap between PCV and GCV for all the characters expect secondary branches per plant under the analysis that means these traits studied had low environmental influence. In addition to the estimation of the genetic advance with the estimation of heritability appears to be more meaningful. The genetic advance as per cent means (GAM) was also estimate along with the estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent mean for all the characters were studied. The results of all are presented in Table 3 and depicted in Figure 1 and 2. In Appendix V, the mean performance of *B. napus* L. F_7 segregating genotypes for various growth characters and yield components are showed.

Table 3. Analysis of variance of different characters in *B. napus* L.

Source Of variation	**Df**	**Mean sum of square**										
		DFF	**D50F**	**DM**	**PH (cm)**	**NPB**	**NSB**	**NSP**	**SL (cm)**	**NSS**	**TSW (g)**	**SYP (g)**
Replication	2	0.71	2.89	5.67	86.67	0.37	0.05	446.10	0.07	15.36	0.26	1.53
Genotype	42	11.36**	44.70**	35.93**	654.01**	6.42**	5.21**	13634.10**	2.67**	46.64**	1.48**	15.98**
Error	84	2.14	4.61	6.28	24.14	0.78	0.99	524.70	0.18	5.76	0.10	0.16

** = Significant at the 0.01 level, Df = Degrees of freedom

Where,

DFF= Days to first flowering
D50F= Days to 50% flowering
DM= Days to maturity
PH= Plant height (cm),
NPB= Number of primary branches
NSB=umber of secondary branches
NSP= Number of siliqua per plant,
SL= Siliqua length
NSS= Number of seeds per siliqua
TSW= Thousand seed weight,
SYP= Seed yield per plant.

4.2.1. Days to first flowering:

There significant variance was observed in days to first flowering and the value was 11.36 (Table-3). Within 24.00 days G8 (Nap200 × Nap2022) showed first flowering as the minimum duration of days first flowering. On the other hand, the maximum duration of days toys first flowering was found in G41 (Nap248 × Nap2022) with 33.00 DAS. The duration of days to first flowering was ranged with 24.00 to 33.00 where the mean of the days to first flowering was 27.83% (Appendix V).

The phenotypic variance (5.21) was higher than genotypic variance (3.07) (Table 4) Same scenario was observed on PCV (Phenotypic co variance 8.20) and GCV (Genotypic co variance 6.30) respectively along with medium heritability of 58.91 with low genetic advance as 5 per cent mean of 2.77 %` and low genetic advance % mean was 9.96% (Table 4).

4.2.2. Days to 50% flowering:

The mean sum of square of days to 50% flowering was observed with significant value of 44.70 (Table 3).). The values ranged from 35.19 to 43.00 days for 50% flowering. The highest days to 50% flowering was found in G22 (Nap94006 × Nap2019) (43 days) and the lowest (35 days) was found in G19 (NAP94006×Nap2013) (Appendix V). The phenotypic and genotypic variance for days to 50% flowering was found as 17.97% and 13.37% respectively (Table 4). The value of PCV is higher than GCV and ECV which indicated that variability for the character was influenced by both genotypes and environment. The highest co-efficient of both for genotypic variance and phenotypic variance was observed by Lekh *et al.* (1998). The higher heritability was observed with the value 74.37% and the moderate Genetic advance was studied with the value 18.45 (Table 4). It was indicating that environmental factors were much influential in respect of their phenotypic expression for the characters of the genotypes because the phenotypic variance was much higher than genotypic variance. The phenotypic coefficient of variation (4.57%) was higher than the genotypic coefficient of variation (3.57%) (Table 4), which suggested that environment had a huge role for the development with the environmental coefficient of variation was observed 1.00. This same kind of result for this trait was also observed by Rameeh (2013) and Katiyar *et al.* (1974). The higher heritability 61.16 with lower genetic advance mean 5.75.

Table 4. Estimation of genetic parameters in 11 characters of 43 genotypes in *B. napus* L.

Parameters	σ 2 p	σ 2 g	σ 2 e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to first flowering	5.21	3.07	2.14	8.20	6.30	1.91	58.91	2.77	9.96
Days to 50% flowering	17.97	13.37	4.61	12.05	10.39	1.66	74.37	6.49	18.45
Days to maturity	16.16	9.88	6.28	4.57	3.57	1.00	61.16	5.06	5.75
Plant height (cm)	234.09	209.96	24.14	11.89	11.26	0.63	89.69	28.27	21.97
Number of primary branches	2.66	1.88	0.78	33.46	28.13	5.33	70.70	2.37	48.73
Number of secondary branches	2.40	1.41	0.99	32.00	24.51	7.49	58.66	1.87	38.67
Number of siliqua per plant	4894.50	4369.80	524.70	36.79	34.76	2.03	89.28	128.67	67.66
Siliqua length (cm)	1.01	0.83	0.18	12.08	10.97	1.11	82.54	1.71	20.54
Number of seeds per siliqua	19.39	13.63	5.76	16.90	14.17	2.73	70.28	6.37	24.47
Thousand seed weight (g)	0.56	0.46	0.10	15.04	13.63	1.41	82.16	1.27	25.45
Seed yield per plant (g)	5.43	5.27	0.16	38.06	37.50	0.56	97.08	4.66	76.11

Where,

σ^2 p = Phenotypic variance

σ^2 g = Genotypic variance

σ^2 e = Environmental variance

GA= Genetic advance

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

ECV = Environmental coefficient of variation

4.2.1. Days to maturity:

There significant variance was observed in days to maturity and the value was 35.93(Table-3). The duration of days to maturity was ranged with 77.33 to 93.00 where the mean of the days to first flowering was 3.82% (Appendix V).The phenotypic variance (16.16) was higher than genotypic variance (9.88) (Table 4).Same scenario was observed on PCV (Phenotypic co variance 4.57) and GCV (Genotypic co variance 3.57) respectively along with medium heritability of 61.16.91 with genetic advance as 5 per cent mean of 5.75 %` and genetic advance % mean was 5.75% (Table 4).

4.2.4. Plant height (cm)

The 2nd highest mean plant height recorded was 128.69 cm. It ranged from 101.55 cm to 127.70 cm (Appendix V). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height with figure 654.01. From Appendix-1 the maximum plant height was studied 169.93 cm by the G16 (Nap 248 × Nap 159) whereas the minimum plant height was recorded 106.43 by G36 (Nap 94006 ×Nap 179). The phenotypic variance was 234.09 that was lower than both genotypic variance 209.96 and environment variance 24.14. The PCV were studied 11.89% and GCV were 11.26% and the lower value of environmental co variance 0.63%. The estimate of heritability was high at 89.69 per cent with high genetic advance in percent of mean (21.97%) (Table 3). The Genetics Advance at 5% was observed 28.27.

4.2.5 Primary branches per plant

It ranged from 2.67 to 8.33 with a mean value of 8.87. The maximum number of primary branches were recorded in G21 (BS 7 × Nap 2013) whereas G8 (Nap200 × Nap 2022) genotype showed the minimum number of primary branches. The PCV, GCV, ECV were observed 33.46, 28.13 and 7.49 percent, respectively. It might provide better scope for improvement through selection because of higher GCV and PCV for primary branches per plant and that also reported by Mekonnen (2014). The PCV was higher than the GCV for number of primary branches and it was supported by Walle *et al.* (2014) findings. Higher heritability of 70.70 per cent coupled with higher genetic advance over percentage of mean 38.67 percent were noticed and these similar findings was found by Alam (2010).

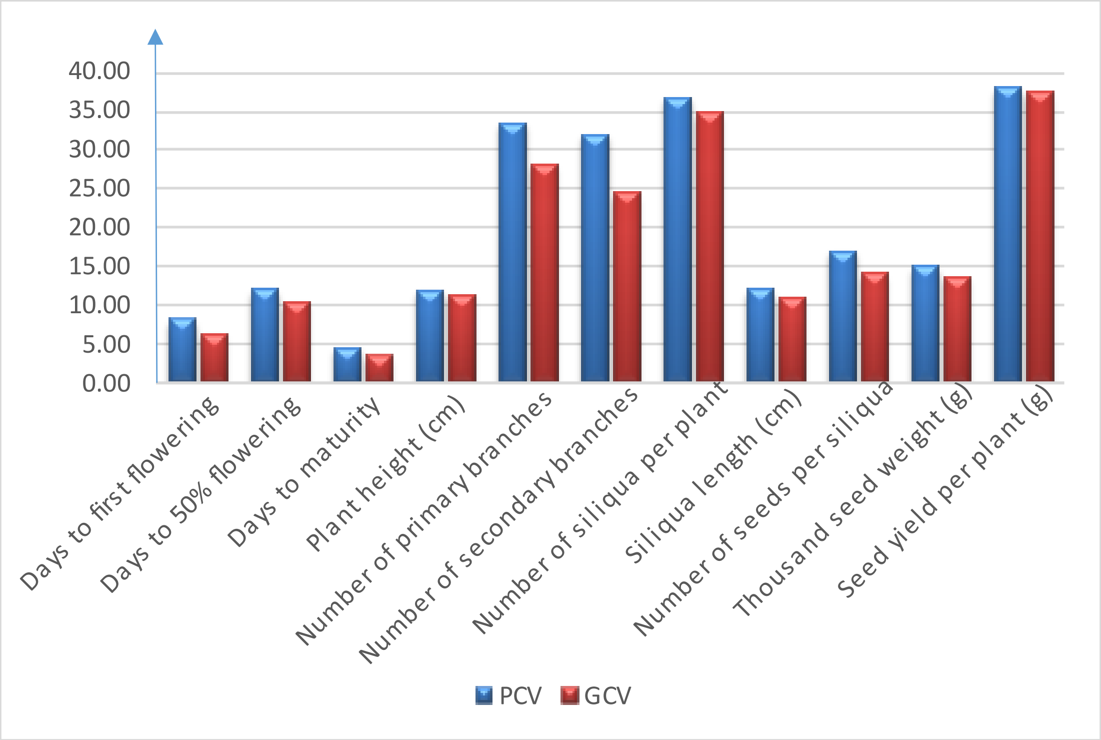


Figure 1. Genotypic and phenotypic variability in *B. napus* L.

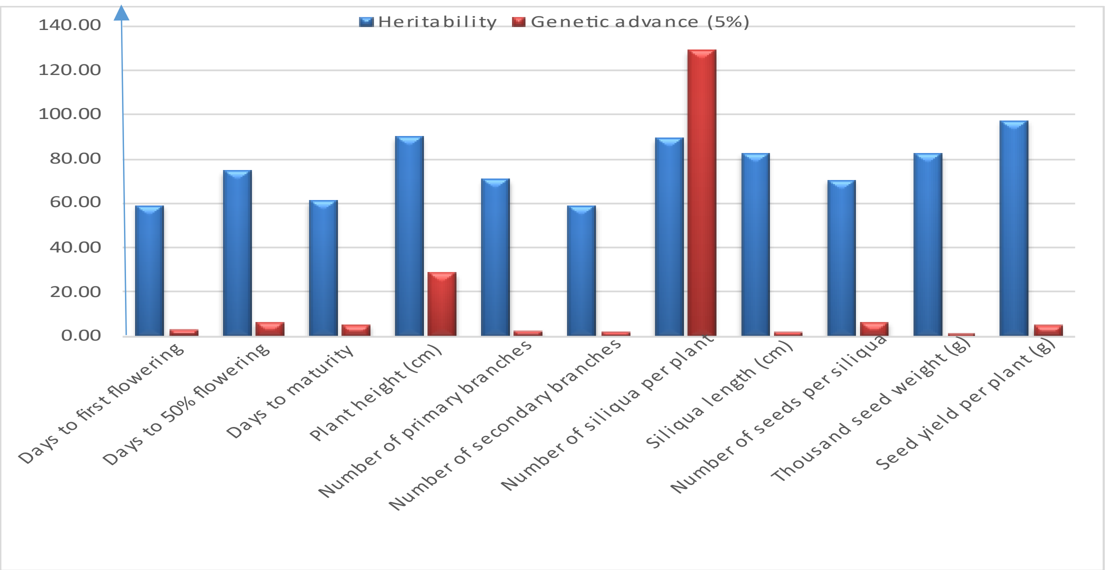


Figure 2. Heritability and Genetic advance (5%) of 43 F_7 populations of *B. napus* L.

