VARIABILITY AND INTERRELATIONSHIP OF *Brassica napus* IN ADVANCED POPULATIONS

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CERTIFICATE

This is to certify that thesis entitled **"VARIABILITY AND INTERRELATIONSHIP OF *Brassica napus* IN ADVANCED POPULATIONS "** submitted to the **DEPARTMENT OF GENETICS AND PLANT BREEDING**, 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 bonafide research work carried out by **SAIKAT BISWAS**, Registration No. 13-05625 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 received during the course of this investigation has duly been acknowledged.

June, 2020

Dhaka, Bangladesh

(Dr. Firoz Mahmud)
Professor
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Dedicated to
My
Beloved Parents

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The Author

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ABSTRACT

A field experiment was conducted with 41 populations of *Brassica napus* at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the variability and interrelationship among the advanced populations during November 2018 to March 2019. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Analysis of variance for each trait showed significance differences among the populations. The first two components with Eigen value were greater than others. The utmost inter cluster distance was observed between cluster I and V and the maximum intra-cluster distance was found in cluster I. Phenotypic variances were higher than the genotypic variances for all the characters studied. Days to 50% flowering (90.45) exhibited the highest value of heritability and number of seeds per siliqua (47.71) exhibited the lowest value of heritability. The significant positive correlation with seed yield per plant was found in days to 1st flowering, days to 50% flowering, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant. Path co-efficient analysis revealed that days to 1st flowering, days to 50% flowering, plant height, number of secondary branches per plant, number of siliqua per plant and thousand-seed weight had the positive direct effect on yield per plant. Considering group distance and other performance populations G_1 (Nap-2037), G_2 (Nap-10020), G_3 (Nap-10015), G_4 (Nap-10019), G_9 (Nap-084), G_{13} (Nap-10009), G_{30} (Nap-0837), G_{31} (Nap-179), G_{32} (Nap-0885), G_{34} (BARI-8) and G_{37} (Nap-205) might be suggested for future hybridization program.

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COMMONLY USED SOME ABREVIATIONS

Full word	**Abbreviation**
At the rate	@
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
By way of	via
Backcross in the sixth generation of a cross between two dissimilar homozygous parents	BC_1F_6
Cultivars	cv.
Centimeter	cm
Canonical Variate Analysis	CVA
Cluster aAnalysis	CA
Degrees of Freedom	df
Days to 50% flowering	D50%F
Days After Sowing	DAS
Days to Maturity	DM
Duncan`s Multiple Range Test	DMRT
Etcetera	etc.
Environmental variance	σ^2_e
Food and Agricultural Organization	FAO

COMMONLY USED SOME ABREVIATIONS (CONT'D)

Full word	**Abbreviation**
Gram	G
Genotype	G
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Genetic Advance	GA
Heritability in broad sense	$h^2{}_b$
International Center for Agricultural Research in Dry Areas	ICARDA
Indian Agricultural Research Institute	IARI
Journal	J.
Kilogram	Kg
Meter	M
Mean sum of square	MS
Murate of Potash	MP
Ministry of Agriculture	MOA
Number	No.
Namely	Viz.
Principal Component Analyais	PCA
Principal Coordinate Analysis	PCO
Phenotypic coefficient of variantion	PCV
Percent	%
Percentage of Coefficient of Variation	CV%

Full word	**Abbreviation**
	σ^2_g
Phenotypic variance	σ^2_p
Plant height	PH
Primary branches per plant	PBP
Residual Effect	R
Randomized Complete Block Design	RCBD
Science	Sci.
Standard Error	SE
Siliqua length	LS
Secondary branches per plant	SBP
Seeds per siliqua	SPS
Seed yield per plant	SYP
Square meter	m^2
Sher-e-Banagla Agicultural University	SAU
Triple Super Phosphate	TSP
Thousand seed weight	TSW
The third generation of a cross between two dissimilar homozygous parents	F_3
University	Uni.
Variety	var.

CHAPTER I

INTRODUCTION

Brassica napus L. is second most important oilseed crop in the international oilseed market after soybean and important source of vegetable oil (Verma *et al.* 2016). *Brassica* is accounting for over 16% of the world's edible oil supply (Anonymous, 2015).*Brassica* oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2013).

The genus *Brassica* has generally been divided into three groups namely rapeseed, mustard and cole. In Bangladesh various species of *Brassica* are grown. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *B. campestris,* BB for *B. nigra* and CC for *B. oleracea* having diploid chromosome number of 20, 16 and 18 respectively (Han, 1990). On the other hand the species *B. juncea* (AABB), *B. carinata* (BBCC) and *B. napus* (AACC) are the amphidiploids (Sharma, 1984). Approximately, 70% of the total cultivated mustard in Bangladesh which is the variety of either *B. rapa* or *B. napus*.

The seeds of *B. rapa* contain 42% oil and 25% protein (Khaleque, 1985). It also serves as important source of raw material for industrial use such as in making soaps, paints, hair oils, lubricants, textile auxiliaries, pharmaceuticals and so on. On the other hand, oil cakes and meals are used as animal feeds and manures. *B. rapa* occupies the first position in respect of area and production among the oil crops grown in Bangladesh (Anonymous, 2011). In Bangladesh, it occupies the 1st position in respect of area and production among the oil crops grown. About 83120 million hectare of land was under rapeseed and mustard cultivation where produced about 0.271 million tons of seed with national average yield of 1.075 ton/ha during 2016-2017 in Bangladesh (BBS, 2018).

The main reasons behind these are the use of low yielding local indigenous cultivars and low management practices (Hasanuzzaman and Karim, 2007).

One of the main objectives of any breeding program is to produce high-yielding and better-quality genotypes for release as variety to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, from which desired populations are to be selected for further exploration to achieve the breeding target. The phenotypic variability is a combined estimation of genetic and environmental causes, of which only the former one is heritable. Although number of high yielding varieties have been released but short duration high yielding varieties are not enough. Thus, farmers still use low yielding indigenous varieties. Therefore, high yielding and short duration *B. rapa* L. varieties need to be developed to fit into the existing cropping pattern (Rice-Mustard-Rice).

Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be of great importance in planning a successful breeding program (Mary and Gopalan (2006). The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations (Shukla *et al.* 2006).

Seed yield is a complex character that can be determined by several components reflecting positive or negative effects upon this trait, whereas it is important to examine the contribution of each of the various components in order to give more attention to those having the greatest influence on seed yield (Marjanovic- Jeromela *et al.*, 2007).

Determination of correlation coefficients is an important statistical procedure to evaluate the association among yield and its contributing traits in breeding programs, as well as to examine direct and indirect contributions to yield (Ali *et al.* 2003). Again, Path-coefficient technique splits the correlation coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation, thus path coefficient analysis can help in formulating an efficient selection strategy (Sabaghnia *et al.* 2010). Therefore, correlation in combination with the path coefficient analysis quantifies the direct and indirect contribution of one character upon another (Dewey and Lu, 1995).

The present study was conducted to find out the variability and interrelationship of *B. napus* in advanced line along with different character association and the direct and indirect effect of different characters on yield per plant which will give an opportunity to select the desired plant types to meet the existing demand. However, the present study was undertaken to achieve the following objectives:

1. To determine the nature of association, direct and indirect relationship of yield and yield contributing characters
2. To select the promising populations considering high yielding capacity.

CHAPTER II

REVIEW OF LITERATURE

B. napus is the major edible oil producing crop of Bangladesh. The nation spent an enormous amount of foreign currency to import edible oil, which could be mitigated through enhancing and ameliorating the existing populations. To do this, the genetic variability and diversity of the existing populations should be assessed. *Brassica* breeding has been immensely researched in different countries to elevate its yield and yield-contributing characters. A large number of literatures are procurable on variability, correlation and path analysis of yield and yield contributing characters of Brassica grown under a particular environment. An endeavor has been made here to recapitulate the findings of this study pertinent to the present investigation. The whole review has been divided into following sections, namely –

- Genetic variability, heritability and genetic advance
- Correlation among different characters
- Path co-efficient analysis
- Genetic diversity analysis

2.1. Genetic variability, heritability and genetic advance

Genetic variability is a precondition for commencing a successful breeding program aiming to build up high-yielding varieties. Huge numbers of literatures concerning the variability in the *Brassica* spp. are available. These literatures are outlined here:

Joya *et al*. (2016) evaluated thirty eight rapeseed populations to estimate the genetic variability and association among the populations, following 8 quantitative characters. A considerable amount of genetic variability were found ranges from 1000 seed weight (11.09 g) to harvest index (44.00%) and phenotypic variability for plant height (13.36 cm) to harvest index (44.14%).

High heritability was found for all characters except 1000 seed weight (67.04 g). Minimum genetic advance was observed for 1000 seed weight (0.63g) and maximum for plant height (29.72 cm). The lowest genetic advance in percent of mean was found in 1000 seed weight (18.70 g) and highest in harvest index (90.35%).

Naznin *et al*. (2015) conducted an experiment with thirty three genotypes of *B. rapa* L. in order to find out their inter-genotypic variability; character association and path coefficient of seed yield/plant and its component characters. BARI sarisha-6 x TORI-7 S-45 showed best result in terms of early maturity (75 days) and higher seed yield/plant (5.28g) than check varieties. The character, plant height, was highly influenced by the environment whereas, all other characters influenced the least. Number of secondary branches/plant showed the highest phenotypic and genotypic coefficient of variation. Moreover, number of siliquae/plant, number of secondary branches/plant and number of primary branches/plant showed high heritability (93.16%, 75.69% and 68.03%, respectively) couple with high genetic advance in percent of mean (37.74%, 73.55% and 26.82%, successively).

An experiment was conducted by Siddika (2015) using F_2 generation of some advanced *Brassica napus* L. populations. The result exposed that days to first flowering, plant height, length of siliqua, number of seeds per siliqua, thousand seeds weight, exhibited low genotypic and phenotypic co-efficient of variation.

Days to first flowering, number of secondary branches per plant and 1000 seed weight showed high heritability with high genetic advance and genetic advance in percentage of mean. Number of primary branches per plant, number of secondary branches per plant, yield per plant and number of siliqua per plant showed moderate genotypic and phenotypic coefficient of variation.

Heritabilities (broad sense) were moderate to high in magnitude for all traits. 1000-seed weight showed significant ($p<0.01$) differences validating the presence of genetic variation among the tested accessions. Greater variability among the accessions for 1000-seed weight was observed.

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

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

Helal *et al.* (2014) conducted an experiment to study genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. The results revealed that varieties produced the highest seed yields and 15% variation at genotypic and phenotypic level.

Shakera (2014) performed an experiment and the result revealed that among twenty F_3 and F_4 progenies for most of the characters wide range of variation observed. In case of days to Plant height and number of siliqua per plant showed higher influence of environment for the expression of these characters. Number of secondary branches per plant, number of siliqua per plant, and yield per plant showed high genotypic and phenotypic coefficient of variation. Days to 50% flowering, days to maturity, plant height and siliqua length exhibited low genotypic and phenotypic coefficient of variation.

An experiment was conducted with twenty four rapeseed populations including two cultivars and 22 advanced populations by Rameeh (2013) based on randomized complete block design with three replications. Significant populations effects were exhibited for phenological traits, plant height, yield components and seed yield, indicating significant genetic differences among the populations. High broad sense heritability was estimated for phenological traits, pods on main axis and seed yield, signifying selection gain for improving these traits. Duration of flowering and pods on main axis had high value of genetic coefficient of variation.

To study variability, heritability and genetic advance, a study was conducted with thirty F_7 segregating genotypes and two parents of *B. rapa* by Khan *et al.* (2013). The result revealed that significant variation was presented among all the populations for all the characters except thousand seed weight. The highest genotypic, phenotypic and environmental variances were observed in plant height while the lowest one was in length of siliqua followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliqua, and siliqua length showed high heritability along with low genetic advance in percent of mean. Considering important performances, the populations G_{15}, G_{19}, G_1, G_3, G_4, G_{10}, G_{18}, G_{21}, and G_{24} were found suitable for future breeding program.