4.2.6. Secondary branches per plant

The maximum number of secondary branches per plant was recorded 7.67 in the G19 (Nap179 × Nap 2012) and the minimum number was recorded 2.67 in the G43 (Nap 179 × Nap 2012). The number of secondary branches per plant ranged from 2.67 to 7.67 with a mean of 4.84. The genotypic, phenotypic and environmental variances observed were 2.40, 1.41 and 0.99, respectively. The PCV and GCV were 32.00 and 24.51 respectively and the ECV was 7.49. The moderate heritability estimates of 58.66 per cent with a high expected genetic advance over mean of 38.67 per cent were recorded for this trait and high genetic gain over mean were 89.28 and 128.67 per cent, respectively. This sort of high heritability with low genetic advance was found by Alam (2010) for this trait that supported the results.

4.2.7 Number of siliquae per plant

There was the highest significant variance 13634.10 was observed in this character. Where the maximum siliquae per plant was observed in G34 (Nap179 X Nap 2022) and the minimum number of siliquae per plant was observed in G23 (Nap 9406 X Nap 2057). The ranged was from 111.33 to 353.67 with mean value was 190.17

The genotypic variance and phenotypic variance were 4894.50 and 4369.80 respectively with the environmental variance was 524.70. The coefficient of variability at phenotypic and genotypic level were 36.79 and 34.76 per cent respectively with environment co efficient was 2.03. The values for high heritability and high genetic gain over mean were 89.28 and 128.67 per cent, respectively.

4.2.8 Siliquae length (cm)

The significance variance was observed in this trait with the value 2.67. It ranged from 6.47 to 10.60 cm with a mean of 8.30 cm. The minimum siliqua length was recorded from the G25 (Nap 94006 × BS-7) and G23 (Nap 94006 × Nap 2057) studied the maximum siliqua length. The PCV and GCV obtained were 12.08 and 10.97 per cent respectively with the ECV was 1.11. The phenotypic variance was 1.01 with low genotypic variance and economic variance were .83 and .18 respectively. The values of high heritability (82.54%) along with high genetic advance as per cent mean (20.54%).

4.2.9 Number of seeds per siliquae

The Number of seeds per siliquae was observed as significance variance with value 46.64 (Table 3). The maximum number of seeds of siliquae was represented from G40 (Nap 9908 × Nap 206) while the minimum number of seeds per siliquae was represented from G39 (Nap 206 × Nap 2012). It was ranged with 35.00 to 16.33.

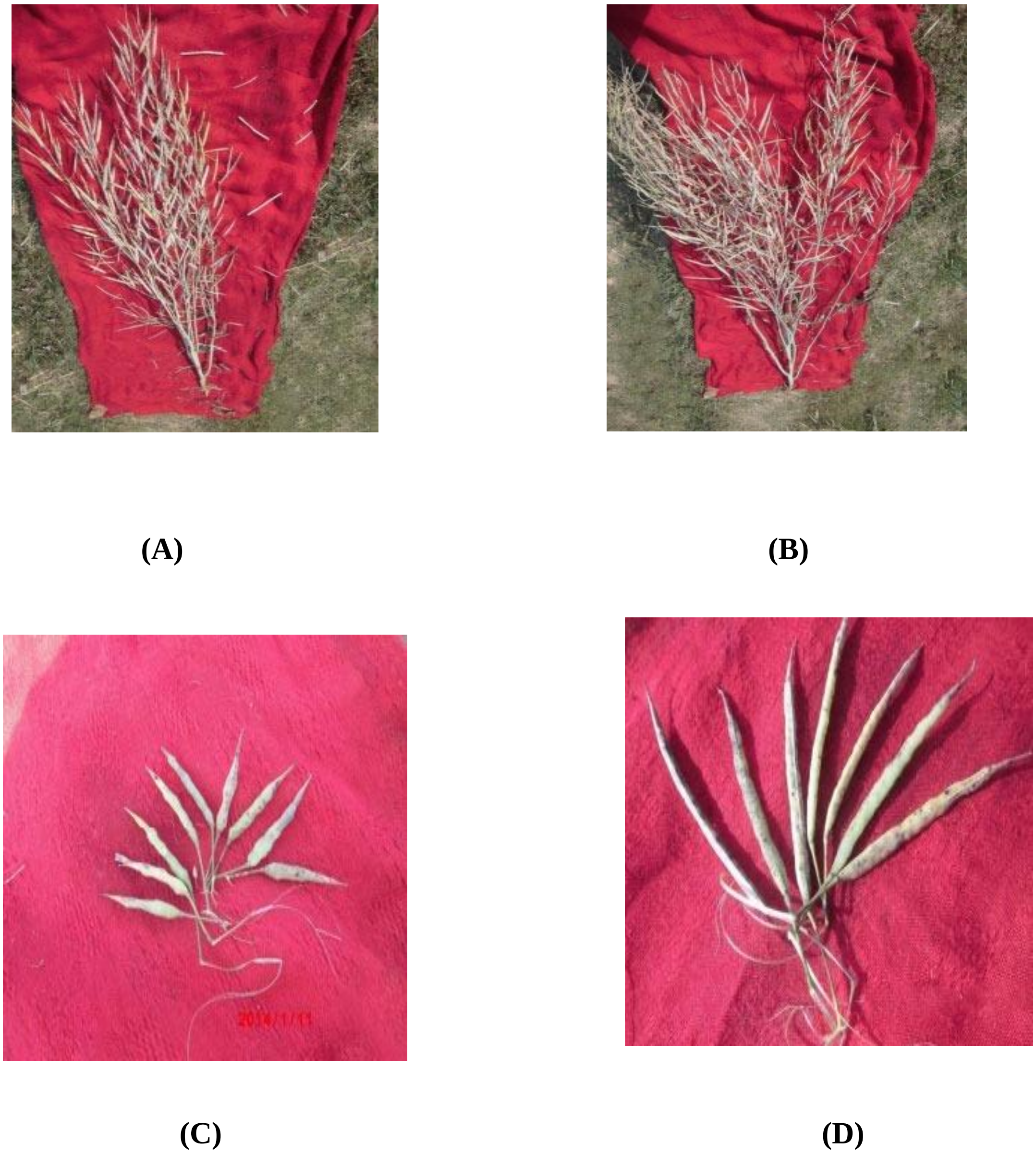
This trait showed high heritability 70.28 % coupled with high genetic advance 4.12 and high genetic advance in percentage of mean 18.18%, indicated that this trait was controlled by additive gene and selection for this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Singh (1985).

4.2.10 thousand seed weight (g)

The weight of thousand seed was estimated the significance variance result (Table 3). The maximum weight of thousand seed was recorded 6.49 from G6 (Nap 2012 × Nap 2013) while the minimum weight of thousand seed was studied 4.98 from G31 (Nap 2057 × Nap 2001). The mean was recorded 4.98. The phenotypic variance and the genotypic variance were recorded 0.56 and 0.46 respectively. The environment variance was estimated 0.10. The PCV was slightly higher than GCV and the score was 38.06 and 37.50. The ECV was 0.56. Higher GCV and PCV for this trait which indicated that, it might be provided better scope for improvement through selection, this founding was also observed by Hira (2015). The higher heritability 97.08 with low genetic advance 4.66 was estimated.

4.2.11 Seed yield per plant (g)

The mean seed yield per plant was noticed 6.12 g with a range from 3.12 g to 10.57 g in the G19, (Nap 179 × Nap 2012) and G6, '(Nap 2012 × Nap 2013)' respectively. Highest phenotypic coefficient of variability (38.06%) while genotype coefficient of variability (37.50%) was recorded. The highest GCV and PCV for seed yield per plant which indicated that, it indicated better scope for improvement through selection which was also reported by Mekonnen (2014). High heritability (98.02%) and genetic advance over mean (76.11%) were studied. Higher heritability along with the highest genetic advance was observed in these traits by Mekonnen (2014) attributed to additive gene actions. The highest heritability and genetic advance over mean was supported this result by Aytac and Kinaci (2009) in their observation.


(A) (B)

(C) (D)

Plate 6. (A) G21 showing highest primary branches per plant, (B) G19 showing highest secondary branches per plant, (C) G25 showing minimum length of silique in 43 genotypes of *B. napus* L. (D) G23 showing maximum length of silique.

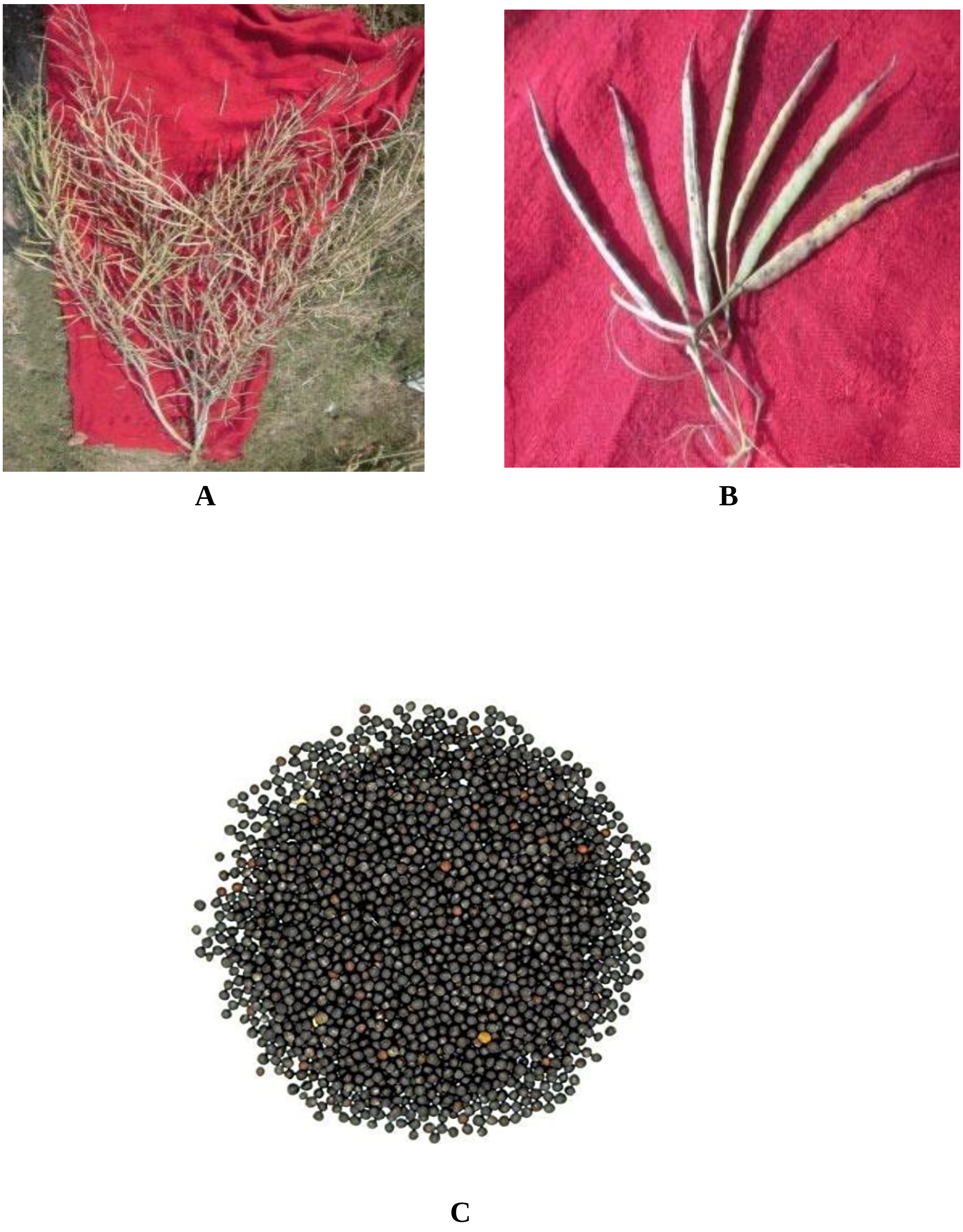


Plate 7: The photograph showing A. the primary and the secondary branches of G6 (Nap 2012 × Nap 2013) B. the siliqua length G6 (Nap 2012 × Nap 2013) C. the seed of G3 (Nap 2012 × Nap 2013) plant.

4.3 Association analysis

Although variability estimation does not focus on the extent the nature of the characters but they gather information for the expanse improvement in different traits. Association analysis might be focus on this by determining the direction of action of different characters. Based on this analysis, the desired character can be selected for improving the variety and also the desired variables can be ascertained.

Yield is a complex character which is predominantly governed by a large number of genes with that it is greatly influenced by environmental fluctuations. Therefore, is not effective if the selection is done on the basis of yield alone. The effect of indirect selection for yield contributing components, those contain high heritability and represent a strong association with yield, could be brought under a better improvement of crop yield. The direct observation of phenotypic correlation does not apprise the tract or the approach of genetic correlation which represents a true genetic figure of relationship among the genes controlling the characters. In the present research, the correlations between seed yield and its component characters were estimated. Relationship between yield and its contributing characters were studied through analysis of correlation among them. This correlation coefficient among all the eleven characters were dedicated in Table 5 and Table 6.

From the present study all the data were recorded in Table 5 which contain heading Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *B. napus* L, here out of 55 associations 21 associations were significant at 1% level and 7 associations were significant at 5% level in phenotypic level. Therefore, the total significance association were 28 in phenotypic level and among the phenotypic 28 significant associations, 23 associations were positively significant and the rest of the 5 were negatively significant. From the phenotypic 27 non- significant associations, the 6 were negatively non-significance and 21 associations were positively non-significant. The additive genetic model was less affected by the environmental fluctuation, suggested the significant and positive association among the characters.

Days to 1st flowering was showed positively significance with 50% flowering (0.701), plant height (0.231), number of primary branches (0.507), number of secondary branches(0.04), number of siliquae/plant(0.395), and siliqua length(0.282). In addition, the trait represented non-significant result with days to maturity, number of seeds /siliquae and was negatively non-significant with yield/plant

Days to 50% flowering was presented positively significance with number of primary branches(0.271), number of secondary branches(0.230), number of siliqua/plants (0.250), and number of seeds/siliqua while the days to maturity represented the negative significant(-0.221). On the other hand, days to 50% flowering showed positively non-significant with plant height, siliqua length, and thousand seed weight. There was negative non-significant recorded with seed yield/plant for the days to 50% flowering.

Days to maturity was estimated positively significant with siliqua length (0.211*), seed yield/plant (0.186*) while it was recorded negative significant with number of secondary branches and amount of siliqua/plant (-0.373). There was the positive non-significant co-efficiency was observed with plant height, number of primary branches and thousand seed weight and negative non-significant was studied with number of seed siliqua(-0.114).

Plant height (cm) was estimated significant genotypic association with days to first flowering. There was 5 positive non-significant observed with this character those were associated with number of primary branches, number of secondary branches, and number of siliquae. In addition to that there was negatively non-significant association in genotypic association with seed yield/ plant (-0.100).The negative significant was observed with number of seed per siliqua (-0.173).

Number of primary branches was recorded no negative significant and positive non-significant. It was recorded positive significant with the number of secondary branches (0.763), number of siliqua/plant (0.238), siliqua length (0.267), number of seed/siliquae (0.212), thousand seed weight(0.255) while with seed yield /plan(-0.077) was recorded negatively non-significant. It indicated if the number of primary branches increases the thousand seed weight also increases.

Number of secondary branches was acquired positively significant with number of siliqua /plants (0.537), siliqua length (0.291), thousand seed weight (0.255) while the negatively significant with number of seeds/siliquae (0.141). The number of secondary branches showed negatively non-significant with seed yield/plant (-0.086).Non-significant association of those traits indicated that the association is largely influenced by environment.

Number of siliqua/plants was attained positively significant with siliqua length (0.423), thousand seed weight (0.213) while with the number of seeds/siliquae, seed yield/plant with the association of amount of siliqua/plant recorded as positively non – significant. The positively significant suggested that the traits were governed by same gene and simultaneous improvement would be effective.

Siliqua length was obtained positively non-significant with number of seed/siliquae (0.046), thousand seed weight (0.098), seed yield/plant (0.107). Indicting simultaneous improvement would be effective because their same gene governed those traits.

Number of siliqua/plants showed insignificant and positive interaction with thousand seed weight,(0. 016) and the traits of this association is largely influenced by environmental factor. Nasim et al. (1994) found negative and significant study for yield per plant where this study also found negative and significant result on yield per plant for number of siliqua per plant. (-0.297)

Thousand seed weight (g) was recorded positively significant with the seed yield /plant (0.659). That same feature was observed Rauf (2016).in his study.

From Table 6 the result of phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *B. napus* L. was estimated that among 55 associations, 17 relationships were significant and 37 were non-significant. Among 17 associations 9 relationships were significant at 1% level and 8 relationships were significant at 5% level. And the 15 association were positively significance and 2 relationships were negative and significant in genotypic level and 26 relationships were positive and non-significant while 11 relationships were negative and non-significant in phenotypic level were observed. The information of inherent relation among the pairs of combination was caused by the positive and non-significant association while the negative and non-significant association referred a complex linked of relation among the pair of combinations.

Days to first flowering was recorded highly significant and positive phenotypic co-relation with days to 50% maturity (0.593), number of primary branches (0.308), number of secondary branches (0.180), number of siliqua per plant (0.326), Siliqua length (0.182), it indicated if days to 1st flowering increases then those traits also increases.

Days to 50% flowering was recorded positively significance with number of primary branches (0.217), number of secondary branches (0.201), number of siliquae per plant (0.245). The negatively non-significance with days to maturity (-0.144), seed yield/plant (-0.094) was recorded while the positively non-significant with plant height, siliqua length, the number of seeds/siliquae, thousand seed weight was observed.Parveen (2007) also estimated days to 50% flowering as insignificant and positive interaction with yield per plant.

Plant height (cm) was estimated no significant association with any traits. The positive non-significant association was recorded with the number of primary branches, number of secondary branches, no of siliqua/plant, siliqua length, thousand seed weight, seed yield/plant. With number of seeds/siliquae and seed yield/plant, plant height was estimated negatively significant.

Number of primary branches was recorded positively significance with the number of secondary branches, number of siliquas/plants, siliqua length. The positive non-significant was recorded with the number of seed/siliqua and thousand seed weight while the negatively non-significant was studied with the association of seed yield/plant.

Number of secondary branches was practiced positively significant association with the number of siliqua /plants while the positively non-significant was observed with siliqua length, number of seeds/siliquae, thousand seed weight. On the other hand, there was a negatively non-significant association with seed yield/plant.

Number of siliqua/plants was studied positively significant association in the genetic advance with siliqua length and thousand seed weight while the non-significant was observed of number of siliqua/plants with number of seeds/siliquae, seed yield/plants.

Number of seeds/siliquae was represented negatively significant association with seed yield/plant.

Thousand seed weight was recorded positively significant relationship with seed yield/plants. This founding was also observed by Sultana *et al.* 2016 on both genotypic and phenotypic level.

Seed yield per plant was significant positive correlation with 1000 seeds weight in both genotypic and phenotypic level (Table 5 and Table 6) suggesting that genotypes with high efficiency gave increase in seed yield per plant. Only number of seed/siliquae was negatively correlated with seed yield per plant indicating that seed yield per plant would be increased with the decreased of that character at both levels supported this result. Maurya *et al.* (2012) and Khayat *et al.* (2012) reported seed yield per plant had significant positive correlation with 1000 seed weight that supports the finding

Table 5. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *B. napus* L.

Characters	**DFF**	**D50F**	**DM**	**PH (cm)**	**NPB**	**NSB**	**NSP**	**SL (cm)**	**NSS**	**TSW (g)**	**SYP (g)**
DFF	1										
D50F	0.701**	1									
DM	0.079^{NS}	-0.221*	1								
PH (cm)	0.231**	0.130^{NS}	0.033^{NS}	1							
NPB	0.507**	0.271**	0.050^{NS}	0.080^{NS}	1						
NSB	0.304**	0.230**	-0.373**	0.169^{NS}	0.763**	1					
NSP	0.395**	0.250**	-0.192*	0.102^{NS}	0.238**	0.537**	1				
SL (cm)	0.282**	0.029^{NS}	0.211*	0.142^{NS}	0.267**	0.291**	0.423**	1			
NSS	0.073^{NS}	0.251**	-0.114^{NS}	-0.173*	0.212*	0.141^{NS}	0.156^{NS}	0.046^{NS}	1		
TSW (g)	0.087^{NS}	0.075^{NS}	0.075^{NS}	0.042^{NS}	0.261**	0.255**	0.213*	0.098^{NS}	0.016^{NS}	1	
SYPS (g)	-0.140^{NS}	-0.122^{NS}	0.186*	-0.100^{NS}	-0.077^{NS}	-0.086^{NS}	0.100^{NS}	0.107^{NS}	-0.297**	0.659**	1

** = Significant at 1%. * = Significant at 5%.

Where,

DFF= Days to first flowering
D50F= Days to 50% flowering
DM= Days to maturity
PH= Plant height (cm),
NPB= Number of primary branches
NSB=umber of secondary branches
NSP= Number of siliqua per plant,
SL= Siliqua length
NSS= Number of seeds per siliqua
TSW= Thousand seed weight,
SYP= Seed yield per plant.

Table 6. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters of *Brassica napus* L.

Characters	**DFF**	**D50F**	**DM**	**PH (cm)**	**NPB**	**NSB**	**NSP**	**SL (cm)**	**NSS**	**TSW (g)**	**SYP (g)**
DFF	1										
D50F	0.593**	1									
DM	0.046^{NS}	-0.144^{NS}	1								
PH (cm)	0.147^{NS}	0.095^{NS}	-0.004^{NS}	1							
NPB	0.308**	0.217*	-0.009^{NS}	0.045^{NS}	1						
NSB	0.180*	0.201*	-0.204*	0.100^{NS}	0.573**	1					
NSP	0.326**	0.245**	-0.133^{NS}	0.085^{NS}	0.219*	0.403**	1				
SL (cm)	0.182*	0.011^{NS}	0.159^{NS}	0.131^{NS}	0.187*	0.172^{NS}	0.367**	1			
NSS	0.111^{NS}	0.152^{NS}	-0.104^{NS}	-0.132^{NS}	0.132^{NS}	0.125^{NS}	0.120^{NS}	0.051^{NS}	1		
TSW (g)	0.105^{NS}	0.097^{NS}	0.010^{NS}	0.037^{NS}	0.171^{NS}	0.172^{NS}	0.207*	0.076^{NS}	0.000	1	
SYP (g)	-0.101^{NS}	-0.094^{NS}	0.130^{NS}	-0.093^{NS}	-0.078^{NS}	-0.081^{NS}	0.091^{NS}	0.107^{NS}	-0.249**	0.584**	1

Where, ** = Significant at 1%. * = Significant at 5%.

DFF= Days to first flowering
D50F= Days to 50% flowering
DM= Days to maturity
PH= Plant height (cm),
NPB= Number of primary branches
NSB=umber of secondary branches
NSP= Number of siliqua per plant,
SL= Siliqua length
NSS= Number of seeds per siliqua
TSW= Thousand seed weight,
SYP= Seed yield per plant.