Rameeh (2012) carried out a study to evaluated twenty rapeseed populations including 4 cultivars and 16 advanced populations. Significant populations effect were found for phenological traits, plant height, seed yield and yield components except seeds per siliqua. High broad sense heritability estimates for phenological traits, plant height, siliquae per plant. 1000-seed weight and seed indicating selection gain for improving these trails will be high. Days to maturity had low value; of genetic coefficient of variation and therefore for improving this trait, the correlated onus *viz,* days to flowering and days to end of flowering can be used.

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

To estimate genetic parameters in 16 rapeseed genotypes in two conditions (irrigation and non-irrigation), a study was conducted by Zebarjadi *et al.* (2011). Statistical analysis showed significant differences among the populations based on the data for 13 different characters, including chlorophyll content (SPAD), sugar solution (SS), stem size (SS), plant height, oil percent, oil yield etc. In stress condition heritability was maximum oil percentage, whereas low genetic advance was observed for thousand kernel weight.

Khan (2010) found with an experiment inter-genotypic variability of 32 genotypes of *Brassica rapa* including two commercially cultivated varieties as checks. Significant variation was observed among ail the populations for all the characters except 1000-seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with low genetic advance in percentage of mean were obtained for 1000-seed eight, number of secondary branches per plant, number of seeds per pod and pod length.

Sharma (1984) performed a field study by using eight F_2 and eight F_4 populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* to study the variation. 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 populations used in the experiment. The value of GCV and PCV indicated that there was least variation present among most of the characters. The days to maturity, length of siliqua, seeds per siliqua and 1000-seed weight showed high heritability with low genetic advance and high genetic advance in percentage of mean. Phenotypic variances were higher than corresponding genotypic variances. Days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, length of siliqua, seeds per siliqua, 1000-seed weight and yield per plant showed least difference between phenotypic and genotypic variances.

Alam (2010) carried out a study using twenty six F_4 populations of some inter-varietal crosses of *B. rapa* L. to study the variation among them. Higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant.

Afrin (2009) studied genetic variability of 22 *B. napus* L. advanced lines. The genotypes were found to differ significantly for all the characters except days to 50% maturity, The characters days to 80% maturity, plant height, number of primary branches per plant, number of seeds per siliqua, number of siliquae per plant and seed yield per plant showed higher influence of environment whereas, siliqua length and 1000-seed weight showed least, Moreover, the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seeds per siliqua, number of siliqua per plant, 1000-seed weight and seed yield per plant showed moderate broad sense heritability while plant height exhibited the highest heritability.

Aytac and Kinaci (2009) performed an experiment with 10 winter rapeseed varieties for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for 2 years. They observed the maximum broad sense heritability get genetic advance seed yield followed.

Hosen (2008) conducted a study using five parental genotypes of *B. rapa* and their ten F_3 progenies including reciprocals. The result revealed that there were large variations present among all the genotypes used in the experiment. Number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, length of siliqua, number of seeds per siliqua, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was considerable variation among the all characters except days to maturity. The plant height, days to 50% flowering and number of siliqua per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

Mahmud (2008) performed a study with 58 populations of *Brassica rapa* L. to study inter-genotypic variability. Significant influence was observed among all the populations for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in percentage of mean were obtained for days to 50% flowering, number of secondary branches per plant, seeds per siliqua, and siliqua length.

Rashid (2007) studied variability of forty oleiferous *Brassica* species. Result revealed that populations showed wider variation for morphological characteristics and thus were categorized under three cultivated species - *B. rapa, B. napus and B. juncea* considering genetic parameters. High GCV (Genotypic Co-efficient of Variation) value was observed for days to 50% flowering, days to maturity, plant height and number of siliqua per plant.

Parveen (2007) performed and experiment to observed variability in F_2 progenies of the inter-varietal crosses of 17 *Brassica rapa* genotypes. The result revealed that there were significant variations among the different genotypes used in the experiment. Number of primary branches/plant and secondary branches/plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage.

Genetic variability was studied by Ahlawat *et al.* (2006); for 12 characters in 19 genotypes of Indian mustard *(Brassica juncea* (L) czern and coss.). Estimate high phenotypic coefficient of variation than genotypic coefficient of variation were used for the characters numbers of primary and secondary branches, number of siliquae per plant and yield per plant, which indicated the presence of considerable amount of variation. Heritability and genetic advance were high for 1000-seed weight, number of siliquae per plant and plant height. Number of siliquae per plant and plant height had moderately high heritability with high genetic advance indicating that additive gene effects were important for these characters and selection pressure could be applied on them for yield improvement. Number of primary branches per plant and oil content had low heritability indicating that these traits were under the influence of environmental factors.

Afroz *et al.* (2004) studied genetic variability of 14 genotypes of mustard and rape. The highest genetic advance was observed in percent of pollen sterility.

Mahak *et al.* (2004) conducted an experiment on genetic variability, heritability, genetic advance and correlation for eight quantitative characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters. High heritability coupled with high genetic advance in percentage of mean was observed for days to flowering, followed by thousand seed weight, days to maturity and plant height.

Niraj and Srivastava (2004) performed a study on variability and character association in Indian mustard of 21 populations of *Brassica juncea.* Among the populations, RH-9704 and IGM-21 recorded the highest seed yield. Phenotypic coefficient of variation was high for oil yield per plant, seed yield per plant and seed weight. Heritability was high for test weight, days to flowering, days to maturity and plant height.

Choudhary *et al.* (2003) conducted a study on variability in Indian mustard for 10 characters during rabi season in India. A wide range of variability was observed for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua and thousand seed weight. Genotypic and phenotypic coefficient of variability was recorded high for secondary branches per plant, seed yield per plant and number of siliqua per plant. High 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, indicating preponderance of additive gene action.

Ali *et al.* (2003) conducted an experiment with twenty-five winter type rapeseed varieties introduced from diverse sources of the world and found genotypic and phenotypic variances were highest for siliquae per plant followed by plant height, whereas the maximum genotypic and phenotypic coefficients of variability were found in seed yield per plant and siliquae per plant, respectively. High heritability for flower duration, seed weight and seed yield coupled with high genetic advance indicated that these trails could be improved through mass selection.

Shen *et al.* (2002) tested 66 F_1 hybrids of *Brassica rapa*and significant differences were found between F_1s and their parents for yield per plant and seed oil content.

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

Pant and Singh (2001) studied genetic variability for nine traits in 25 genotypes which revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. All traits showed high heritability, with the highest value estimated for seed yield per plant. The estimates of genetic advance were comparatively low for oil content and days to flowering. The GCV and heritability estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

An experiment was conducted by Shalini *et al.* (2000) to study variability in *B. juncea* . Different genetic parameters was 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 populations for all 10 characters studied. Genotypic coefficient of variation, estimates of variability, heritability values and genetic gain were moderate to high for 1000 seed weight, number of siliqua per plant and number of secondary branches per plant, indicating that the response to selection would be very high for these yield components. For the other characters, low coefficient of variation, medium to low heritability and low genetic gain were observed.

Khulbe *et al.* (2000) carried out a study to estimate variability, heritability and genetic advance for yield and its components in Indian mustard revealed maximum variability for seed yield. All the characters except oil content performed high heritability with high or moderate genetic advance, suggesting the role of additive gene action in conditioning the traits. Non-additive gene action appeared to influence the expression of days to maturity, while environment had a major influence on oil content. The use of pedigree selection or bi-parental mating in advanced generations was advocated to achieve substantial gains.

Thousand seed weight is a very important character of rapeseed and mustard, where highest consideration is on the seed yield. This character has been found to vary widely from populations to populations and from environment to environment. A good number of literatures are procurable 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 (gm) and number of primary branches per plant was observed by Sheikh *et al.* (1999); while working with 24 populations of toria.

In a study, Lekh *et al.* (1998) reported that secondary branches showed the highest genotypic co- efficient of variation. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering. Thousand seed weight is also an important trait of *Brassica* oil crops, where the highest consideration is on the seed yield. This trait has been found to vary widely from population to population and from environment to environment including macro and micro environments. The coefficient of variation was high for thousand seed weight. pod length and number of seed per pod for both population and phenotypic variability.

Nanda *et al.* (1995) observed that days to 1st flowering varied by genotypes and date of sowing, while working with 65 strains of *B. napus*, *B. juncea*, *B. carinata* and *B. rapa.* Many other researchers like Kumar and Singh (1994).

2.2 Correlation among different characters

Analysis of correlation among different character is important in breeding program. A good number of literatures are available on correlation among characters of *Brassica sp.* Some of these literatures are reviewed here:

Islam *et al*. (2016); conducted a study using twenty one (21) F_9 populations derived from inter-varietal crosses of *Brassica rapa* L. Correlation study revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua, and siliqua length (genotypic or phenotypic level). Based on the variability study, some F9 plants showed high heritability for short duration and yield contributing characters were selected from some of the crosses combinations of the intervarital crosses of Brassica rapafor further selection.

In an experiment undertaken by Sultana (2016) by using F_4 generations of Brassica napus revealed that significant positive correlation with seed yield per plant with all most all the characters except days to 50% flowering which was positive but non-significant and days to maturity (non-significant negative) with seed yield per plant.

Naznin *et al*. (2015) conducted an experiment with thirty three genotypes of *B. rapa* L. were evaluated in order to find out their inter-genotypic variability; character association and path coefficient of seed yield/plant and its component characters. The seed yield/plant showed significant positive correlation with number of siliquae/plant (rg = 0.7011**, rp = 0.5684**), number of primary branches/plant (rg = 0.5611**, rp = 0.4016*) and number of secondary branches/plant (rg = 0.5160**, rp = 0.4098*) revealing that selection based on these traits would be judicious. Path analysis showed that the number of siliquae/plant (0.4679), number of primary branches/plant (0.2823) and number of secondary branches/plant (0.0092) were the most important contributors to seed yield/plant. The results indicated that number of siliquae/plant, number of primary branches/plant and number of secondary branches/plant can be used as selection criteria to increase seed yield/plant in rapeseed.

Siddika (2015) observed correlation revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, 1000 seeds weight both genotypic and phenotypic level. A significant genotypic positive correlation also observed for days to first flowering and length of siliqua.

Rameeh (2015), studied 36 rapeseed *(Brassica napus* L.) genotypes including four checks and 32 advanced lines and found that pods per plant, seeds per plant and 1000- seed weight traits were positively correlated with seed yield.

Bilal *et al*. (2015) evaluated 23 genotypes of rapeseed to study the correlation between the yield and yield contributing characters. Positive significant correlation was observed between days to maturity and yield per plant (r = 0.279) as well as with 1000-seed weight (r = 0.057). Negative significant correlation was observed between plant height and pods per plant and 1000-seed weight. Number of pods per plant revealed positive significant correlation with 1000-seed weight and positive correlation with pod length, number of seeds per pod, yield per plant.

Another study on correlation by Shakera (2014) revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, thousand seed weight (Both genotypic & phenotypic level).

Halder *et al.* (2014) conducted an experiment by using 14 genotypes including 11 advanced lines and 3 check varieties to study the correlation and observed that days to first flowering showed positive non-significant relationship with yield but high positive significant correlation with the days to 50% and 80% flowering. Highly significant negative correlation was found with number of secondary branches per plant and siliqua length.

Helal *et al.* (2014) conducted an experiment to study Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. Correlation between seed yield and yield contributing characters showed significant and positively correlated with number of siliqua/plant, 1000 seed weight, straw yield, plant height, biological yield and harvest index. Correlation coefficient analysis of yield attributes had the highest and positive association with seed yield.

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

A research was conducted by Mili (2014) using 66 F5 genotypes of *Brassica napus* L. to study correlation and path coefficient analysis. The significant positive correlation with seed yield per plant was found in number of siliqua per plant,siliqua length, number of seed per siliqua and thousand seed weight.

Abideen *et al.* (2013); studied with eight genotypes of *Brassica napus* and the resulted that positive phenotypically correlation was observed in plant height, pod length and seed yield. Significant positive correlation was also found in seed yield per plant and pods per plant.

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

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

Afrin *et al.* (2011) studied on *B. napus* and found positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliqua per plant. Highest significant positive correlation was found between days to 50% flowering and plant height.

Khan (2010) conducted a field experiment with 32 genotypes of *Brassica rapa* including two *commercially* cultivated van dies as checks to study correlation. Highly significant positive association of seed yield per plant was observed with number of primary brandies per plant, number of secondary' branches per plant and number of pods per plant.

A research was conducted by Alam (2010) using 26 F_4 populations of some intervarietal crosses of *B. rapa* to study the correlation between pairs of different characters. Correlation study revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of siliquae per plant, number of seeds per siliqua and siliqua length.

Singh *et al.* (2004) studied sixty two Fi and twenty four parental lines of *B. juncea* and observed that positive correlation was present in plant height, primary branches per plant, secondary branches per plant, seed per siliqua, thousand grain weight with seed yield.

Esmaeeli Azadgoleh *et al.* (2009) mentioned positively significant correlation of seed yield with number of pod per plant, number of pods in sub branches and number of seeds per pod. An experiment was conducted by Basalma (2008) in Ankara conditions using 25 winter oil seed rape cultivars. Correlation analysis showed a high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, thousand seed weight and oil ratio.

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of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, 1000 seed weight and oil ratio.

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

Marjanovie-Jeromela *et al.* (2007) conducted an experiment using 20 rapeseed cultivars. They found highest seed yield per plant for cultivars ‘Sremica’, ‘B-009’, ‘Jet Neuf’ and ‘Falcon’. There was a complete correlation between plant height and height of the first lateral branch and a very strong one between plant height and seed oil content, as well as between plant height and seed yield per plant. 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 investigation helps rapeseed breeders to optimize their breeding *programs.*

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica* species to estimate correlation and observed that, highly significant positive association of yield per plant with number of primary branches per plant , number of secondary branches per plant, number of seeds per siliqua and number of siliqua per plant.

Siddikee (2006) undertaken an experiment on oleiferous *B. campestris* L. to study the correlation analysis. The results revealed that yield per plant had highest significant positive correlation with number of siliquae per plant.

Tusar *et al.* (2006) reported an experiment to study the phenotypic correlation and observed that seed yield per plant was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliquae per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield.

An experiment on *oleiferous B. campestris* was conducted by Siddikee, (2006) to study the correlation analysis. The results revealed that yield per plant was the highest significant positive correlation with number of siliqua per plant.

The significant and positive correlation of seed yield per plant with plant height and 1000 seed weight, but high negative and significant correlations with seeds per siliqua, at both the genotypic and phenotypic levels were observed by Uddin *et al.* (1995). Seeds per siliqua, 1000 seed weight had high positive direct effects on seed yield per plant. Days to maturity and plant height had considerable negative direct effects on seed yield per plant.

An experiment conducted by Niraj and Srivastava (2004) on character association studies in Indian mustard of 21 genotypes of *B. juncea*. Seed and oil yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

A field experiment was conducted to determine the genetic potential of *Brassica* accessions. Eight accessions were sown in randomized complete block design in four replications. Result revealed that plant height, number of primary branches, number of secondary branches, number of siliqua per plant and seed index were found positively correlated with seed yield. So, the emphasis should be given during experimentation for improvement of plant height, number of primary branches, number of secondary branches, number of siliqua per plant and seed index for improvement in yield of seed in *Brassica* (Khan and Khan, 2003).

Srivastava and Singh (2002) studied correlation in Indian mustard *[Brassica juncea* L. Czern and Coss] for 10 characters was conducted with 24 strains of Indian mustard along with two varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and oil percent were positively associated with seed yield.

Association of yield components in Indian mustard among 12 yield components were studied in 36 genotypes selected from different geographical regions by Ghosh and Gulati (2001) seed yield exhibited significant positive association with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliquae on main shoot and oil content.

Malek *et al.* (2000) studied correlation analysis and reported that days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. He also reported that number of branches per plant and number of siliqua per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight.

According to Kumar *et al.* (1999) genotypic correlation co-efficient were higher in magnitude than corresponding phenotypic correlation co-efficient for most characters. The plant height, siliquae on main shoot, siliquae per plant and thousand seed weight were positively correlated with seed yield.

Das *et al.* (1998) carried out an experiment with 8 genotypes populations of Indian mustard *(B. juncea*) and reported that the length of siliqua, seeds per siliqua had high positive genotypic correlation with seed yield per plant.

Tyagi *et al.* (1996) carried out and experiment with six yield components in three cultivars of mustard and observed that plant height, siliqua per plant, siliqua length, seed weight, and seeds per siliqua had positive and significant effects on seed yield per plant.

Arthamwar *et al.* (1995) studied correlation and regression in *B. juncea.* Results revealed that weight of siliqua per plant showed the highest correlation with seed yield followed by number of siliqua per plant, number of seeds per siliqua and thousand seed weight.

Uddin *et al.* (1995) while studied correlation analysis in 13 Indian mustard *(B. juncea*) and reported that seed yield per plant had high positive arid significant correlations with plant height and 1000 seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

Ghosh and Mukhopadhyay (1994) studied Tori-7 *(B. campestris var. toria)* for evaluation of seed yield and five seed yield contributing characters and found that plant height, siliqua per plant, seeds per siliqua and thousand seed weight was significant and positively correlated with seed yield.

Ahmed (1993) worked with eight cv. of *B. campestris* and *B. juncea* for study of nature and degree of interrelationship among yield components and observed that siliqua length, number of siliquae per plant, number of seeds per siliqua and seed weight per siliqua was positively and linearly associated with seed yield per plant. He also observed that seed oil content was positively correlated with seed weight, but negatively correlated with number of seeds per siliqua.

2.3 Path coefficient analysis

When more characters are involved in correlation study, it becomes difficult 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.

Islam *et al*. (2016) conducted a study using twenty one (21) F_9 populations derived from inter-varietal crosses of *B. rapa* .Path coefficient analysis revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua, and siliqua length had the positive direct effect on yield per plant and days to 50% flowering, number of secondary branches per plant, and thousand seed weight had the negative direct effect on yield per plant.

Joya *et al*. (2016) evaluated thirty eight rapeseed genotypes to estimate the genetic variability and association among the populations, following 8 quantitative characters. Plant height, raceme length and 1000 seed weight have significant positive association with yield with harvest index. Plant height, raceme length, 1000 seed weight and harvest index have imposed direct positive effect on yield per plant (g). As plant height, raceme length, 1000 seed weight and harvest index are mainly driven by the additive genes so that selection criteria based on this characters should be effective.

Path coefficient analysis by Sultana (2016) revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 80% maturity, plant height, number of primary branch and siliqua length had the negative direct effect on yield per plant.

Path coefficient analysis experiment carried out by Siddika (2015) with using F2 seggregating generation of some advanced populations of *Brassica napus* L. revealed that days to number of primary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua and thousand seed weight had the positive direct effect on yield per plant and days to first flowering, plant height and number of secondary branches per plant had the negative direct effect on yield per plant.

In an experiment undertaken by Shakera (2014) by using some advanced lines of *Brassica rapa* revealed that days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua and thousand seed 92 weight had the positive direct effect on yield per plant. Siliqua length had the negative direct effect on yield per plant.

Helal *et al.* (2014) conducted an experiment to study genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. Path coefficient analysis of different yield contributing characters showed biological yield contributed maximum to seed yield with the highest correlation.

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

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

Afrin *et al.* (2011) studied with *B. napus* to identify the path coefficient among the characters. The plant height was found the highest positive and direct effect on seed yield per plant followed by number of siliqua per plant and siliqua length.

A research was conducted by Alam (2010) using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the direct and indirect effect of different characters on seed yield. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliqua and siliqua length had the positive direct effect on yield per plant, days to 50% flowering, number of secondary branches per plant and 1000-seed weight had the negative effect on yield per plant.

Khan (2010) conducted a field experiment wilh 32 genotypes of *B. rapa* including two commercially cultivated varieties as check's to study path coefficient. Path analysis showed that, yield per plant had the highest direct effect on number of primary brandies per plant, number of pods per plant, number of secondary branches per plant and number of seeds per pod,

Esmaeeli-Azadgoieh *et al.* (2009) performed path coefficient analysis and identified number of pods in sub branches, number of seeds per pod and number of pods per plant as having the greatest effect on seed yield, respectively.

The path coefficient analysis by Hosen (2008) exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F3 progenies including reciprocals.

An experiment was carried out by Mahmud (2008) with 58 genotypes of *Brassica rapa*. Path analysis showed that yield per plant had the highest direct effect on number of primary branches per plant, number of siliqua per plant, number of secondary branches per plant and number of seeds per siliqua.

Aytac *et al.* (2008) evaluated on six genotypes of spring rape seed and studied path coefficient and the result stated that plant height, number of siliqua per plant, seeds per siliqua had highest and positive direct effect on yield per plant for all cultivars except cv. Star.

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

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

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

Khan *et al.* (2006) studied correlation for some quantitative traits relating to yield and quality. The results indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

An experiment was conducted by Singh (2004) in Jammu and kashmir, India, during 2001-02 rabi season to study path coefficient analysis and mentioned that siliqua per plant had a high positive direct effect. Seed per siliqua, primary branches and 1000-seed weight were highly correlated with seed yield and had a maximum indirect effect on siliqua per plant.

Pant *et al.* (2002) conducted a field experiment with 25 accessions of Indian mustard were used in Uttar Pradesh, India, and reported that the major yield-contributing characters, which consisted of days to flowering, plant height, number of primary and secondary branches, number of siliquae on main raceme, 1000-seed Weight and oil content, may be used for developing cultivars with high yield potential.

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

Khulbe and Pant (1999) studied path coefficient analysis in eight Indian mustard *(B. juncea)* parents and their 28 F_1 hybrids. The results revealed that harvest index, siliqua length, seeds per siliqua, siliqua per plant, thousand seed and days to initial flowering were the major traits influencing seed yield.

Sheikh *et al.* (1999) worked with 24 diverse genotypes of toria for assess the direct and indirect effect of seven quantitative and developmental traits on seed yield. Results revealed that thousand seed weight and siliqua per plant had highly positive direct effect on seed yield.

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

Dhillor *et al.* (1990) reported that the plant height had the highest positive direct effect on seed yield per plant in *B. juncea,* but Singh *et al.* (1997); also found negative direct effect of the trait on seed yield.

2.4 Genetic diversity analysis

Diversity is the basis of crop improvement. If there were no diversity in nature no improvement would possible. But amid incessant selection process for better quality and productivity, the gene pool of the selected final varieties has been made narrow down due to eliminating of genes for undesirable traits for example, declining amount of erucic acid in oil and glucosinolates in seeds. Due to which the differences at genetic level in *B. napus* has been made very limited which were so much important for many other promising characters.

Rout *et al*. (2019) carried out a study with 71 genotypes of Indian mustard [*B. juncea* (L.) Czern and Coss] under sub-Himalayan condition to examine the genetic diversity within them. All the 71 populations were tested in randomized complete block design with three replications during rabi 2017-18. The genetic divergence was studied among the populations of Indian mustard [*Brassica juncea* (L.) Czern and Coss] using Mahalanobis D2 statistics. Populations were found to be grouped into seven clusters. Cluster I had the largest number of populations (31) followed by cluster IV (21), V (12), II (two), III (two), VI (two) and VII (one). Maximum intra cluster divergence was found in cluster VI followed by cluster V, IV and I. Maximum inter cluster distance was found between cluster VII and V followed by cluster VII and VI, cluster VII and IV and cluster VII and I, which indicates that efficient breeding programme can be formulated to improve yield potential by hybridization between populations from these clusters. Based on the maximum intra cluster distance value the crosses could be made among the populations having the highest divergence like PHR-2, RNWR-09-3, Giriraj, Kranti, SKJM-05, DRMR-15-16, RW-85-59 and NPJ-194 from various clusters like IV, V, VI and VII to get desirable transgressive segregants. Cluster III having the highest seed yield (11.80 g plant-1) had not shown highest genetic divergence from the other clusters. However, other clusters like cluster IV, V, VI, and VII had shown higher genetic divergence among themselves. Plant height (18.71) contributed maximum towards genetic divergence followed by 1000 seed weight (18.35) as well as penetration force (18.35), aphid count (12.76) and seed yield per plant (10.62). For the characters like plant height,1000 seed weight, penetration force, seed yield and aphid count contributing substantially high to the total genetic divergence, it was found that genetically divergent clusters namely IV, V, VI and VII performed optimally and amongst these clusters only. Cluster VII was the poorest seed yielder. This clearly reflected that the genetically divergent populations were distributed in the different clusters like cluster IV, V, VI and VII.