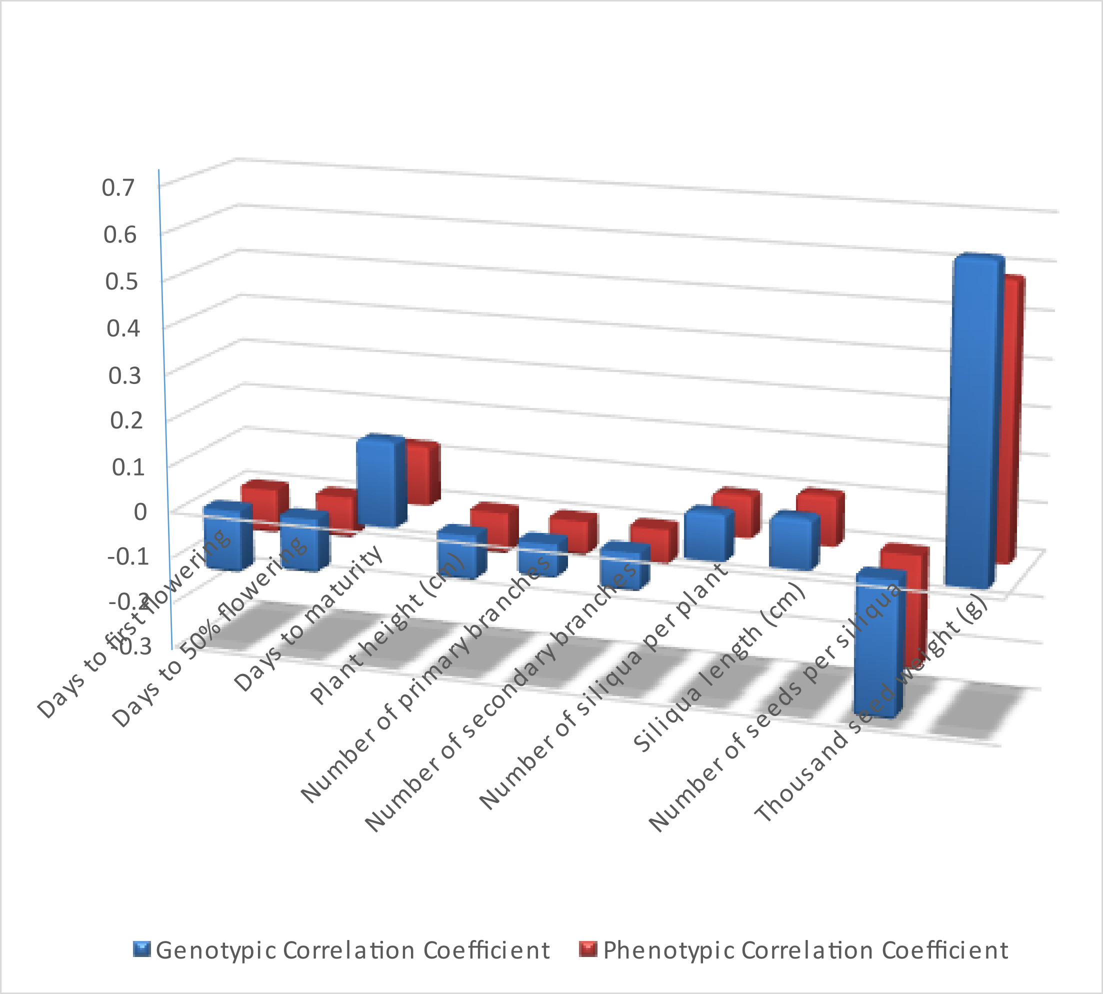


Figure 3: Figure representing the Genotypic and phenotypic correlation

4.4 Path coefficient analysis

At first Wright (1921) suggested the path analysis and later it modified by Dewey and Lu (1957). Path Analysis provides an effective measure of direct and indirect effect of association and describes the related importance of each components which are contributing to the final product that is seed yield. It is important because the judgment of correlation coefficient points out only the case and nature of coalition between yield and its contributing virtues which does not represent the direct and indirect effects of different yield contributing attributes on yield, such as seed yield is dependent on several elements which are mutually associated with each other. These associations make a reciprocal collaboration with existing the elements and seed yield. After that, if one component of this collaboration change, there changes will occur in others components and so fur there is likely to disturb the whole network of cause and effect. Thus, each element has two paths of action viz.

(1) Direct effect on seed yield

(2) Indirect effects through components which are not identified from the correlation studies.

In this study the path coefficient analysis was estimated by using correlation coefficient to determine the direct and indirect effect of considering eleven characters viz. days to 1st flowering, days to50% flowering, days to 80% maturity, plant height, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliquae and 1000 seeds weight to seed yield per plant. The Estimation of direct and indirect effects of eleven yield contributing characters where seed yield the complex outcome of those characters, was considered as the resultant variable and other characters as causal variable are presented bellow in Table 7.

4.4.1 Direct effect:

Among the characters, the positive direct effect on seed yield per plant were bear by days to 50% flowering (0.208), number of primary branches per plant (0.318), siliqua length (0.141) and 1000 seeds weight (0.671). The genotypic and phenotypic correlation of days of maturity and thousand seeds weight with seed yield per plant was also high and positive. This high positive correlation with seed yield per plant was mainly due to the high positive direct effect with those components The path co-efficient analysis showed highest positive direct effect on thousand seed weight with seed yield per plant and Hosen (2008) and Siddikee (2006) also exhibited that thousand seed weight had the highest positive direct effect that supported this finding. Uddin *et al.* (2013) and Alam (2010) reported that days to 50% maturity, primary branches per plant, siliqua per plant, siliquae length and thousand seed weight recorded the direct positive association with seed yield per plant that also supported this finding.

4.4.1.1 Days to 1st flowering:

This element showed negative direct effect with yield per plant (-0.452) while days to 1st flowering represented positive indirect effect on yield per plant through days to 50% maturity, number of primary branches, number of siliquae, siliqua length, thousand seed yield. On the other hand, days to 1st flowering showed negative indirect effect with the association of days to maturity, plant height, number of secondary branches, and number of seeds/siliquae. The highest indirect positive effect was observed with yield per plant through number of primary branches.

4.4.1.2 Days to 50% flowering:

Path co-efficient analysis estimated that, days to 50% flowering revealed positive direct effect (0.208) on yield per plant. Days to maturity (0.005), number of primary branches (0.091), number of siliquae per plant (0.080), thousand seed weight (0.051) had positive indirect effect on yield per plant. On contrast days to 1st flowering (-0.317), plant height (-0.013), number of secondary branch (-0.131), number of seed per siliqua (-0.099), had negative indirect effect (table 5). chauhan and singh (1995) and nabi (2014) were revealed that days to 50% flowering had positive direct effect on yield per plant that supported this result.

4.4.1.3 Days to maturity:

In path co-efficient analysis days to maturity showed negative direct effect (-0.022) on yield per plant. This trait had positive indirect effect through number of primary branches (0.017), number of secondary branches (0.212) and siliqua length (0.030) number of seed per siliquae and Rauf (2016) got similar result in his funding. On the other hand, days to maturity had negative indirect effect via days to 1st flowering (-0.036), days to 50% flowering (-0.04), plant height (-0.003), number of seed per siliqua (-0.061).

Table 7. Partitioning of genotypic correlations into direct and indirect effects of 11 important characters by path analysis of *B. napus* L.

Character	Direct Effect	Days to first flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliqua per plant	Siliqua length (cm)	Number of seeds per siliqua	Thousand seed weight (g)	Genotypic correlation with yield
Days to first flowering	-0.452		0.146	-0.002	-0.023	0.170	-0.173	0.126	0.040	-0.029	0.059	-0.140^{NS}
Days to 50% flowering	0.208	-0.317		0.005	-0.013	0.091	-0.131	0.080	0.004	-0.099	0.051	-0.122^{NS}
Days to maturity	-0.022	-0.036	-0.046		-0.003	0.017	0.212	-0.061	0.030	0.045	0.050	0.186*
Plant height (cm)	-0.101	-0.105	0.027	-0.001		0.027	-0.097	0.032	0.020	0.068	0.028	-0.100^{NS}
Number of primary branches	0.335	-0.229	0.056	-0.001	-0.008		-0.434	0.076	0.038	-0.084	0.175	-0.077^{NS}
Number of secondary branches	-0.570	-0.138	0.048	0.008	-0.017	0.255		0.171	0.041	-0.055	0.171	-0.086^{NS}
Number of siliqua per plant	0.318	-0.179	0.052	0.004	-0.010	0.080	-0.306		0.060	-0.061	0.143	0.100^{NS}
Siliqua length (cm)	0.141	-0.128	0.006	-0.005	-0.014	0.089	-0.166	0.135		-0.018	0.066	0.107^{NS}
Number of seeds per siliqua	-0.394	-0.033	0.052	0.003	0.017	0.071	-0.080	0.049	0.007		0.011	-0.297**
Thousand seed weight (g)	0.671	-0.040	0.016	-0.002	-0.004	0.087	-0.145	0.068	0.014	-0.006		0.659**

Residual effect: 0.32 ** = Significant at 1%. * = Significant at 5%.

4.4.1.4 Plant height (cm):

Plant height had recorded negative direct effect (-0.101) on yield per plant on path analysis. It presented positive indirect effect on days to 50% flowering (0.027), number of primary branches per plant (0.027), number of siliquae per plant (0.032), siliquae length (0.02), Number of seed per siliquae, thousand seed weight (0.028) (table 5). Varshney (1986) worked with several strains of *Brassica* family and experienced that plant height had the negative direct effect on yield. In addition to that, plant height also had negative indirect effect via days to 1st flowering (-0.105), days to maturity (-0.001), number of secondary branches (-0.097) (table 7). These results indicated that if plant height increases than seed yield also decreases mostly through the negative indirect effect of plant height with other characters. Mili (2014). got this negative direct effect (-0.263) in her funding, that strongly supported this study.

4.4.1.5 Number of primary branches per plant:

Number of primary branches per plant had the positive direct effect on yield per plant (0.335). This trait had positive indirect effect on number of days to 50% flowering (0.05), number of siliquae per plant (0.076) and thousand seed weight (0.028). On the other hand, negative indirect effect was recorded on days to 1st flowering (-0.2291), days to maturity (-0.001), Plant height (-0.008), number of secondary branches (-0.434), number of seeds per silique (-0.084) (Table 7). Number of primary branches per plant finally makes significant positive correlation with see yield (0.332). Mahla *et al.* (2003), Gupta *et al.* (1987) and Singh *et al.* (2001) also recorded that number of primary branches per plant had direct positive effect on seed yield. Gupta *et al.* (1987) observed that primary branching had the direct effect on seed yield. Mili (2014), also observed this same result.

4.4.1.6 Number of secondary branches per plant:

Path co-efficient analysis revealed that number of secondary branches had negative direct effect (-0.570) on yield per plant. It had positive indirect effect via days to 1st flowering (0.048), days to maturity (0.008), number of primary branches per plant (0.080), number of siliquae per plant (0.171), siliqua length (0.060) and thousand seed weight (0.171) on seed yield per plant. On the contrary, days to 1st flowering (0.138), plant height (-0.017) and number of seed per siliquae (-0.055) had negative indirect effect on yield per plant (Table 5). Mili (2014). Hira (2015)., Afrin (2017). Found same negative direct effect, that founding support this study.

4.4.1.7 Number of siliquae per plant:

In this Path co-efficient analysis revealed that number of siliquae per plant had the positive direct effect (0.318) on seed yield followed by positive indirect effect on days to 50% flowering (0.052), days to maturity (0.004), number of primary branches (0.080), siliquae length (0.060) and thousand seed weight (0.143). This trait had negative indirect effect on yield via days to 1st flowering (-0.179), plant height (-0.010), number of secondary branches (-0.306), number of seed per siliquae (-0.061) (Table 7). Sheikh *et al.* (1999) revealed that siliqua per plant had highly positive direct effect on seed yield and Mili (2014), Hira (2015), Rauf (2016) also observed same result that strongly support this funding.