Rameeh (2015) carried out an experiment to study genetic diversity of twenty one rapeseed genotypes. These populations were assessed based on randomized complete block design with three replications. On the basis of cluster analysis, the populations were classified in three groups and the group with high seed yield had high mean values of plant height, days to maturity and pods per plant. All the populations were classified in three groups with different mean values of the traits. The high seed yield populations with high mean value of pods on main axis and pods per plant were classified in group1 (C1). Group 1 (C1) and group 2(C2) had 1545.56 and 2160.55 kg per ha of seed yield.

In an another experiment Iqbal *et al.* (2014) studied different genotypes to determine the genetic variability and diversity among different mustard populations and reported that all the characters demonstrated high heritability (D80%) irrespective of any genotypes. The genotypes were grouped into four clusters by using Euclidean distance following Ward's method. The cluster III had higher intra cluster distance and the maximum inter cluster distance was observed between populations of clusters I and IV followed by clusters III and IV.

Pandey *et al.* (2013) conducted an experiment with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. D^2 analysis was conducted to measure the genetic diversity among the genotypes. The 45 genotypes were grouped in eight clusters using Tocher's method. Intra-cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. The maximum contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield per plant (20.91%) and number of siliqua on main raceme (8.38%). Evaluation of genotypes through genetic divergence which quantifies variation among populations on the basis of a group of characters (yield and yield contributing) helps in identification of promising parental materials for crop improvement. Genotypes collection was also valuable gene pools providing diverse genetic material that may be applied for the improvement of cultivars and advanced agronomic productivity. An assessment of genetic and genomic diversity within these collections can be used to assign lines and populations to diverse groups, to study the evolutionary history of wild relatives, to verify pedigrees and fill in the gaps in incomplete pedigree or selection history, to monitor changes in allele frequencies in cultivars or populations.

Zare and Sharafzadeh (2012) evaluated 8 genotypes of rapeseed to determine the genetic divergence. The genotypes were grouped into four clusters. Based on the results, Modena and Sarigol, which had the highest grain yield, were located in a major cluster and Okapi, which had the lowest grain yield, was located in a single cluster else. SLM046, RGS003 and Hyola308 cultivars, which had lower grain yield, were placed in the third cluster that was partitioned into two small clusters. The fourth cluster included Licord and Zarfam cultivars also had high grain yield.

A field experiment was conducted by Zaman *et al.* (2010) which comprised eighteen advanced lines of mustard for estimation of divergence among advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of populations (6) and the cluster III contained the lowest (3). The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials. The populations from cluster I had dwarf plant along with earpopulationss in days to 50% flowering, days to maturity and maximum number of primary branches per plant.

The genetic diversity of 22 rapeseed *(B. napus*) advanced populations was studied by Mahmud *et al.* (2008); using principal component analysis non-hierarchical clustering and canonical vector analysis. The populations were grouped into four clusters. Cluster II contained the maximum number of populations (9) and cluster III contained the lowest (2). The highest inter cluster distance was found between cluster I and cluster III and the lowest between cluster I and cluster II. The highest intra-cluster distance was noticed for cluster III and the lowest for cluster II. Cluster I had the highest mean values for siliqua length and thousand seed weight. Cluster III had the lowest cluster mean values for the number of days to 50% flowering and the number of days to maturity with moderate seed yield. Crosses between populations belonging to cluster II with those of cluster I and cluster IV might therefore produce high heterosis in yield as well as ear populationss.

Vivek *et al.* (2007) studied the genetic diversity in 81 true breeding advanced generation cultivars of Indian mustard based on yield and yield components. They are followed by cluster analysis and showed that out cluster XII, which was most diverse, had very high seed yield and number of siliquae per plant. Cluster VII also represented entries with high seed yield, number of siliquae per plant and highest number of seed per siliqua. Cluster XI with the lowest number of days to maturity could be considered as a good source for ear populationss.

Goswami *et al.* (2006) reported the moderate genetic diversity between parents had the good general combining ability (GCA) effect and high specific combining ability (SCA) and high mean values in F_2, had the highest frequency of transgressive segregates in F_2 and the magnitude of transgression were high in Indian Mustard.

Goswami and Behl (2006) carried out a study on 43 genotypes of Indian mustard using D statistics. They recorded data for plant height, primary branches, secondary branches, main shoot length, number of siliqua on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant and oil content. The genotypes were grouped into six clusters. The intra cluster distances were almost equal and relatively lower than the inter-cluster distances.

Singh *et al.* (2005) performed an experiment on response of selection in generation for main shoot length, seeds per siliqua, seed mass and seed yield were studied in *Brassica* species. Observations were recorded on individual plant basis in one generation of three crosses of Indian mustard *(B. juncea L.)* for each trait. Five plants with high and five with low values were selected for each trait. On the other hand a bulk was constituted by taking one seed from each plant in each cross. These selected plant- as well as the constructed bulks were raised to advance from generation to generation, comparisons were made between high and low selections for each trait as well as between high selection and bulk. It was observed that differences between high and low selection were non-significant for all traits except seed mass. On the other hand mean values under bulk were comparable to that of high selection group for each trait. Bulk was advised to be followed in early generation. Transgressive segreegates were more frequent for main shoot length: seeds per siliqua and seed yield than for seed mass.

Goswami *et al.* (2005) carried out an experiment on variability studies for number of secondary branches per plant, siliquae on main shoot, seed per siliqua, 1000-seed weight and seed-yield per plant. Results showed that the coefficient of variation of pods per plant.

Aunwinithul *et al.* (2004) studied 33 genetically diverse genotypes of Indian mustard or diversity. The genotypes were grouped into eight different clusters. The cluster III was the biggest with 11 populations followed by cluster-I with nine populations, cluster V and VI consisted of four and three populations respectively. The cluster II and VII both had two populations each and similarly, cluster IV and VIII included one population each.

Kumar *et al.* (2003) noted that the generation of mean analysis was carried out in six crosses of Indian mustard *(B. juncea)* to identify gene effects for plant height, primary and secondary branches per plant and seed yield. Both additive and non-additive gene effects were found for plant height with the latter being more important. For seed yield and primary and secondary branches additive gene effects were more important than non-additive gene effects. Among the epistatic interactions identified, additive x additive and dominance x dominance interactions were important for plant height, whereas for number of branches and seed yield these interactions were significant in one or two crosses only. To improve these traits, crossing followed by delayed selection to obtain transgressive segregates and reciprocal recurrent selection could be utilized to exploit both types of gene effects.

Ali *et al.* (2003) conducted experiment on 25 winter type rapeseed cultivars introduced from diverse sources of the world were studied for variability of seed yield and yield components. Significant differences among genotypes for most of the traits indicated that there was sufficient variability available to have an effective selection. Genotypic and phenotypic variances were the highest for pods per plant followed by plant height, whereas the maximum genotypic and phenotypic co-efficients of variability were found in seed yield per plant and pods per plant, respectively.

Choudhary and Joshi (2001) determined genetic diversity among the 88 entries including eighty F_4 derivatives i.e., 20 each selected from *Brassica crosses* viz., *B. junceax B. napus*, *B. juncea x B. rapa* var. toria, *B. junceaxB. rapa* var. yellow sarson and *B. tournefortii x B. juncea*, and eight parent populations through multivariate analysis (D^2 statistic). The genetic distances calculated among different *Brassica* species revealed that *B. tournefortii* had the maximum diversity with *B. juncea* followed by *B. napus*, *B. rapa* var. toria and *B. rapa* var. yellow sarson. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters.

The characters, namely, plant height, secondary branches per plant, days to flowering and 1000-seed weight was contributed the maximum towards genetic divergence.

Jagadev et *al.* (1999) studied on some 19 genotypes of rapeseed *(B. napus).* They studied yield and yield contributing characters grouped the populations into 5 clusters with clusters I comprising these populations, clusters II and 1112 each and clusters IV and V one each.

Khulbe and Pan (1999) reported that siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight were positively associated with grain yield. Analysis of variance revealed that siliqua per plant, siliqua length, 1000 seed weight and seeds per siliqua were the major characters influencing grain yield.

Singh *et al.* (1997) studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and inter - intra cluster distances. On the basis of stability, high yield and divergence among the populations, nine crosses were recommended as suitable for use in breeding program.

Peter and Rai (1995) studied genetic divergence using the D^2 statistics and canonical analysis among 25 genotypes of *B. napus.* They reported that genetic and geographical divergence was highly related with the genotypes. The genotypes were grouped into six clusters of which cluster I was the largest accommodating among these populations. The cluster VI had large genetic distance from the remaining clusters.

Rawhat and Anad (1981) conducted a study on genetic divergence using Mahalanobis D^2 statistic on 27 strains of Indian brown mustard *(Brassica juncea* L. Czern and Coss) for seven characters related to yield and fitness. The various strains were grouped in seven clusters on three diverse lines. Parallel variation was observed between clusters III, IV and VII on one line, and I, II and V on the other, with cluster VI diverging from the rest. The geographical diversity of strains was found not to be related with the genetic diversity.

CHAPTER III

MATERIALS AND METHODS

To perform the experiment, 41 selected populations were used in Rabi season 2018-2019. The populations were grown in the experimental farm.

3.1 Experimental site

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka – 1207 during November 2018 to March 2019. The location of the experimental site was situated at 23°74′ N latitude and 90°35′ E longitudes with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix I).

3.2 Soil and Climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agro ecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine 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 experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

The healthy seeds of 41 populations of *B. napus* 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 is shown in Table 1.

Table1. Populations used for the experiment

Designation	Advanced populations	Source
G_1	Nap-2037	GEPB,SAU
G_2	Nap-10020	GEPB,SAU
G_3	Nap-10015	GEPB,SAU
G_4	Nap-10019	GEPB,SAU
G_5	Nap-9906	GEPB,SAU
G_6	Nap-206	GEPB,SAU
G_7	Nap-108	GEPB,SAU
G_8	Nap-9904	GEPB,SAU
G_9	Nap-084	GEPB,SAU
G_{10}	Nap-2022	GEPB,SAU
G_{11}	Nap-0869	GEPB,SAU
G_{12}	Nap-2013	GEPB,SAU
G_{13}	Nap-10009	GEPB,SAU
G_{14}	Nap-2012	GEPB,SAU
G_{15}	Nap-9901	GEPB,SAU
G_{16}	Nap-0876	GEPB,SAU
G_{17}	Nap-0762	GEPB,SAU
G_{18}	Nap-0865	GEPB,SAU
G_{19}	BARI-13	GEPB,SAU
G_{20}	Nap-248	GEPB,SAU
G_{21}	Nap-2066	GEPB,SAU
G_{22}	Nap-0733-1	GEPB,SAU
G_{23}	Nap-0733-2	GEPB,SAU
G_{24}	Nap-9905	GEPB,SAU
G_{25}	Nap-10007	GEPB,SAU
G_{26}	Nap-0136	GEPB,SAU
G_{27}	Nap-9908	GEPB,SAU
G_{28}	Nap-2037	GEPB,SAU
G_{29}	Nap-94006	GEPB,SAU
G_{30}	Nap-0837	GEPB,SAU
G_{31}	Nap-179	GEPB,SAU
G_{32}	Nap-0885	GEPB,SAU
G_{33}	Nap-0017	GEPB,SAU
G_{34}	BARI-8	GEPB,SAU
G_{35}	Nap-10012	GEPB,SAU
G_{36}	Nap-1005	GEPB,SAU
G_{37}	Nap-205	GEPB,SAU
G_{38}	Nap-2001	GEPB,SAU
G_{39}	Nap-10014	GEPB,SAU
G_{40}	Nap-1007	GEPB,SAU
G_{41}	Nap-2057	GEPB,SAU

GEPB = Genetics and Plant Breeding, SAU = Sher-e-Bangla Agricultural University

3.4 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 tilt. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. A pictorial view showing prepared land in Plate 1.

3.5 Application of manure and fertilizer

The crop was fertilized @ 10 tons of Cow dung, 250 kg Urea, 175 kg Triple Super Phosphate (TSP), 85 kg Muriate of Potash (MP), 250 kg Gypsum, 3 kg Zinc Oxide and Boron 1 kg per hectare. The half amount of urea, total amount of Cowdung, 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 of sowing.

3.6 Experimental design and layout

Having finished final land preparation, field lay out was done. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 19 m × 13 m = 247 m^2. Each replication size was 19 m × 3m, and the distance between replication to replication was 1 m. The spacing between line to line was 30 cm and plant to seed was 10 cm.

3.7 Sowing of seeds

Seeds of 41 populations were grown in separate line in the experimental field on 15 November, 2018. The row spacing was 30 cm having plant spacing 10 cm within the row. The seedlings emerged with in four days.

3.8 Irrigation and drainage

One post sowing irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of 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.

3.9 Intercultural operation

Necessary intercultural operations were done during the crop period to ensure normal growth and development of the plants. Thinning and 1st weeding were done after 15 days of sowing. Top-dressing, weeding and necessary thinning were done after 25 days of sowing. Malataf was sprayed two times one just before flowering and the other of the middle of flowering for protecting the crop from the attack of aphids and Rovral-50 WP was sprayed @ 20-g/10 L water first one at the time of siliquae setting of fruiting and second one after 1 days of 1st spraying to control Alternaria leaf spot.

Plate 1. Photograph showing Land preparation & seed sowing

Plate 2. Photograph showing harrowing & thinning

Plate 3. Field visited by respected Supervisor

3.10 Harvesting of sample plants

When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stem and desirable seed color in the matured siliqua, the crop was assessed to attain maturity. At maturity, 10 plants were selected at random from the middle row of each plot. The sample plants were harvested by uprooting and then they were tagged properly. Data were recorded from these 10 plants.

Plate 4. Photographs showing harvested samples collection

3.11 Data collection

For studying different genetic parameters and inter-relationships, ten characters were taken into consideration. A pictorial view of observation and data collection is presented in Plate 3. The data were recorded on ten selected plants for each cross and ten selected plants for each parent on the following characters

1) **Days to 1st flowering:** Days to 1st flowering were recorded from sowing date to the date of 1st flower appear to plants.
2) **Days to 50% flowering:** Days to 50% flowering were recorded from sowing date to the date of 50% flowering of every entry.
3) **Plant height (cm):** It was measured in centimeter (cm) from the base of the plant to the tip of the longest inflorescence. Data were taken after harvesting.
4) **Number of primary branches per plant:** The total number of branches arisen from the main stem of a plant was counted as the number of primary branches per plant.
5) **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.
6) **Number of siliqua per plant:** Total number of siliquae of each plant was counted and considered as the number of siliquae per plant.
7) **Siliqua 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.
8) **Number of seeds per siliqua:** All siliqua from the sample plants was collected and 10 siliqua was randomly selected. Seeds obtained from them, were counted and average numbers of seeds per siliqua was recorded.
9) **1000-seed weight (g):** Weight in grams of randomly counted thousand seeds of each entry was recorded.
10) **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.

3.12 Statistical analysis

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTAT-C software program and then phenotypic and genotypic 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 co-efficient 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); and path co-efficient analysis was done following the method outlined by Dewey and Lu (1959). Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Multivariate analysis *viz.*. Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO). Cluster Analysis (CA) were done by using GENSTAT-5 software program.

3.12.1 Estimation of genetic parameters

Estimation of phenotypic (σ^2p), genotypic **(**σ^2g) and environmental (σ^2e) variance were calculated by the following formula by Johnson *et al.* 1955.

$$\text{Genotypic variance } (\delta^2 g) = \frac{MSG - MSE}{r}$$

Where,

MSG = Mean Square due to Populations.

MSE = Mean Square Error

r = Number of replication

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

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental variance

Environmental variance ($\sigma^2 e$) = MSE

Where,

MSE = Mean Square Error

3.12.2 Estimation of genotypic coefficient of variation and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to the formula given by Burton (1952) and Singh and Chudhary (1985).

$$\text{Genotypic Co-efficient of Variation (GCV \%)} = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\overline{X}$ = Population mean

$$\text{Phenotypic Coefficient of Variation (PCV \%)} = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\overline{x}$ = Population mean

3.12.3 Estimation of heritability

Heritability in broad sense was estimated using the given formula suggested by Johnson *et al*. (1955).

$$\text{Heritability, } h^2b = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$=Phenotypic variance

3.12.4 Estimation of genetic advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al.*(1955).

$$\text{Genetic advanced (GA)} = \frac{\sigma^2 g}{\sigma^2 p} \times K \times \sigma p$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$=Phenotypic variance

$\sigma\, p$ = Phenotypic standard deviation

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

3.12.5 Estimation of genetic advance in percent of mean GA(%)

Estimate by the following formula suggested by Comstock and Robinson (1952).

$$\text{Genetic advance in percent of mean GA(\%)} = \frac{\text{GA}}{\overline{\text{X}}} \times 100$$

Where,

GA = Expected Genetic Advance

$\overline{\text{X}}$ = Population mean

3.12.6 Estimation of correlation

The genotypic and phenotypic correlation estimated by the formula suggested by Miller *et al.* (1958).

$$\text{Genotypic correlation } r_{gxy} = \frac{Cov_{gxy}}{\sqrt{(\sigma^2 g_x \times \sigma^2 g_y)}}$$

Where,

Cov_{gxy}= Genotypic covariance between the trait x and trait y
$\sigma^2 g_x$ = Genotypic variance of the trait x
$\sigma^2 g_y$ = Genotypic variance of the trait y

Similarly,

$$\text{Phenotypic correlation } r_{pxy} = \frac{Cov_{pxy}}{\sqrt{(\sigma^2_{px} \times \sigma^2_{py})}}$$

Where,

$Cov_{px\,y}$ = Phenotypic covariance between the trait x and y
σ^2_{px}= Phenotypic variance of the trait x
σ^2_{py} = Phenotypic variance of the trait y

3.12.7 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable. In order to estimate direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x1 and y is thus partitioned as follows:

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

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

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

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):$P^2_{RY} = 1- \sum P_{iy} .riy$

Where,

$P^2_{RY} = (R^2)$; and hence residual effect, $R =(P^2_{RY})^{½}$

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

riy = Correlation of the character with yield.

3.12.8 Estimation of Genetic Diversity

3.12.8.1 Principal component analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and population scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jager *et al.* 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.12.8.2 Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Digby *et al.* 1989).

3.12.8.3 Canonical vector analysis (CVA)

The canonical vector analysis compute a linear combination of original variability that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variability that can be used to discriminate between groups. Finally, a series of orthogonal transformations sequentially maximizing the ratio among groups within the group variations.

3.12.8.4 Average intra-cluster distances

The average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D2/n, where D2 is the sum of distances between all possible combinations (n) of the population included in the cluster. The square root of the average D2 values represents the distances (D) within cluster.

3.12.8.5 Clustering

To divide the populations of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the populations into required groups, the algorithm repeatedly transfers populations from one group to another so long as such transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two populations of different classes and so on.

CHAPTER IV

RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among 41 materials of *B. napus* populations and also to study the variability and interrelationship of *B. napus* in advanced populations through correlation and path coefficient for seed yield and different yield contributing characters.

The data were recorded on different characters such as days to 1st flowering, days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, 1000 seed weight (gm) and seed yield per plant (m). The data were statistically analyzed and thus obtained results are described below under the following heads:

- Mean performance
- Variability study in *Brassica napus*
- Heritability and genetic advance
- Correlation coefficient of characters
- Path coefficient analysis
- Genetic diversity analysis

4.1 Mean performance

Mean performance of 41genetic and yield related traits of populations were presented in Appendices IV. In the study significant variations were observed for most of the characters among 41 materials of *Brassica napus L.*

4.1.1 Days to 1st flowering

Considerable variations were observed among 41 materials for days to 1st flowering (table 2). In case of days to 1st flowering for line, it was ranged from 26.00 to 32.00 days. The days to 1st flowering were observed lowest (26.00 days) in Nap-2037 and Nap-179 and highest (32.00 days) was observed in

Nap-10015 and Nap-10019 (Appendix IV). The days to 1st flowering were observed in varieties 27.33 days in BARI-8 and 29.00 days in BARI-13 (Appendix IV). Singh *et al.* (2005); obtained ear populations on YSK-S501 × SS-2 in *B. campestris/rapa.* Singh *et al.* (1997); observed ear populations in PR-1108 × BJ-1235 in *Brassica juncea* L.

4.1.2 Days to 50% flowering

Considerable variations were observed among 41 materials for days to 50% flowering. In case of days to 50% flowering for line, it was ranged from 31.00 to 39.00 days. The days to 50% flowering were observed lowest (31.00 days) in Nap-0837 and Nap-179 and highest (39.00 days) was observed in Nap-10019 (Appendix IV). The days to 50% flowering were observed in varieties 32.33 days in BARI-8 and 34.00 days in BARI-13 (Appendix IV).

4.1.3 Plant height (cm)

Considerable variations were observed among 41 populations for plant height and it is ranged from 81.47 cm to 121.13 cm. In this study, the maximum plant height was observed in Nap-10019 (121.13 cm) whereas the minimum plant height was observed in Nap-0733-2 (81.47 cm). Plant height observed in the variety BARI-13 was 101.40 cm (Appendix IV). Chowdhury *et al.* (2004) observed dwarfness in PT-303 × Tori-7 in *B. rapa* L Tyagi *et al.*(2001); observed the highest variation in plant height among parents and their hybrid. These findings were closed resemblance to the reports of Chowdhury *et al.* (1993) and Yadava *et al.*(1993).

Plate 5 . Photograph showing 1st flowering in Nap- 2037

Plate 6. Photographs showing the maximum plant height of Nap-10019 and the minimum plant height of Nap-0733-2

4.1.4 Number of primary branches per plant

Significant variation on number of primary branches per plant was found among 41 populations including populations of *Brassica napus* and it is ranged from 2.00 – 3.67 (Appendix IV). Among the 41 plant materials, the highest number of primary branches per plant was observed in Nap-084, Nap-0885 and BARI-8 (3.67) whereas the minimum number of primary branches per plant was observed in Nap-0733-1, Nap-0733-2 and Nap-94006 (2.00) (Appendix IV). Number of primary branches per plant observed in the populations 2.67 in BARI-8 (Appendix IV). Number of primary branches per plant showed little differences. The value indicating the apparent variation not only due to populations but also due to the large influence of environment (Appendix IV). Chowdhury *et al*. (2004) found more primary branches in Sampad × Tori7 in *Brassica rapa* L. Singh *et al.* (2005) obtained maximum number of primary branches per plant in YSK-8501 × SS-1 in *B. jucea*. Chowdhary *et al*. (1993) found significant differences for number of primary branches per plant. Similar results were obtained by Rashid (2007) and Kumar *et al*. (1996).

4.1.5 Number of secondary branches per plant

For the number of secondary branches per plant, parents showed at a range from 1.00 to 3.67 (Appendix IV). However, among the 41 plant materials, population BARI-8 showed the highest number of secondary branches per plant (3.67) whereas the lowest (1.00) was found from Nap-9901, Nap-0864 Nap-0762 and Nap-0865 (Appendix IV). Number of secondary branches per plant were noticed 1.67 in the populations in BARI-13 (Appendix IV). Chowdhury *et al.* (2004) found the maximum secondary branches in Sampad × Din-2 in *Brassica rapa* L. Singh and Murty (1980) observed more secondary branches per plant in YSC-68 × SS-2 in *Brassica campestris* L. These findings are closing similar to the reports of Choudhary *et al*. (1993) and Mahmud (2008).

4.1.6 Number of siliqua per plant

Number of siliqua per plant were varied from 88.00 to 204.00 table (2) and it was significantly varied among the 41 plant materials (Appendix IV). The number of siliqua per plant was observed the highest in Nap-10019 (204.00) followed by BARI-8 (203.00). Whereas the minimum number of siliquae per plant observed in Nap-0865 (88.00) (Appendix IV). Number of siliqua per plant observed105.33 in the variety in BARI-13 and 203.00 in BARI-8 (Appendix IV). These combinations could be selected for the future breeding program to obtain desirable higher number of siliqua per plant. Chowdhury *et al.* (2004); found the maximum siliquae in Sampad × Din-2 in *Brassica rapa* L. Singh and Murty (1980), observed more siliquae per plant in YSP842 × SS-3 in *Brassica campestris L.*

4.1.7 Length of siliqua (cm)

Siliqua length of poplation ranged from 6.98 to 9.27 cm. Length of siliqua was observed the highest in Nap-10009 (9.27 cm) followed by Nap-10015 (9.21 cm) whereas the minimum length of pod was observed in Nap-2037 (6.98 cm) (Appendix IV).