4.4.1.8 Siliqua length (cm):

Path analysis revealed that siliqua length revealed direct positive effect (0.141) on yield per plant. This trait had also indirect positive effect on days to 50% flowering (0.006), number of primary branches (0.089), number of secondary branches (0.135), thousand seed weight (0.066). On the contrary, length of siliqua showed indirect negative effect on days to 1st flowering (-0.128), days to maturity (-0.005), plant height (-0.014), number of secondary branches (-0.166), number of seed per siliquae (-0.018) (Table 7). Hence, selection should be practiced for this trait which had longer siliquae in order to improve seed yield. The direct positive effect was also observed by Rauf (2016), Afrin (2017), Bhuiyan (2018).

4.4.1.9 Number of seeds per siliqua:

Path analysis estimated that number of seeds per siliqua had direct negative effect (-0.394) on yield per plant. This trait had also indirect positive effect on days to 50% flowering (0.179), days to maturity (0.010), plant height (0.017), number of primary branches (0.71), and number of siliquae per plant (0.049), siliqua length (0.007), and thousand seed weight (0.011). On the other side, number of seeds per siliquae presented indirect negative effect on days to 1st flowering (-0.033), number of secondary branches (- 0.080), siliqua length (-0.061) (Table 7). The direct effect was negative and the maximum traits had indirect effect was positive. The negative direct effect was mainly converse balanced by indirect positive effect of different characters. Hira (2015), reported that number of seeds per siliqua had direct negative effect on yield per plant.

4.4.1.10 Thousand seed weight (g):

Thousand seed weight had the highest positive direct effect on yield per plant (0.671) and positive indirect effect on days to 50% flowering (0.016), number of primary branches (0.112), number of siliquae per seeds (0.068), siliqua length (0.014) (Table 5). On the other hand, this trait showed negative indirect effect on days of 1st flowering (-0.040), days to maturity (-0.002), plant height (-0.004), number of secondary branches (-0.145), number of seeds/siliqua (-0.006) (Table 5).Paul (2017) found same findings. The positive direct effect on yield per plant also observed Rauf (2016) that strongly support this finding.

4.4.1.11 The residual effect (R):

The magnitude of residual effect (0.32) indicated that traits included in the path analysis explained about 68% of the variation in seed yield. However, the remaining variation in seed yield (32%) can be attained by incorporating other yield related components in the path analysis as far as studies involving association of traits is concerned. The residual effects towards seed yield in this study may be occurred due to several reasons such as may be other causal factors (characters) that not included in the analysis contribution more towards yield and other may be happened by sampling errors.

4.4.1.12 Genotypic correlation with yield:

Both genotypic correlation and path co-efficient studies revealed positive result for thousand seeds weight, the most important components for getting higher yield. Recent breeding research also emphasized giving importance of these characters. Days to maturity showed positive significant result (0.186) while number of seed/siliquae showed negative significant result (-0.297) on genotypic correlation. On contrary days to 1st flowering (-0.140), days to 50% maturity (-0.122), plant height (-0.077), number of secondary branches (-0.086). Therefore, the present study suggested that 1000 seeds weight should be given more importance in selecting the genotypes for higher seed yield in *B. napus* L.

CHAPTER V

Summary and Conclusion

The experiment which was undertaken to analysis the variability, character association and diversity among the 43 genotypes of *Brassica napus* L. at the Sher-e-Bangla Agricultural University Farm, Bangladesh during November 2019 to February 2020. Seeds were sown in the main field in Randomized Complete Block Design (RCBD) with three replications (Plate:2).Data on various yield attributing characters such as, days to 1st flowering, days to 50% flowering, days to 80% maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g) and seed yield per plant (g) were recorded. On the basis of those characters studied from the research, the principal findings of the present study have been summarized.

It was revealed from the analysis of variance that there were highly significant differences among the genotypes for all the characters (Table:3).It means, there was observed the significant variation existing for those characters. From the mean performance, it was observed that the minimum value for days to 1st flowering was observed in both G8 while the highest value of days to 1st flowering was observed in G41.On the other hand, the maximum days to 50% flower was observed 43.00 in G22 and the minimum days for 50% flowering was recorded 30.33 in G9.The maximum days to 80% maturity was revealed by G1 plant whereas the minimum days to 80% maturity was observed in G18.The longest height of plant was recorded in G16 and smallest height was studied in G41.The maximum number of primary branches was studied by the G21 and the minimum number of secondary branches was studied by the G8 plant. Whereas, the maximum number of secondary branches was estimated from G19 and the minimum number of secondary branches was estimated from G43. The highest number of siliquae per plant was observed by the genotype G23 whereas the lowest number of siliquae per plant was observed by G34. Siliqua length was resulted the longest by G23 whereas the shortest siliqua length was observed by G25. The maximum seeds per siliqua were observed in G40 whereas the minimum seeds per siliqua were observed in G39. Thousand seed weight was found the maximum in G6 whereas the minimum thousand seed weight was found in G31. Yield is the most outstanding character in all over the research work and objectives are depending on yield. The highest yield per plant was observed in G6 whereas the lowest yield per plant observed in G19 (Appendix:IV)

However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study (Table 5and Table 6). In case of Plant height and number of siliquas per plant showed higher influence of environment for the expression of these characters. On the other hand, rest of the characters like days to 80% maturity, days to 1st flowering, days to 50% flowering, number of primary branches, number of secondary branches, number of seeds per siliqua, siliqua length, 1000-seed weight and seed yield per plant estimated the least difference between the phenotypic and genotypic variance which was suggesting additive gene action for the expression of the characters.

Seed yield per plant (g) (97.08) exhibited the highest value of heritability while Number of secondary branches (58.66) exhibited the lowest value of heritability (Table:4). High heritability with high genetic advance in percent of mean was observed for plant height, number of primary branches, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, 1000 seed weight and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. High heritability with moderate genetic advance was observed for days to 50% flowering indicating medium possibility of selecting genotypes. Moderate heritability with low genetic advance in percent of mean was observed for days to 1st flowering, days to 80%maturity indicating that non-additive gene effects were involved for the expression for this character.

For determining the association between yield and yield contributing characters, the Correlation coefficients among the characters were studied. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient which suggested that a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive genotypic correlation co-efficient with seed yield per plant were found in days to 80% maturity and thousand seed weight. Insignificant and negative correlation with seed yield per plant were found in days to 1st flowering, days to 50% maturity, number of primary branches, number of secondary branches, siliqua length. Significant but positive interaction was found for number of seed per siliqua with seed yield per plant. In addition to that, thousand seed weight gave the positive significant record on phenotypic correlation co-efficient analysis. On contrary, number of seed per siliqua showed negative significant result on the phenotypic correlation co-efficient.

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering eleven characters.(Table7) It was revealed that days to 50% flowering, number of primary branches per plant, number of secondary branches, number of siliquae per plant, siliqua length, thousand seed weight had the positive direct effect on yield per plant, whereas, days to 1st flowering, days to maturity, plant height, number of secondary branches, number of seed per siliqua had the negative direct effect on yield per plant. The path coefficient studies indicated that days to 50% flowering, number of primary branches per plant, number of secondary branches, number of siliquae per plant, siliqua length, and thousand seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

The residual effect was 0.32 indicating that the eleven characters contributed 68 percent of variability in seed yield per plant studied in path analysis. Therefore, the present study suggested that days to maturity number seed per siliqua, and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher seed yield in *B. napus* L.

The following conclusions and recommendations may be drawn based on the results of the study:

- the high heritability with high genetic advance in percent of mean observed in plant height, number of primary branches, number of siliquae per plant, siliqua length, number of seed per siliquae, 1000-seed weight, seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective for breeding.
- the significant positive correlation with seed yield per plant were found in days to maturity, thousand seed weight. Significant and negative correlation with

seed yield per plant was found in number of seed per siliqua. This result suggested that yield per plant can be increased by improving these characters.

- the days to 50% flowering, number of primary branches, siliquae length, number of siliquae per plant, siliquae length and thousand seed weight had the positive direct effect on yield per plant. So, yield improvement was associated with these characters.
- the role days to maturity, number of secondary branches, number of siliquae per plant, number of seeds per siliquae both the vectors were important components for genetic divergence in these materials.

Recommendations:

Considering the magnitude of genetic variability and agronomic mean performance the genotypes G6 (Nap 2012 X Nap 2013) for the highest seed yield per plant and thousand seed weight ,G40 (Nap 9908 X Nap206) for the highest number of seed per siliqua, G23 (Nap 9406 X Nap 2057) for the highest length of siliqua and number of seed per siliqua per plant, G19 (Nap 179 X Nap 2012) for the highest number of secondary branches, G 21(BS-13 X Nap-2013) higher number of primary branches per plant, G8 (Nap200 X Nap 2013) for days toys first flowering, G9 (Nap-94006 X Nap-2001) for the lowest days to 50% flowering and G18 (BS-13 X Nap-94006) for the lowest day to maturity. Considering genetic analysis and other agronomic performance G6 (P1), G14 (P2), G18 (P2) and G9 (P3) could be considered high yielding with early maturity genotypes for improving crop yield.

CHAPTER VI

REFERRENCE

Abideen S.N.U., Nadeem, F. and Abideen, S.A. (2013). Genetic Variability and Correlation Studies in *Brassica napus. Intl. J. Innov. Appl. Stud.* **2**(4): 574-581.

Abraham, V. (1994). Rate of out-crossing in Indian mustard, *Brassica juncea. Cruciferae Newsl.* **16**: 69-70.

Afrin, K. S., Mahmud. F., Bhuiyan, M. S. R. and Rahim, M. A. (2011). Assessment of genetic variation among advanced lines of *Brassica napus L. Agronomski Glasnik.*, **4**(5): 201-226.

Afrin.F.(2017). Genetic variability and character association in BC_1 F_6 population of *Brassica napus L* M.S. Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

AIS (Agricultural Information Service) (2015) Krishi Diary (In Bangla). Agril Inform Ser Khamarbari, Farmgate, Dhaka, Bangladesh, p. 16.

AIS (Agricultural Information Service). (2013). Krishi Diary (In Bangla). Agril. Inform. Ser. Khamarbari, Farmgate, Dhaka, Bangladesh. p.16.

Akbar, M., Saleem, U., Tahira, Yaqub, M. and Iqbal, N. (2007). Utilization of genetic variability, correlation And path analysis for seed yield improvement in Mustard, *Brassica juncea. J. Agric.* Res., **45**(1): 25-31.

Alam, M.F. (2010). Variability studies in F4 progenies of *Brassica rapa* obtained through intervarietal crosses. M.S. thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Ali, Y., Farhatullah, H. Rahman, A. Nasim, S.M. Azam and A, Khan. (2013). Heritability and correlation analysis for morphological and biochemical traits in *Brassica J. Agric.* **29**(3): 35-37

Anonymous (2012). Bangladesh Bureau of Statistics. Monthly Statistical Bulletin of Bangladesh.January, Statistics Div., Ministry of Planning, Govt. People's Repub. Bangladesh. p. 46.

Aytac, Z. and Kinaci, G. (2009). Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus L.). African J. Biotech***. 8**(15): 3547-3554.

Aytac, Z., Kinaci, G. and Kinaci, E. (2008). Genetic variation, heritability and path analysis of summer rape seed cultivars. *J. Appl. Biol. Sci.* **2**(3): 35- 39.

Baradaran, R., Majidi, H. E., Darvish, F., and Azizi, M. (2007). Study of correlation relationships and path coefficient analysis between yield and yield components in rapeseed *(Brassica napus L.). J Agr Sci,* **12**(4).

Basalma, D. (2008). The correlation and path analysis of yield and yield components of different winter rapeseed *(Brassica napus ssp. oleiferaL.) cultivars.Res. J. Agric. Biol. Sci.***4** (2): 120-125

BBS, (2015). Statistical Yearbook of Bangladesh 2010. Bangladesh Bureau of Statistics. Ministry of Planning, Govt. of the People's Republic of Bangladesh. Dhaka.