Plate 7. Photograaphs showing maximum and minimum lengh of siliqua between G_{13}= Nap-10009 and G_1= Nap-2037

The varieties length of siliqua was observed 8.43 cm in BARI-13 and 8.33 cm in BARI-8 (Appendix IV).

4.1.8 Number of seeds per siliqua

Number of seeds per siliqua varied from 18.00 to 28.33. The number of seeds per siliqua was observed the highest in Nap-10015 (28.33) whereas the second highest was found in Nap-10009 (27.33). The minimum number of seeds per siliqua observed in Nap-2057 (18.00) (Appendix IV). The number of seeds per siliqua observed 23.33 in BARI-13 and 22.00 in BARI-8 (Appendix IV). Choudhury *et al.*(2004) found the highest seeds per siliqua in Dhali × Sampad in *Brassica rapa* L. Singh *et al.* (2005); obtained more seeds per siliquae in YSP-842 × YSK-8501 in *B. juncea.*

4.1.9 Thousand seed weight (gm)

Thousand seed weight in B. napus varied with some extent i.e. from 3.00 to 4.33 gm in line. Thousand seed weight was found maximum in Nap-205 (4.33 g) where as the minimum thousand seed weight was found in Nap-2037, Nap-2013 and Nap-2012 (3.00 g) (Appendix IV). Thousand seed weight observed in the varieties 3.67 g in BARI-13 and BARI-8 (Appendix IV). Singh *et al.* (2005); observed more seed weight per plant in YSC-68 × SS-2 in *Brassica campestris* L. Chowdhury *et al*. (2004); obtained the highest seed weight in Dhali × Sampad in *B. rapa*.

4.1.10 Seed yield per plant (g)

Seed yield per plant was found at diversely in different populations including populations. Seed yield of the populations varied from 4.20 to 8.87 g in populations. Yield is the most outstanding character and all the research work and objectives are dependent on yield. The highest amount of yield per plant was observed in Nap-100208 (8.87 gm) followed by Nap-10019 (8.60 g) whereas the minimum yield per plant was observed in Nap-108 (4.20 g) (Appendix IV). The yield per plant of the varieties were 5.93 in BARI-13 and

8.33 in BARI-8. The highest seed yield in Agroni × Tori 7, Agroni × BARI sar-6 and Shafal × BARI sar-6 in *Brassica rapa* L. Choudhury *et al.* (2004); obtained the highest seed yield in M-27 × Din-2 in *Brassica rapa L*. Singh *et al.* (2005); observed more seed yield per plant in YSP-842 × YSK-8501 in *Brassica campestris* L.

4.2 Variability study in *Brassica napus*

Significant variations were observed for most of the characters among 41 materials of *Brassica napus*. The values of mean, CV%, phenotypic variances, genotypic variances, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters were shown in Table 2 and 4.

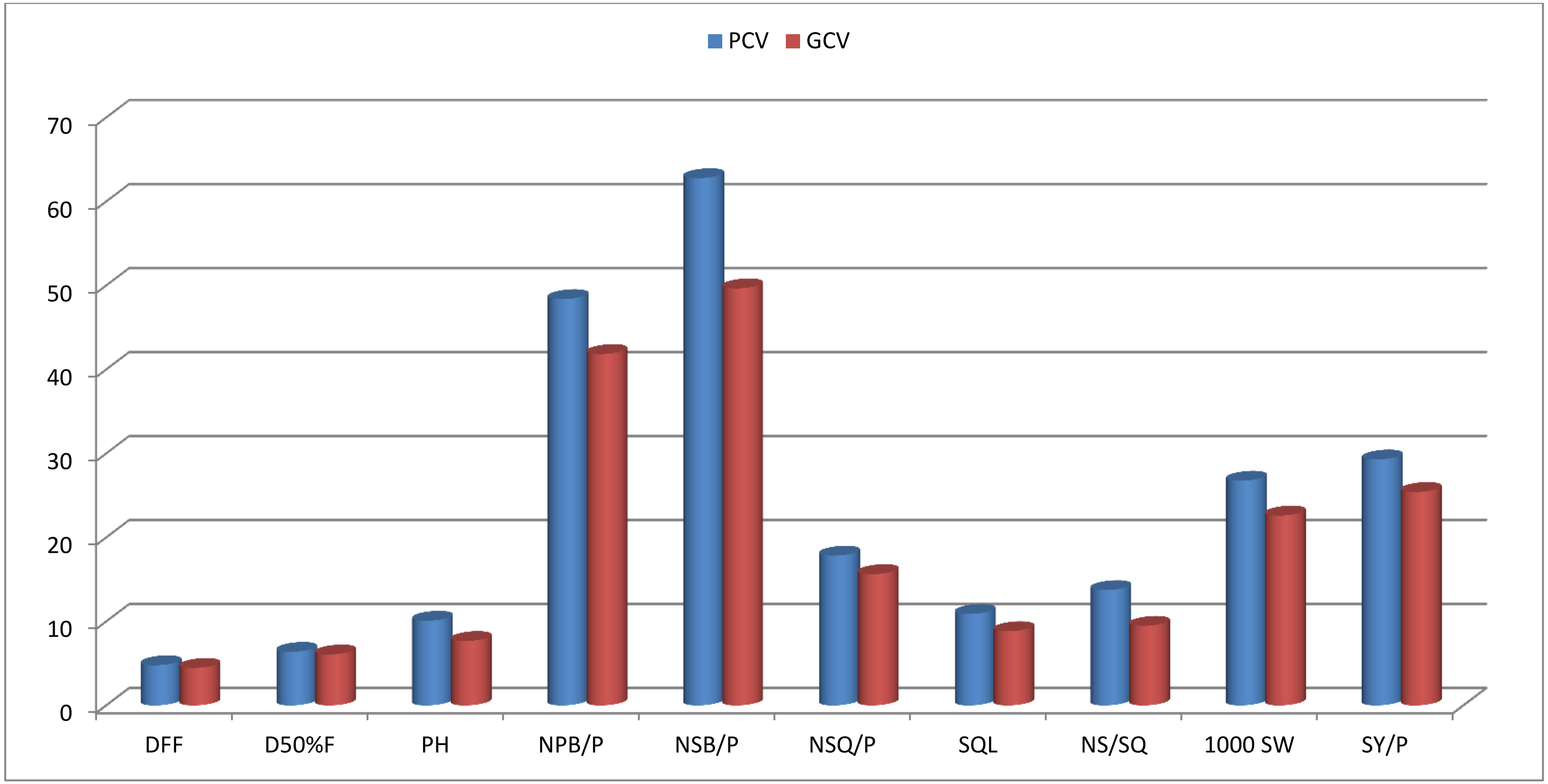

Figure 1. Genotypic and phenotypic coefficient of variation in *Brassica napus* .

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

Table 2. Range, Mean, CV (%) and standard deviation of 41 *Brassica napus* populations

Parameters	**Range**		**Mean**	**CV(%)**	**SD**	**SE(±)**
	Maximum	**Minimum**				
DFF	32.00	26.00	28.54	3.91	1.306	0.174
D50%F	39.00	31.00	33.97	3.54	2.099	0.188
PH	121.13	81.47	100.77	6.56	8.620	1.032
NPB/P	3.67	2.00	2.80	12.27	0.441	0.106
NSB/P	3.67	1.00	1.86	13.34	0.596	0.112
NSQ/P	204.00	88.00	134.58	7.12	28.647	5.701
SQL	9.27	6.98	8.27	6.38	0.542	0.082
NS/SQ	28.33	18.00	23.01	13.89	2.550	0.499
1000 SW	4.33	3.00	3.63	14.32	0.309	0.081
SY/P	8.87	4.20	6.27	9.08	1.218	0.285

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant.

Table 3. Analysis of variance for different characters in *Brassica napus* populations

Parameters	**Mean sum of square**		
	Replication (r-1) = 2	**Population (G-1) = 40**	**Error (r-1)(G-1) = 80**
DFF	0.317	5.12**	0.242
D50%F	8.691	13.21**	0.449
PH	12.500	222.90*	43.655
NPB/P	0.463	4.58**	0.463
NSB/P	0.618	3.07**	0.51
NSQ/P	44.083	1461.99*	133.49
SQL	0.598	1.88**	0.278
NS/SQ	12.326	19.50**	5.218
1000 SW	0.886	2.29**	0.27
SY/P	3.996	8.45**	0.832

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

4.2.1 Days to 1st flowering

Phenotypic and genotypic variance for days to 1st flowering was observed as 1.87 and 1.63, respectively with low differences between them, suggested low influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (PCV) (4.79) was higher than the genotypic coefficient of variation (GCV) (4.47) which suggested that environment had a significant role on the expression of this trait (Table 4). High genotypic and phenotypic coefficient of variation was recorded by Lekh *et al*. (1998). Significant genetic variability in days to 1st flowering in *B. napus* was also observed by Singh *et al*. (2005).

4.2.2 Days to 50% flowering

Considerable variations were observed among 41 materials for days to 50% flowering. Phenotypic and genotypic variance for days to 50% flowering was observed as 4.70 and 4.25, respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (PCV) (6.38) was higher than the genotypic coefficient of variation (GCV) (6.07) (Table 4), which suggested that environment had a significant role on the expression of this trait.

4.2.3 Plant height (cm)

Phenotypic variance and genotypic variance were observed as 103.40 and 59.75, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait.

Table 4. Estimation of genetic parameters in ten characters of 41 *Brassica napus* populations

Parameters	**σ^2p**	**σ^2g**	**σ^2e**	**PCV**	**GCV**	**ECV**	**Heritability**	**GA (5%)**	**GA in % mean**
DFF	1.87	1.63	0.24	4.79	4.47	1.72	87.04	2.34	8.205
D50%F	4.70	4.25	0.45	6.38	6.07	1.97	90.45	3.91	11.513
PH	103.40	59.75	43.66	10.09	7.67	6.56	57.78	10.26	10.182
NPB/P	1.84	1.37	0.46	48.38	41.84	24.30	74.77	0.68	24.260
NSB/P	1.36	0.85	0.51	62.78	49.66	38.39	62.59	0.77	41.316
NSQ/P	576.32	442.83	133.49	17.84	15.64	8.59	76.84	45.34	33.693
SQL	0.81	0.53	0.28	10.90	8.84	6.38	65.76	0.73	8.879
NS/SQ	9.98	4.76	5.22	13.73	9.48	9.93	47.71	2.51	10.891
1000 SW	0.94	0.67	0.27	26.76	22.61	14.31	71.38	0.45	12.517
SY/P	3.37	2.54	0.83	29.28	25.42	14.55	75.32	1.89	30.142

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

The estimates of PCV (10.09%) and GCV (7.67%) also indicated presence of considerable variability among the populations for this trait (Table 4). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al*. (2001).

4.2.4 Number of primary branches per plant

Phenotypic variance and genotypic variance were observed as 1.84 and 1.37, respectively. Relatively low differences between them indicating low environmental influences on these character and relatively high difference between PCV (23.193%) and GCV (11.93%) value indicating the apparent variation not only due to populations but also due to the large influence of environment (Table 4). Choudhury *et al.* (1993) also found significant differences for number of primary branches per plant.

4.2.5 Number of secondary branches per plant

Phenotypic variance and genotypic variance were observed as 1.36 and 0.85, respectively. Higher estimate of PCV (62.78%) and GCV (49.66%) values indicated presence of considerable variability among the populations for this trait (Table 4). Lekh *et al.* (1998) found highest genotypic coefficient of variation for number of secondary branches while working on 24 populations of *Brassica napus*. Choudhury *et al.* (1993) found significant differences for number of secondary branches per plant.

4.2.6 Number of siliqua per plant

Number of siliqua per plant showed the highest phenotypic variance (576.32) and genotypic variance (442.83) with large environmental influence and the difference between the PCV (17.84%) and GCV (15.64%) indicated existence of adequate variation among the populations (Table 4).