BBS, (Bangladesh Bureau of Statistics).(2015). Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Stat. Div., Ministry Planning, Govt. Peoples Rep. Bangladesh, Dhaka. p.477

Begum, F, Hossain, F. and Mondal, M. R. I. (2012). Influence of Sulphur on morpho-physiological and yield parameters of rapeseed *(Brassica campestris L.)* Bangladesh *J. Agril Res.* **37(**4): 645-652.

Begum, H., Alam, A.K.M.M., Chowdhury, M.J.A. and Hossain, M.I. (2007). Genetic Divergence in Linseed (*Linum usitatissimum*.). *Int. J. Sustain. Crop Prod***.2** (1): 04-06.

Bhardwaj, R.P. and Singh, R.R. (1969). Morphological and genetic variability in brown sarson *(Brassica campestris var. brown sarson). Madras Agric. J.* **56**(1): 28-31.

Bhuiyan.F. A. (2018) Genetic analysis in yield and its contributing characters in F_5 population of *B. napus L.*SAU, Dhaka.

Burton, G.W. 1952. Quantitative inheritance in grasses. pp. 277-283. Proceeding 6th International Grassland Congress, Pennsylvania. 17-23 August. Pennsylvania State College, State College, Pennsylvania, USA.

Chaudhury, P.K., Singh, P. and Kumar, A. (1990). Association and Interdependence of morphophysiological characters under moisture stress in *Brassica. Beitrage Zar Tropichen Landuitshaft*. **18(**1): 43-47.

Chauhan, J. and Singh, P. (1985). Association of some morphophysiological determinants with seed yield in Toria *(Brassica campestris L. var. Toria).*Thesis Abs. **XI-**1: 4243.

Choudhary, B., Joshi, P. (2001) Genetic diversity in advanced derivatives of ***Brassica*** interspecific hybrids. *Euphytica* **121,** 1–7

Choudhary, B.D., Singh, P., Singh, D.P. and Pannu, R.K. (2003). Path analysis in Indian mustard. *Haryana J. Agron.* **9**(2): 161-166.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518

Dhillor, S.S., Labana, D.S. and Ahuja, K.L (1990). Association analysis in Indian mustard. *J. Agric. Res*. **27**(3): 385-388.

Downey R. and Robbelen G. (1989) Brassica Species: Oil Crops of the World, Their Breeding and Utilization. McGraw Hill Publishing Co., New York, USA, pp. 339–374.

Ejaz-Ul-Hasan, Mustafa, H.S.B., Bibi, T. and Mahmood, T. (2014). Genetic variability, correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. *Cerce. Agro.in Moldova*. XL**.**1: (157).

FAO (Food and Agriculture Organization). (2019). Production Year Book. Food and Agriculture Organization of the United Nations, Rome. Italy

FAO. (2020). Food and Agriculture Organization of the United Nations, FAOSTAT. FAO Statistics Division.

Friedt, W. and Ordon, F. (2007). Molecular Markers for Gene Pyramiding and Disease Resistance Breeding in Barley. 10.1007/978-1-4020-6297-1_4.

Genetic variability and character association in f5population of *Brassica napus L.* MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Ghosh, D.V. and Mukhopadhyay, D. (1994). Path analysis of yield and yield attributes of toria (*B. rapa var. napus*) as affected by date of sowing and plant density. *Indian J. Agril. Sci*. **64**(1): 56-58.

Ghosh, S.K. and Gulati, S.C. (2001). Genetic variability and association of yield components in Indian mustard (*Brassica juncea L.*). *Crop Res. Hisar.* **21**(3): 345- 349.

Gomez-Campo, Cesar and Shyam Prakash. (1999). "Origin and Domestication." Biology of *Brassica Cenospecies. Amsterdam J. Els.* 33-58.

Goswami, P.K. and Behl. R.K. (2006). Exploitation of heterosis and selection of superior combiners in Indian mustard. Department of Plant Breeding, CCS Haryana Agricultural University, Hissar. *Indian Ann. Agril. Res.* **26**(1): 56-58.

Goswami, P.K., Ghosh, D.V. and Behl, R.K. (2005). Genetic divergence in Indian mustard. *Ann. Agril. Res*. **27**(2): 187-190.

Gupta, M., Labana, K.S. and Badwal, S.S. (2002). Correlation and path coefficient of metric traits contributing towards oil yield in Indian mustard. In the International rapeseed congress, pozan, Poland, 107(En).

Han, J.X. (1990). Genetic analysis of oil content in rape *Brassica napus* L. Chainese Oil Crop. 2: 1-6.

Heiliger, A. (2012). Quantitative trait locus mapping of yield and yield components in canola (*Brassica napus* L.*)* Under irrigated and rain fed treatments.CSU Theses and Dissertations - Department of Soil & Crop Sciences

Hira. U.K. (2015). Genetic variability, correlation and path analysis in F_6 generation of rapeseed (*Brassica napus* L.). MS Thesis, Department of Genetic and Plant Breeding, SAU, Dhaka.

Hosen, M. (2008). Variability, correlation and path analysis in F_3 materials of Brassica rapa. MS Thesis, Department of Genetic and Plant Breeding, SAU, Dhaka.

Hossain, A., Salini, R.P., Malik, B.P.S. and Singh, D.P. (2008). Variation for morph physiological characters in genotypes of Indian rapeseed. *Indian J. Agril. Sci.* **57**(4): 225-230.

https://fdc.nal.usda.gov/fdc-app.html#/food-details/748278/nutrients

https://www.exportgenius.in/import-data/bangladesh/mustard-seeds.php

Iqbal, Md & Haque, Md & Nath, Ujjal & Hamim, Islam. (2014). Genetic diversity analysis of mustard germplasm based on phenotypic traits for selection of short duration genotypes. *Int. J. Agril Sci Res*. **3**. 141-156.

Islam, M. S. and M. O. Islam. 2000. Genetic diversity in rapeseed and mustard (*Brassica sp.*). *Bangladesh J. Genet. Pl. Breed*. **13** (2): 25-30.

Jagadev, P.N., Samal, K.M. and Lenka, D. (1999). Genetic divergence in rape mustard. *Indian J. Genet.* **51**(4): 465-467.

Jahan, N. (2008). Inter-genotypic variability and genetic diversity analysis in F_4 lines of *Brassica rapa*. MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Jeromela, A.M., Nagl, N., Varga, J.G., Hristov, N., Spika, A.N., Mirjana Vasicand, M. and Marinkovic, R. (2011). Genotype by environment interaction for seed yield per plant in rapeseed using AMMI model. *Pesq. agropec. bras*. **46**(2): 99-102

Johnson, R.W., Robinson, H.F. and Comstock, RE. 1955. Estimates of genetic and environmental variability in soybeans. *Agron. J.,* 47: 314-318.

Joshi AB, Dhawan NL (1966). Genetic improvement of yield with special reference to self-fertilizing crop. *Indian J Genet Pl Breed.* **26**A:101-113

Kardam, D.K. and Singh, V.V. (2005). Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern & Coss) grown under rainfed condition. Department of Plant Breeding and Genetics, SKN College of Agriculture, Jobner - 303 329, Rajasthan. *Indian J. Spices Aromatic Crop***.** **14**(i): 56-60.

Katiyar, R. P., Mishra Singh, S.N. and Chauhan, Y. S. (1974). Genetic variability, heritability and genetic advance of yield and its components in Indian mustard. *Indian J. Agril. Sci,* **44**(5): 291-93

Khaleque, M.A. (1985). A guidebook on production of oil crops in Bangladesh. DAE and FAO#UNDP Project BGD#79#034, Strengthening the Agricultural Extension Service" Khamarbari, Firmgate, Dhaka.

Khan S., Farhatullah, Khalil I. H., 2008 Phenotypic correlation analysis of elite F3:4 *Brassica* populations for quantitative and qualitative traits. *J. Agric. and Bio. Sci.,* **3**(1):38-42.

Khan, F.A., Sajid-Ali., Amir-Shakeel., Asif-Saeed.and Ghulam-Abbas (2006). Correlation analysis of some quantitative characters in *Brassica napus* L. Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. *J. Agril. Res. Lahore*. **44**(1): 7-14.

Khan, M. H., Bhuiyan, S. R., Rashid, M.H., Ghosh, S. and Paul, S.K. (2013). Variability and heritability analysis in short duration and high yielding *Brassica rapa* L. *Bangladesh*

J. Agril. Res. **38**(4): 647-657.

Khatun. A. (2018). Genetic diversity and characters association analysis of advanced line of *Brassica napus* L. MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Khayat, M., Lack, Sh. and Karami, H. (2012). Correlation and path analysis of traits affecting grain yield of canola *(Brassica napus* L.*) Varieties. J. Basic. Appl. Sci. Res***. 2(**6): 5555-5562.

Khera, M.K. and Singh, P. (1988). Sensitivity and performance of some *Brassica napus* genotypes in stress and non-stress environments. *Crop improve*. **15**(2): 209-211.

Khulbe. R.K.and Pan, D.P. (1999). Comparative analysis of yield and correlation for yield and its component in Indian Mustard. *Crop Res. Hisar***. 17**(3): 371-375. 94

Kimber, D.S. and McGregor, D.I. (1995) .The Species and Their Origin, Cultivation and World Production. In: Kimber, D. and McGregor, D.I., Eds., *Brassica Oilseeds, Production and Utilization*, CAB International, Wallingford, 1-7.

Kumar, C.H.M.V., Arunachalam, V. and Rao, P.S.K. (1996). Ideotype and relationship between morpho-physiological characters and yield in Indian mustard (*B. juncea*). *Indian J. Agric. Sci.* **66**(1): 14-17.

Kumar, S., Sangwan, R.S. and Yadava, I.S. (1999). Path coefficient analysis in Brassica species under rainfed conditions. *Cruciferae News*l. **24**:59-60.

Kumar, S., Snagwan, R.S. and Yadav, I.S. (2009). Correlations studies in Brassica species under dry land conditions. *Cruciferae Newsl***.** 21:151-152.

Kumar, V. and Singh, D. (1994). Genetics of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss*). Crop Res*. **7**(2): 243-246.

Lebowitz, R.J. (1989). Image analysis measurements and repeatability estimates of siliqua morphological traits in *B. campestris L. Euphytica*. **43**(1-2): 113-116.

Lekh R, Hari S, Singh VP, Raj L, Singh H. 1998. Variability studies in rapeseed and mustard. *Ann. Agril. Res*. 19: 87-88.

Lodhi, G.P., Singh. R.K. and Sharma, S.C. (1979). Correlated response in brown sarson. *Indian J. Genet*. 39: 373-377.

Lush, J.L. 1949. Inter size correlation, regression of offspring on dams as a method of estimating heritability of characters. *Proc. Amer. Soc. Anim. Prod.*, 33: 293-301.

Mahak, S., Singh, H.L. and Dixit, R.K. (2004). Studies on genetic variability, heritability, genetic advance and correlation in Indian mustard *(Brassica juncea L. Czem and Coss). Indian Pl. Arc.* **4**(2): 291-294.

Mahalanobis, P.C. (1936). On the generalized distance in statistics *Indian. Proc. Natl. Acad. Sa.* 12: 49-55.

Mahmud, F., Rasul, M.G and Rahim, M.A. (2008). Genetic diversity analysis in some advanced lines of *Brasssica napus*. *Sci. Asia*. 34:432-434.

Malik, M.A., Das. M.L. and Rahman, A. (2000). Genetic variability, character association and path analysis in rapeseed. *Bangladesh J. Agric. Sci.* **27**(1): 25-59.

Malik.V., Singh,H.and Singh,D. (1995). Gene action of seed yield and other desirable characters in rapeseed. *Anal. Biol (Ludhiana)*. **11**(1/2): 94-97.

Masood, T., Gilani, M.M. and Khan, F.A. (1999). Path analysis of the major yield and quality characters in *Brassica campestris*. *J. Animal P1ant. Sci***. 9**(4): 69-72. 95

Maurya, N., Singh, A.K. and Singh, S.K. (2012). Inter-relationship analysis of yield and yield components in Indian mustard, *Brassica juncea L. Indian J. Plant Sci*.**1** (23): 90-92.

Mekonnen, T.W., Wakjira, A. and Genet, T. (2014). Correlation and path coefficient analysis among yield component traits of Ethiopian mustard *(Brassica carinata a. Brun)* at Adet, Northwestern, Ethiopia. *J. Plant Sci.* **2**(2): 89-96.

Mukhtar MS, Rahman M, Zafar Y (2002). Assessment of genetic diversity among wheat *(Triticum aestivum L.*) cultivars from a range of localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. *Euphytica***.** 128: 417-425.

Nair, K.R., and Mukherjee, H.K. (1960). Classification of natural and plantation teak (Tectona grandis) grown at different localities of India and Burma with respect to its mechanical and physiological properties. Sankhya. 22: 1-20.

Nanda, R., Bhargava, S.C. and Tomar, D.P.S. (1995). Rate and duration of siliqua and seed filling and their rotation to seed yield in Brassica species. *Indian J. Agric. Sci.* **64**(4): 227-232.

Nath, U.K., S. Naz, and M.M. Rahman. 2003. Genetic divergence of Brassica campestris, *Brassica juncea* parents and their hybrids. Pakistan *J. Biol. Sci.* **6**(10): 936-938.

Niraj, K. and Srivastava, S. (2004). Variability and character association studies in Indian mustard*. J. Appl. Biol.* **14**(1):9-12.

Olsson, G. (1960) Species crosses within the genus Brassica. II. Artificial *Brassica napus.* L. *Hereditas* 46. 351 396

Pandey, R., Kumar, B. and Kumar, M. (2013). Genetic Divergence for Quantitative Traits in Indian mustard (*Brassica juncea L. Czern & Coss)*. American-*Eurasian J. Agric. Environ. Sci.* **13**(3): 348-351.

Pankaj, S., Gyanendra, T., Gontia, A.S., Patil, V.D. and Shah, P. (2002). Correlation studies in Indian mustard. Dept. of Genetics and Plant Breeding, Marathwada Agricultural University, India. *Agric. Sci. Digest***. 22**(2): 79-82.

Parveen, S. (2007). Variability study in F2 progenies ofiInter-varietal crosses of *Brassica rapa*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Paul. J. (2017). Genetic variation and correlation analysis in agro morphological traits of f4 generation in *Brassica napus L*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Peter, K.V. and Rai, B. (1995). Genetic divergence in rapeseed. *Indian J.* **36**(3): 379-383.

Poonam, S. and D.N. Sing. 2004. Path coefficient analysis in Indian mustard *(Brassic Juncea L.). J. Res. Bisra Agric. Uni. Ranchi*. **16**(2): 293-295.

Rakow, G. and D. L. Woods. “Outcrossing in rape and mustard under saskatchewan prairie conditions.” *Canadian J. Plant Sci* 67: 147-151.

Rameeh, V. (2011). Correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. *J. Oilseed Brassica*. **2**(2): 56-60.

Rameeh, V. (2012). Correlation analysis in different planting days of rapeseed varieties. *J. Agril. Sci*.**7** (2). 96

Rao CR (1952). Advance statistical method in biometrical research. Ednl John Willey and Sons, New York.

Rashid, M. H. (2007). Characterization and diversity analysis of the *oleiferous Brassica species*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Rauf M. A. (2016). Genetic variability and character association among yield and its contributing traits in mustard *(Brassica napus L.)* MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Rawhat, D.S. and I.J. Anand. 1981. Analysis of genetic divergence in Brown Mustard.

Reddy, N.N. (1991). Correlation studies in Indian mustard (*Brassica juncea L. Czern and Coss.). J. Oilseeds Res***. 8**(2): 248-250.

Robinson, H.I., R.E. Comstock, and P.H. Harvey. (1949). Estimation of heritability and degree of dominance in corn. *Agron. J*. 41:353-359.

Sabaghnia, N., Dehghani H., Alizadeh, B. and Mohghaddam, M. (2010) Interrelationships between seed yield and 20 related traits of 49 canola genotypes in non-stressed and water stressed environments. Spanish *J. Agri. Res*. 8: 356-370.

Shalini, T.S. Sheriff, R.A., Kulkarni, R.S. and Venkataramana, P. (2000). Variability studies in Indian mustard [*Brassica juncea* L. Czern and Coss]. *Res. Crops*. **12**(3): 230-234.

Shalini, T.S., Sheriff, R.A., Kulkarmi, R.S. and Venkataramana, P. (2000). Correlation and path analysis in Indian mustard germplasm. Research on. Crops Dept. of Genetics and Plant Breeding. *Indian.Univ. Agril. Sci***. 1**(2): 226-229.

Sharma, S.K. (1988). Variation and correlation studies in Indian mustard (*B. juncea*). Thesis Abst. **10(**2): 146-147.

Sharma, S.K., Rao, D., Singh, D.P., Harbir, S. and Singh, H. (1994). Correlation analysis of yield, biomass and its partitioning components in Indian mustard (*Brassica juncea* L. Czern. Coss.). Hariana Agril. Univ. *J. Res***. 27**(2-4): 149-152.

Sheikh, F.A., Rathen, A.G. and Wani, S.A. (1999). Path analysis in toria (Brassica campestris L.) var. toria. *Adv. P1ant. Sci***. 12**(2): 385-388.

Siddikee, M.A. (2006). Heterosis inter genotypic variability, correlation and path analysis of quantitative characters of *oleiferous Brassica campestris L*. MS Thesis, Dept. of

Genetics and Plant Breeding, SAU, Dhaka. Rashid, M. H. (2007).

Singh, M., Singh, S.P. and Dhirendra, S. (2001). Genetic analysis for seed yield and its genotypes in yellow sarson (Brassica compestris L.). *Indian J. Agril. Sci*. **70**(9): 624-626. 97

Singh, R.K., and B.D. Chaudary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India.p.56.

Singh, R.P., Khera, M.K. and Gupta, V.P. (1991). Variability and correlation studies for oil and seed yield in gobhi sarson. *Crop improv*. **18** (2): 99-102.

Singh, R.P., Malik, B.P. and Singh, D.P. (1997). Variation for morpho-physiological characters in genotypes of Indian mustard. *Indian J. Agric. Sci*. 57: 227-230.

Srivastava, M.K. and Singh, R.P. (2002). Correlation and path analysis in Indian mustard. Crop Res. Hisar, Dept. of Genetics and Plant Breeding. *Indian Univ. Agril. Tech*. **23**(3): 517-521.

Sudan, R.S., Singh, S.P. and Kashyap, S.C. (2004). Path analysis of yield and its components in Indian mustard *(Brassica juncea L. Czern and Coss*). *Ann. Agric. Bio. Res*. **9**(2): 119-122.

Tang, Z.L., Li, J.N., Zhang, X.K., Chen, L., and Wang, R. 1997. Genetic variation of yellow-seeded rapeseed lines (*Brassica napus* L.) from different genetic sources. Plant Breed. 116: 471–474.

Thakral, N.K. (2004). To study the association of some morphophysiological attributes with yield in toria. *Thesis Abst.* **8**(11): 66-67.

Thurling, N. (1983). Variation in pod length in spring rape (*B. napus*) and its relationship to yield. In Proceedings. Australian Plant. Breed. Conf. pp. 14-18.

Tuncturk, M. and Ciftci, V. (2007). Relationships between yield and some yield components in rapeseed *(Brassica napus SSP. oleifera L.)* cultivars by using correlation and path analysis. *Pakistan Journal of Botany*, **39**(1):81–84.

Tusar, P., Maiti, S. and Mitra, B. (2006). Variability, correlation and path analysis of the yield attributing characters of mustard *(Brassica sp.). Res. Crops***. 7**(1): 191-193.

Tyagi, M.K. Chauhan, J.S., Kumar, P.R. and Singh K.H. (2001). Estimaiton of heterosis in Indian mustard [*Brassica juncea. (L) Czren and Coss]. Annl. Agril. Bio. Res***. 6**(2): 193-200.

Uddin, M.J., Chowdhury, M.A.Z. and Miah, M.F.U. (1995). Genetic variability, character association and path analysis in Indian mustard *(Brassica juncea L.). Bangladesh Ann. Agric.* **5**(1): 51-52.

Uddin, M.J., Chowdhury, M.A.Z. and Miah, M.F.U. (1995). Genetic variability, character association and path analysis in Indian mustard *(Brassica juncea L.). Bangladesh Ann. Agric***. 5**(1): 51-52.

Uddin, M.J., Chowdhury, M.A.Z. and Miah, M.F.U. (2005). Genetic variability, character association and path analysis in Indian mustard (*Brassica juncea L.*). *Bangladesh Ann. Agric.* **5**(1): 51-52. 98

Uddin, M.S., Bhuiyan, M.S.R., Mahmud, F. and Kabir, K. (2013). Study on correlation and path coefficient in F2 progenies of rapeseed. *Acad. J. Plant Sci.* **6**(1): 13-18.

USDA(U.S. department of agriculture). (2019). USDA, United States Department of Agriculture. Grain and Feed Annual. USDA Foreign Agricultural Service, Bangladesh, 2019.

Varshney, S.K., Rai, B. and Singh, B. (1986). Component analysis of harvest index in *Brassica oilseeds. Indian J. Agric. Res.* **20** (3): 129-134.

Vivek, S., Ram, B. and Kamlesh K. (2007). Genetic diversity in Indian *mustard (Brassica juncea L. Czem and Coss.). Prog. Agril*. **7**(1/2): 105-109.

Walle, T., Wakjira, A. and Mulualem, T. (2014). Analysis of genetic parameters on Ethiopian mustard (*Brassica carinata A. Braun*) genotypes in northwestern *Ethiopia. Agric. Sci. Res. J.* **4(**4): 83-88.

Warwick, S.I. and L.D. Black (1991) Molecular systematics of *Brassica* and allied genera (Subtribe *Brassicinae, Brassiceae*) chloroplast genome and cytodeme congruence. Theor. Appl. Genet. 82: 81–92.

Wright, S. (1921). Correlation and causation. *J. Agric. Res*. 20: 557-585.

Yadava V.P., Deb S. and Singh H., 1996. Morpho-physiological determinates of yield under water stress conditions in Indian Mustard. *Acta Hort* 407, 155-60.

Yadava, C.K. Yadav, A.K. and Singh, H. (2006). Studies on genetics of yield and its components in Indian mustard (*Brassica juncea L. Czern and Coss). Thesis Abst*. **9**(2): 186-187.

Yadava, C.K. Yadav, A.K. and Singh, H. (2006). Studies on genetics of yield and its components in Indian mustard *(Brassica juncea L. Czern and Coss*). Thesis Abst. **9**(2): 186-187.

Yadava, O.P., Yadav, T.P. and Kumar, P. (1996). Combining ability studies for seed yield, its components characters and oil content in Indian mustard (*Brassica juncea L. Czern and Coss.*). *J. Oil Seed Res*. **9**(1): 14-20.

Yadava, T.P., Yadav, A.K. and Singh, H. (1993). A concept of plant Ideotype in Indian mustard (*B. juncea L. Czern and Coss*). 5th Intl. Rapeseed Conf, June.1978: 7.

Yadava, T.P., Zada, A.K. and Hari, S. (2004). Selection Indices for Seed Yield in Indian Mustard (*Brassica juncea L. Czern & Coss*), I. Based on Physiological Attributes. *Indian J. Genet. Plant Breed.* **48**(1):23-29.

Yadava, T.P., Zada, A.K. and Hari, S. (2004). Selection Indices for Seed Yield in Indian Mustard (*Brassica juncea L. Czern & Coss*), I. Based on Physiological Attributes. Indian J. Genet. Pl. Breed. **48**(1):23-29. 99

Yadava, T.P., Zada, A.K. and Hari, S. (2007). Selection Indices for Seed Yield in Indian

Mustard (*Brassica juncea L. Czern & Coss*), I. Based on Physiological Attributes. *Indian J. Genet. Pl. Breed*. **48**(1):23-29.