4.2.7 Length of siliqua (cm)

Length of siliqua showed phenotypic variance (0.81) and genotypic variance (0.53) with little difference between them indicating that they were less responsive to environmental factors for their phenotypic expression and relatively medium PCV (10.90%) and GCV (8.84%) indicating that the population has moderate variation for this trait (Table 4). High co-efficient of variation for this trait for both genotypic and phenotypic variability was recorded by Masood *et al.* (1999). High genetic variability for this trait was also found by Olsson (1990).

4.2.8 Number of seeds per siliqua

The phenotypic and genotypic variances for this trait were 9.98 and 4.76 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 13.73% and 9.48% respectively for number of seeds per siliqua which indicating that medium variation existed among different populations (Table 4). Similar variability was also recorded by Kumar and Singh (1994).

4.2.9 Thousand seed weight (g)

Thousand seed weight showed very low genotypic (0.94) and phenotypic (0.67) variance with low differences indicating that they were low responsive to environmental factors. The phenotypic co-efficient of variation (PCV) (26.76%) and genotypic coefficient of variation (GCV) (22.61%) were close to each other (Table 4). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Significant variability for this trait was also found by Kumar and Singh (1994).

4.2.10 Yield per plant (g)

The phenotypic variances and genotypic variances for this trait were 3.37 and 2.54 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The values of GCV and PCV were 25.42% and 29.28% indicating that the population has considerable variation for this trait (Table 4). Similar variability was also found by Khera and Singh (1988).

4.3. Heritability and genetic advance

4.3.1 Days to 1st flowering

Days to 1st flowering exhibited high heritability (87.04%) with low genetic advance (2.34) and genetic advance in percentage of mean (8.205%) indicated that this trait was controlled by non-additive gene (Table 4). This results support the reports of Malik *et al.* (2000).

4.3.2 Days to 50% flowering

Days to 50% flowering exhibited high heritability (90.45%) with low genetic advance (3.91) and genetic advance in percentage of mean (11.513%) indicated that this trait was controlled by non-additive gene (Table 4).This results supported the reports of Malik *et al.* (1995).

4.3.3 Plant height (cm)

Plant height shows moderately high heritability 57.78% with low genetic advance of 10.26 and genetic advance in percentage of mean of 10.182% (Table 4), revealed that this trait was controlled by non-additive gene (Table 4). High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *et al.* (1986).

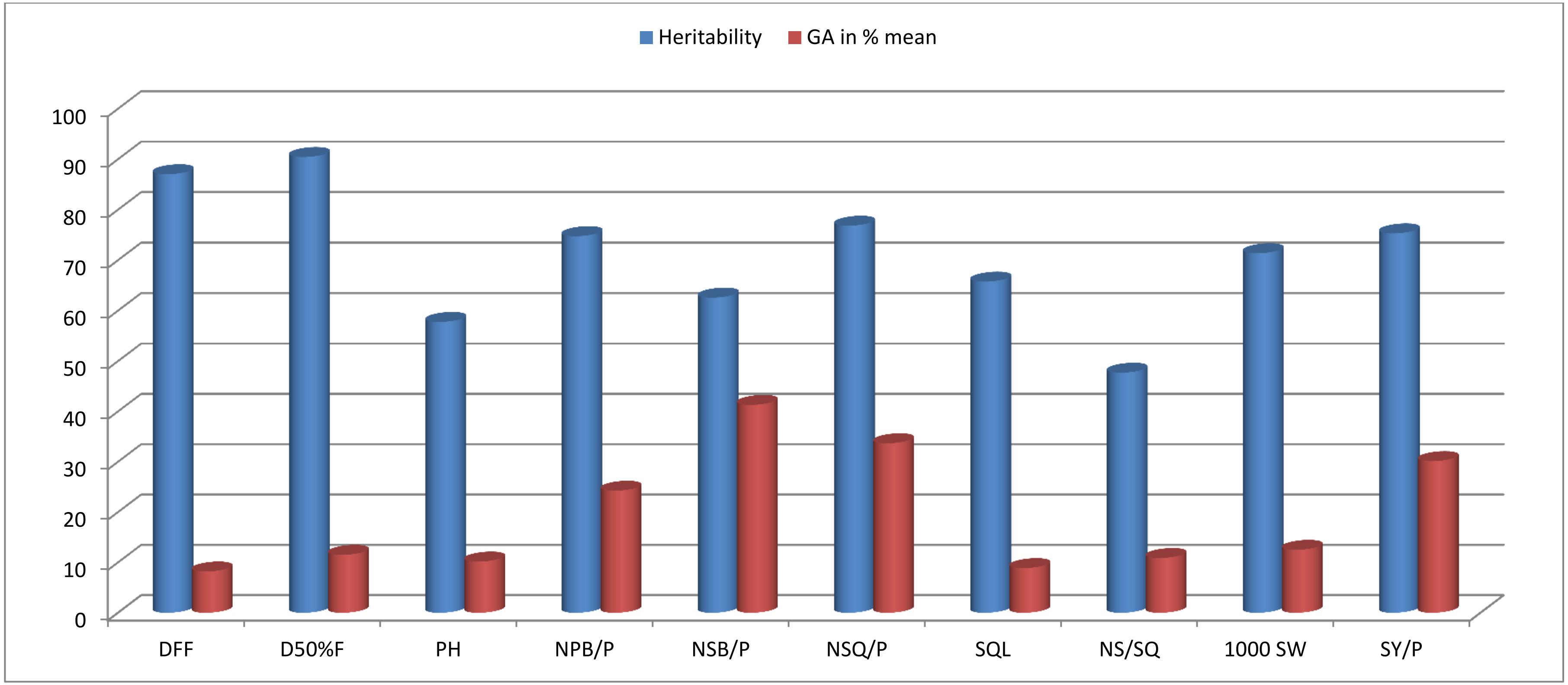

Figure 2. Heritability and genetic advance over mean in *Brassica napus*

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seedyield per plant.

Heritability and genetic advance in percentage of mean are shown in Figure 1.

4.3.4 Number of primary branches per plant

Number of primary branches per plant exhibited moderately high heritability 74.86 with low genetic advance of 0.68 and genetic advance in percentage of mean of 24.26%, which revealed that this trait was controlled by non-additive gene (Table 4). As a whole, the high heritability and the consequent low genetic advance indicated the lower possibility of selecting populations for this trait. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by Singh *et al.* (1997). Yadava *et al.* (1993) found high heritability and genetic advance for number of primary branches per plant.

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant exhibited moderately high heritability (62.50%) with low genetic advance 0.77 and genetic advance in percentage of mean (41.316%), such results revealed that this trait was controlled by non-additive gene (Table 4). As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting populations. Moderately high heritability coupled with low genetic advance was also found by Singh *et al.* (1997). Sheikh *et al.* (1999); found high heritability coupled with high genetic advance for number of secondary branches per plant while working with 24 populations of toria.

According to johson *et al.* (1955)

Low heritability – Below 30 %

Medium heritability – 30-60 %

High heritability – Above 60%

4.3.6 Number of siliqua per plant

Number of siliqua per plant exhibited moderately high heritability 76.84% with high genetic advance 45.34 and genetic advance in percentage of mean 33.693% (Table 4). These results revealed the possibility of predominance of additive gene action in the inheritance of this trait. This indicates that selection for traits with high heritability with lead to fast genetic improvement of a trait that is by increasing the frequency of favorable allelles by repeated mass selection or hybridization between selected genotypes, showing varying degree of variation for such traits. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). Mahmud *et al.* (2008); reported that the number of siliqua per plant were highly heritable coupled with high genetic advance.

4.3.7 Siliqua length

Siliqua length showed moderately high heritability (65.76%) with low genetic advance (0.73) and genetic advance in percentage of mean 8.879% indicated that this trait was controlled by non-additive gene (Table 4). High heritability for this trait was observed by Chaudhury *et al.* (1993).

4.3.8 Number of seeds per siliqua

Number of seeds per siliqua showed moderately high heritability 47.71% coupled with high genetic advance 2.51 and high genetic advance in percentage of mean 10.891%, indicated that this trait was controlled by additive gene and selection for this character would be effective (Table 4). High heritability coupled with high genetic advance for this trait was also observed by Singh (2004).

4.3.9 Thousand seed weight (g)

Thousand seed weight exhibited high heritability 71.28% with low genetic advance 0.45 and genetic advance in percentage of mean 12.517%, revealed that this trait was controlled by non-additive gene (Table 4).

Johnson *et al*. (1955) ;reported that heritability estimates along with genetic group were more useful in prediction selection of the best individual. High heritability for this trait was also observed by Yadava *et al.* (1993). Singh *et al.* (1997); reported the high heritability and genetic advance for thousand seed weight.

4.3.10 Seed yield per plant

Seed yield per plant showed high heritability 75.37% with high genetic advance (1.89) and high genetic advance in number of seed per sliliqua that is hghly significant . Moderate seed yield found in plant hight 0.41 that is significant .Percentage of mean 30.142% indicated this trait was controlled by additive gene and selection for this character would be effective (Table 4). High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999).

High heritability and genetic advance for seed yield per plant was reported by Singh (2004) while working with 22 populations of *B. napus*.

4.4 Correlation coefficient of characters

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for 41 populations of *B. napus* are shown in Table 5 and 6.

Table 5. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different population of *Brassica napus*

Characters	**D50%F**	**PH**	**NPB/P**	**NSB/P**	**NSQ/P**	**SQL**	**NS/SQ**	**1000 SW**	**SY/P**
DFF	0.726**	0.525**	-0.036	0.121	0.383*	0.226	0.037	-0.016	0.389*
D50%F		0.637**	-0.11	0.146	0.510**	0.171	0.032	-0.248	0.347*
PH			0.115	0.225	0.689**	0.205	0.145	-0.239	0.401**
NPB/P				0.507**	0.349*	-0.15	-0.027	-0.142	0.334*
NSB/P					0.549**	-0.001	0.147	-0.195	0.359*
NSQ/P						0.166	0.278	-0.181	0.728**
SQL							0.462**	0.022	0.197
NS/SQ								-0.158	0.256
1000 SW									0.108

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

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

Characters	**D50%F**	**PH**	**NPB/P**	**NSB/P**	**NSQ/P**	**SQL**	**NS/SQ**	**1000 SW**	**SY/P**
DFF	0.266	0.174	-0.144	0.036	0.107	0.079	0.114	-0.032	0.168
D50%F		0.258	-0.042	0.072	0.288	0.066	0.078	-0.103	0.152
PH			0.048	0.057	0.314*	0.107	0.063	-0.088	0.272
NPB/P				0.311*	0.411**	-0.044	-0.048	-0.116	0.396**
NSB/P					0.308*	-0.033	0.036	-0.094	0.317*
NSQ/P						0.054	0.436**	-0.106	0.307*
SQL							0.247	0.124	0.092
NS/SQ								-0.071	0.185
1000 SW									0.044

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

4.4.1 Days to 1st flowering

Days to 1st flowering showed highly signifcant and positive correlation with days to 50% flowering (G = 0.726) indcated that if days to 1st flowering increased then days to 50% flowering also increased.Days to 1st flowering exhibited signifcant and positive correation with plant height (G = 0.525**, P = 0.174), number of siliqua per plant (G = 0.383*, P = 0.107) and seed yield per plant (G = 0.389, P = 0.168) also found. It also exhibited insignificant and positive interaction with number of primary branches per plant (G = 0.121, P = 0.036), siliqua length (cm) (G = 0.226, P = 0.079) and number seeds per siliqua (G = 0.037, P = 0.114). However, it had insignificant and negative interaction with NPB/P (G = -0.036, P = -0.144) and 1000 seed weight (g) (G = -0.0.016, P = -0.032) (Table 5 and 6). Significant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Parveen (2007) also revealed that days to 1st flowering had insignificant and positive interaction with yield per plant.

4.4.2 Days to 50% flowering

Days to 50% flowering showed genotypically significant and positive correlation with plant height (G = 0.637) and number of siliqua per plant(G = 0.510,) indicated that if days to 50% flowering increased then plant height and number of siliqua per plant also increased. Significant and positive correlation was also fond with seed yield per plant (G = 0.347, P = 0.152). It also exhibited insignificant and positive interaction with number of secondary branches per plant(G = 0.146, P = 0.072), Siliqua length (G = 0.171, P = 0.066) and number of seeds per siliqua(G = 0.032, P = 0.078). However, it had insignificant and negative interaction with number of primary branches per plant(G = -0.11, P = -0.042) and 1000 seed weight (G = -0.248, P = -0.103) (Table 5 and 6). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Parveen (2007) also revealed that days to 50% flowering had insignificant and positive interaction with yield per plant.