Zahan, M.I. (2006). Morphological characterization and genetic diversity in oleiferous Brassica species. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Zajac, T., Bieniek, J., Witkowiez, R. and Gierdziewicz, M. (1998). Individual share of field components in winter oilseed rape yield formation. Academia Rolniezaw Kraikowie, Poland. **19**(2): 413-422.

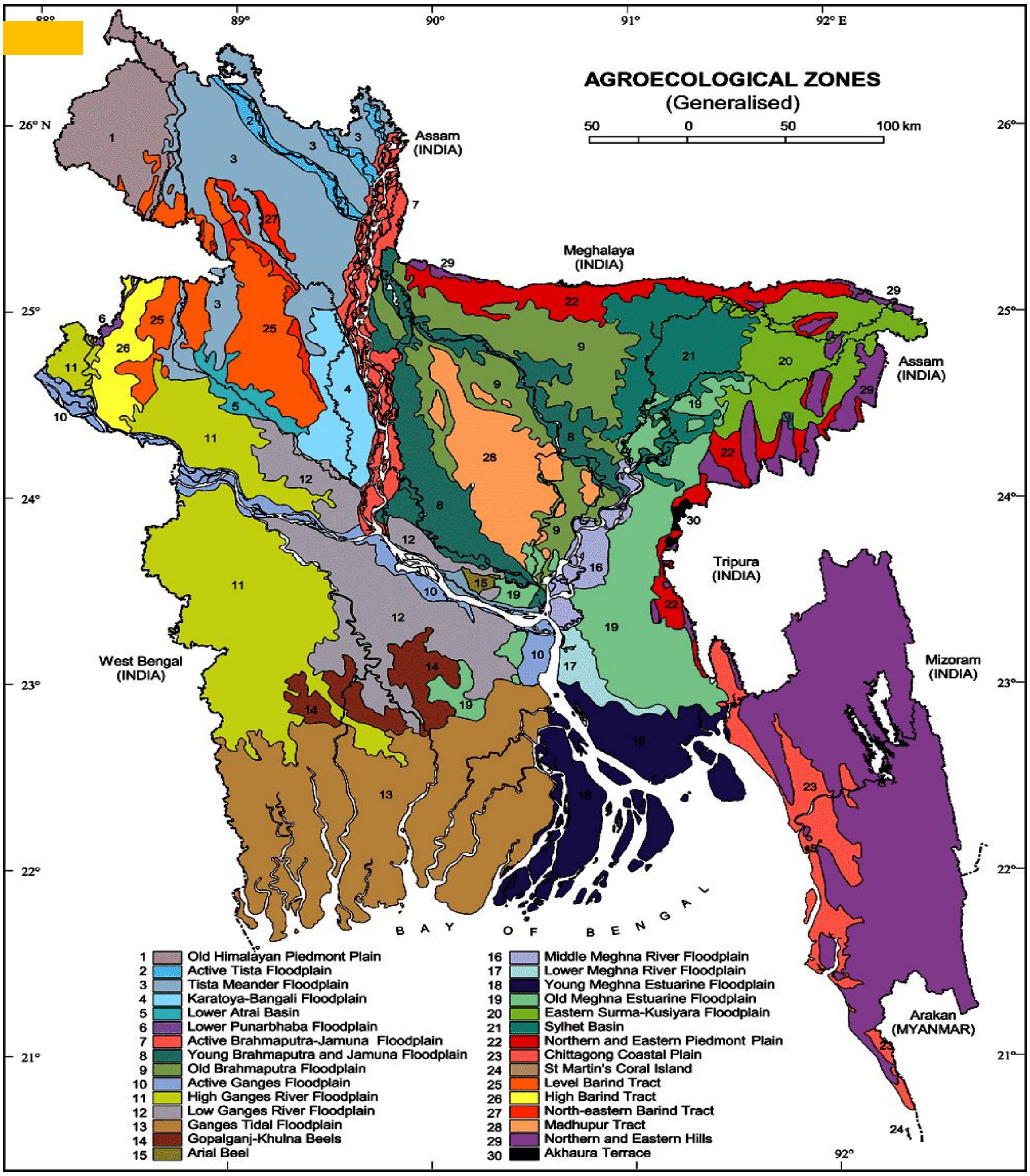
Zaman, M.A., Tuhina-Khatun, M., Ullah, M.Z., Moniruzzamn, M. and Rahman,M. Z. (2010). Multivariate analysis of divergence in advanced lines of mustard *(Brassica sp.).* Bangladesh *J. Plant Breed. Genet.* **23**(2): 29-34.

Zaman, M.W., Talukder, M.Z.I., Biswas, K.P. and Au, M.M. (1992). Development allometry and its implication to seed yield in *Brassica napus L.* Sveriges Utsades foreign Tidskrift. **102**(2): 68-71.

Zebarjadi, A., Kakaei, M. and Mostafaie, A. (2011). Genetic variability of some traits in rapeseed (*Brassica napus L.*) under draught stress and non-stress condition. Biharean Biologist**. 5**(2):127-131.

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 IV: Monthly average temperature, average relative humidity and total rainfall and total sunshine of the experimental site during the period from November, 2018 to February, 2019.

Month	**Air temperature (ºC)**		**Relative humidity (%)**	**Total rainfall (mm)**	**Sunshine (hr)**
	Minimum	**Maximum**			
November, 2018	18	31	63	12.6	5.8
December, 2018	16	28	61	1.9	7.9
January, 2019	13.0	27	57	3.5	3.9
February, 2019	18	28	58	12.3	5.7

Source: https://www.timeanddate.com/weather/bangladesh/dhaka/climate

Appendix V. Mean performance of different characters of 43 *Brassica napus*

Genotypes	**DFF**	**D50F**	**DM**	**PH (cm)**	**NPB**	**NSB**	**NSP**	**SL (cm)**	**NSS**	**TSW (g)**	**SYP (g)**
G1	25.00	32.33	93.00	119.83	8.00	6.00	165.00	8.37	**23.36**	**6.15**	**9.94**
G2	25.00	32.33	83.67	120.55	4.30	4.53	158.77	8.70	**24.83**	**5.48**	**8.53**
G3	28.00	42.33	78.67	127.37	3.25	3.93	232.33	7.87	**23.88**	**6.07**	**10.28**
G4	30.00	31.33	90.00	114.87	4.01	3.59	161.25	7.90	**25.00**	**5.00**	**6.54**
G5	27.33	32.00	90.00	165.23	3.67	4.00	139.33	8.87	**19.00**	**5.11**	**7.82**
G6	27.33	32.00	89.33	141.20	7.67	7.33	261.00	8.90	**26.67**	**6.49**	**10.57**
G7	25.00	31.33	90.00	136.33	3.33	3.00	143.67	8.20	**27.00**	**5.02**	**4.04**
G8	24.00	30.67	83.00	121.87	2.67	3.67	150.67	8.40	**22.33**	**3.82**	**4.89**
G9	25.00	30.33	89.67	116.63	3.33	4.33	123.33	8.27	**25.33**	**5.58**	**9.59**
G10	29.00	32.00	91.00	128.13	7.00	6.00	335.00	10.13	**21.33**	**5.23**	**6.53**
G11	28.00	32.00	90.00	114.67	4.67	5.00	198.33	9.47	**28.00**	**5.08**	**6.08**
G12	28.67	32.00	91.67	160.03	4.33	3.33	246.00	7.97	**24.67**	**5.20**	**9.32**
G13	30.00	31.67	90.33	138.33	6.00	7.33	312.33	9.60	**29.33**	**4.87**	**4.66**
G14	28.67	40.33	90.33	127.33	6.33	7.00	237.67	9.67	**26.33**	**5.53**	**9.37**
G15	29.00	41.00	90.00	138.07	3.67	6.33	242.33	8.97	**24.00**	**4.93**	**3.99**

G16	31.00	42.00	87.33	169.93	5.00	5.33	204.00	9.13	**26.00**	**4.73**	**3.53**
G17	29.67	39.00	85.67	118.40	5.67	6.00	307.00	8.67	**31.33**	**5.27**	**4.84**
G18	27.67	35.00	77.33	123.60	5.67	7.33	282.67	7.10	**27.33**	**5.17**	**3.73**
G19	28.67	36.00	77.67	132.10	7.33	7.67	250.67	8.43	**33.00**	**4.87**	**3.12**
G20	27.33	36.00	86.67	133.43	6.00	6.00	142.67	6.67	**22.67**	**5.27**	**7.43**
G21	30.67	40.00	85.67	161.70	8.33	7.33	138.67	8.43	**27.00**	**4.87**	**3.30**
G22	31.00	43.00	90.67	124.67	7.00	5.33	206.33	9.77	**24.67**	**5.17**	**3.48**
G23	28.00	36.67	88.67	124.10	3.33	4.00	353.67	10.60	**31.67**	**4.93**	**8.33**
G24	28.67	38.33	85.33	133.17	4.00	5.00	242.00	7.83	**21.33**	**3.36**	**3.90**
G25	28.67	37.67	89.33	127.77	4.33	4.67	247.00	6.47	**28.00**	**5.17**	**5.07**
G26	26.00	33.67	90.33	134.77	4.00	4.00	191.67	7.73	**25.00**	**4.80**	**4.93**
G27	25.00	32.67	90.33	116.47	3.67	4.00	136.00	7.17	**28.00**	**3.36**	**4.19**
G28	26.33	31.33	87.33	123.87	3.33	4.33	211.00	8.63	**27.33**	**5.20**	**7.23**
G29	28.67	36.33	88.67	119.77	5.33	3.33	149.33	7.37	**25.33**	**5.20**	**5.70**
G30	26.67	36.00	88.33	118.53	4.67	4.00	147.67	8.77	**29.00**	**4.73**	**7.04**
G31	26.33	35.33	87.33	126.57	5.67	5.00	125.33	8.60	**30.67**	**3.05**	**3.19**
G32	26.67	32.00	90.00	119.90	6.00	4.00	131.33	8.80	**33.67**	**5.17**	**3.40**
G33	26.67	36.67	88.67	128.70	4.00	4.67	140.33	7.17	**33.00**	**5.03**	**3.44**
G34	25.67	33.00	89.33	124.87	4.00	4.00	111.33	6.53	**25.33**	**5.10**	**4.10**

G35	25.67	33.00	86.33	125.47	3.00	5.00	134.67	7.23	**20.00**	**5.53**	**8.40**
G36	27.33	32.33	87.67	106.97	4.00	5.00	129.33	8.57	**24.33**	**4.87**	**6.44**
G37	27.33	31.67	89.00	113.97	5.00	3.67	118.67	7.47	**22.67**	**3.20**	**3.51**
G38	28.00	31.67	89.33	127.13	4.00	3.67	138.00	8.37	**23.67**	**5.00**	**5.14**
G39	28.33	32.00	90.33	124.47	4.33	4.33	143.33	8.60	**16.33**	**4.93**	**8.87**
G40	29.00	39.33	89.67	123.53	4.00	3.67	114.33	7.40	**35.00**	**5.47**	**8.64**
G41	33.00	42.33	90.00	106.43	6.67	4.00	139.67	8.33	**27.00**	**5.13**	**6.71**
G42	30.00	41.33	89.00	115.80	5.33	4.67	298.00	7.37	**25.67**	**5.27**	**8.22**
G43	28.67	35.33	89.33	157.03	3.67	2.67	135.67	8.53	**24.00**	**4.73**	**5.31**
MIN	24.00	30.33	77.33	106.43	2.67	2.67	111.33	6.47	**16.33**	**3.05**	**3.12**
MAX	33.00	43.00	93.00	169.93	8.33	7.67	353.67	10.60	**35.00**	**6.49**	**10.57**
Mean	27.83	35.19	88.05	128.69	4.87	4.84	190.17	8.30	**26.05**	**4.98**	**6.12**
CV (%)	5.26	6.1	2.85	3.82	18.11	20.57	12.05	5.05	**9.22**	**6.35**	**6.51**