4.4.3 Plant height (cm)

Plant height showed significant and positive interaction with number of siliqua per plant(G = 0.689, P = 0.314) and Seed yield per plant (G = 0.401, P = 0.272) (Table 5 and 6). Significant positive associations between plant height and other characters indicate that the traits were governed by same gene and simultaneous improvement would be effective. However, it had insignificant and negative interaction with 1000 seed weight (G = -0.239, P = -0.088) (Table 5 and 6).

Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. These findings are showed resemblance to the reports of Parveen (2007).

Significant positive correlation between plant height and seed yield was found by Verma and Sachan (2000). Chaudhary *et al.* (1993); found positive correlation of plant height with number of seed per siliqua, number of siliqua per plant. Basalma (2008) reported opposite result for this trait.

4.4.4 Number of primary branches per plant

Number of primary branches per plant showed positive and significant interaction with number of secondary branch (G = 0.507, P = 0.311) and seed yield per plant (g) (G = 0.334, P = 0.396). These suggesting if number of primary branches increases then yield per plant also increases. Malik *et al.* (2000) reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. However, it had insignificant and negative correlation was found with Siliqua length (G = -0.15, P = -0.044), NS/SQ (G = -0.027, P = -0.048) and 1000 seed weight (G = -0.142, P = -0.116) (Table 5 and 6). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Similar results were obtained by Rashid (2007).

4.4.5 Number of secondary branches per plant

Number of secondary branch showed highly significant and positive interaction with number of siliqua per plant (G = 0.549, P = 0.308) that the traits were governed by same gene and simultaneous improvement would be effective and branching was an important contributor to yield , independent of its association with plant size (Table 5and 6). It had significant and positive interaction with Seed yield per plant (G = 0.359, P = 0.317) which indicates that seed yield per plant increases with the increasing of number of secondary branches per plant. It had insignificant and negative correlation with siliqua length (G = -0.001, P = -0.033) and 1000 seed weight(G = -0.195, P = -0.094) (Table 5 and 6).

4.4.6 Number of siliqua per plant

Siliqua per plant showed highly significant genotypically and positive correlation with Seed yield per plant (G = 0.728, P = 0.307) (Table 5 and 6). Whereas the insignificant and positive interaction was found in Siliqua length (G = 0.166, P = 0.054) and number of seed per siliqua (G = 0.278, P = 0.436) (Table 5 and 6). It had insignificant and negative interaction with 1000 seed weight (G = -0.181, P = -0.106). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Tyagi *et al.* (2001) reported that number of seed per siliqua had positive and insignificant effect on seed yield per plant.

4.4.7 Siliqua length (cm)

Siliqua length showed genotypically significant and positive correlation with number of seeds per siliqua (G=0.462) indicated that the traits were governed by same gene and simultaneous improvement would be effective. It also showed insignificant and positive correlation with 1000 seed weight(G = 0.022, P = 0.124) and yield per plant (G=0.197, P=0.092) (Table 5 and 6). Indicated that if siliqua length increased then yield per plant increased. Nasim *et al*. (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.4.8 Number of seeds per siliqua

Number of seeds per siliqua showed insignificant and negative interaction with 1000 seed weight (G = -0.158, P = -0.071) (Table 5 and 6). However, it had insignificant and negative interaction with thousand seed weight but positive interaction with yield per plant (G = 0.256, P = 0.185) (Table 5 and 6). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.4.9 Thousand seed weight

Thousand seed weight showed insignificant and positive interaction with yield per plant (G=0.108, P=0.044) (Table 5 and 6). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors.

4.5 Path Coefficient analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on seed yield per hector. In order to find out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and days to 1st flowering, days to 50% flowering, plant height , number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, length of siliqua , number of seeds per siliqua and thousand seed weight were causal (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for *B. napus* is presented in Table 7.

4.5.1 Days to 1st flowering

Path co-efficient analysis revealed that, days to 1st flowering had positive direct effect (0.2941) on yield per plant. Days to 50% flowering (0.4028), number of secondary branches per plant (0.0924), number of siliqua per plant (0.0157) and length of siliqua (cm) (0.0018) had positive indirect effect on yield per plant. Plant height (cm) (-0.1026), number of primary branches (-0.0240), number of seeds per siliqua (-0.0256) and thousand-seed weight (g) (-0.0071) had negative indirect effect on yield per plant (Table 7). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant.

4.5.2 Days to 50% flowering

Path co-efficient analysis revealed that, days to 50% flowering had positive direct effect (0.3944) on yield per plant. Days to 1st flowering (0.3012), number of secondary branches per plant (0.0627), number of siliqua per plant (0.0214) and length of siliqua (cm) (0.0043), had positive indirect effect on yield per plant, whereas plant height (cm) (-0.2014), number of primary branches (-0.1623), number of seeds per siliqua (-0.0133) and thousand-seed weight (g) (-0.0092) had negative indirect effect on yield per plant (Table 7).

4.5.3 Plant height

Path analysis revealed that plant height had positive direct effect (0.3011) on yield per plant. It had positive indirect effect on days to 1st flowering (0.2946), days to 50% flowering (0.3217), number of secondary branches (0.0529), number of siliqua per plant (0.0244) and thousand-seed weight (0.0314) (Table 7). Varshney (1986),worked with several strains of *B. rapa* and observed that plant height had the negative direct effect on yield. On the other hand, plant height had negative indirect effect on number of primary branches per plant (-0.1271), siliqua length (cm) (-0.0244) and number of seeds per siliqua (-0.0177) (Table 7). These results indicated that if plant height increases than seed yield also increases mostly through the positive indirect effect of plant height with other characters. Han (1990) also reported direct positive result for this character.

4.5.4 Number of primary branches per plant

Number of primary branches per plant had the negative direct effect on yield per plant (-0.2136). This trait had positive indirect effect on days to 1st flowering (0.1322), days to 50% flowering (0.3314), plant height (0.1124), number of secondary branches per plant (0.1024), and number of seed per siliqua . On the other hand, number of primary branches per plant effect number of siliqua per plant (-0.0086), siliqua length (-0.0063) and thousand-seed weight (g) (-0.0421) had the negative direct effect on yield (Table 7). Singh *et al.* (2005) in *B. juncea* reported that number of primary branches per plant had direct positive effect on seed yield.

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

Characters	**DFF**	**D50%F**	**PH**	**NPB/P**	**NSB/P**	**NSQ/P**	**SQL**	**NS/SQ**	**1000 SW**	**Genotypic correlation with yield**
DFF	**0.2941**	0.4028	-0.1026	-0.0240	0.0924	0.0157	0.0018	-0.0256	-0.0071	0.389*
D50%F	0.3012	**0.3944**	-0.2014	-0.1623	0.0627	0.0214	0.0043	-0.0133	-0.0092	0.347*
PH	0.2946	0.3217	**0.3011**	-0.1271	0.0529	0.0244	-0.0244	-0.0177	0.0314	0.401**
NPB/P	0.1322	0.3314	0.1124	**-0.2136**	0.1024	-0.0086	-0.0063	0.0058	-0.0421	0.334*
NSB/P	0.5291	0.8153	0.0523	0.1426	**0.2513**	0.0307	-0.2152	-0.0171	0.0337	0.359*
NSQ/P	0.6253	0.5162	0.0633	-0.0324	0.0733	**0.1031**	0.0052	0.0013	0.2015	0.728**
SQL	-0.2044	-0.1072	-0.0572	-0.0128	0.0529	0.0049	**-0.0820**	-0.0084	0.0197	0.197
NS/SQ	0.7021	0.6123	-0.0628	-0.0728	0.0622	-0.0024	-0.0087	**-0.0529**	0.0244	0.256
1000 SW	0.2316	0.2157	0.0218	0.0193	-0.179	0.0436	0.0044	-0.0033	**0.3813**	0.108

Residual Effect (R) = 0.3014

** Correlation is significant at the 0.01 level

* Correlation is significant at the 0.05 level

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

4.5.5 Number of secondary branches per plant

Path coefficient analysis revealed that number of secondary branches per plant had positive direct effect (0.2513) on yield per plant. It had positive indirect effect on days to 1st flowering (0.5291) days to 50% flowering (0.8153), plant height (0.0523), number of primary branches (0.1426), number of siliqua per plant (0.0307) and thousand-seed weight (0.0337). On the other hand, plant height had negative indirect effect on siliqua length (-0.2152) and number of seeds per siliqua (-0.0171) (Table 7). Yadava *et a*l. (1993) found the number of secondary branch had the highest positive direct effect on seed yield. Rashid (2007) observed that number of secondary branches per plant had the highest direct effect on seed yield per plant.

4.5.6 Number of siliqua per plant

Path coefficient analysis revealed that number of siliqua per plant had the positive direct effect (0.1031) on seed yield per plant. It had positive indirect effect on days to 1st flowering (0.6253), days to 50% flowering (0.5162), plant height (0.0633), number of secondary branch (0.0733), siliqua length (0.0052), number of seeds per siliqua (0.0013) and thousand-seed weight (0.2015). This trait had negative indirect effect on yield via number of primary branches per plant (-0.0324) (Table 7). This trait had significant positive genotypic correlation with yield per plant. Shalini *et al.* (2000) in *B. juncea* found the number of siliqua per plant had the highest direct effect on seed yield. Sheikh *et al.* (1999) revealed that siliqua per plant in *B. campestris* had highly positive direct effect on seed yield.

4.5.7 Length of siliqua

Path analysis revealed that length of siliqua had direct negative effect (-0.082) on yield per plant. This trait had also indirect positive effect on number of secondary branches per plant (0.0529), number of siliqua per plant (0.0049) and thousand-seed weight (g) (0.0197). On the other hand, length of siliqua showed indirect negative effect on days to 1st flowering (-0.2044), days to 50%

flowering (-0.1072), plant height (cm) (-0.0572), number of primary branches (-0.0128) and number of seeds per siliqua (-0.0084) (Table 7). Han (1990) reported that siliqua length had negative direct effect on yield per plant.

4.5.8 Number of seeds per siliqua

Path analysis revealed that number of seeds per siliqua had direct negative effect (- 0.0529) on yield per plant. This trait had also indirect positive effect on days to 1st flowering (0.7021), days to 50% flowering (0.6123), number of secondary branches per plant (0.0622) and 1000 seed weight (0.0244). Similarly, this trait showed indirect negative effect on plant height (-0.0628), number of primary branches per plant (-0.0728), number of siliqua per plant (-0.0024) and siliqua length (-0.0087) (Table 7). The negative direct effect was mainly counter balanced by indirect positive effect of different characters. Rashid (2007) reported that number of seeds per siliqua had direct positive effect on yield per plant. Parveen (2007) also found similar results for this trait.

4.5.9 Weight of 1000 seeds

Thousand seed weight had positive direct effect on yield per plant (0.3813). It had positive indirect effect on days to 1st flowering (0.2316), days to 50% flowering (0.2157), plant height (0.0218), number of primary branches per plant (0.0193), number of siliqua per plant (0.0436) and siliqua length (0.0044) (Table 7). Accordingly, this trait showed negative indirect effect on number of secondary branches per plant (-0.179) and number of seeds per siliqua (-0.0033) (Table 7). Siddikee (2006) reported that thousand seed weight had the highest positive direct effect on seed yield per plant.

4.6 Genetic diversity of the *Brassica napus*

Genetic diversity was analyzed using GENSTAT software program. Genetic diversity analysis involves several steps i.e. estimation of distance between the varieties, clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique were required to illustrate the results more clearly and it was obvious from the results of many researchers used multivariate techniques.

4.6.1 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1-Z_2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 3. The position of the populations in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the populations.

4.6.2 Principal component analysis (PCA)

The PCA gives Eigen values of principal component axes of coordination of populations with the first axes totally accounted for the variation among the populations, whereas three of these Eigen values above unity accounted for 66.36% (Table 8). The first two principal axes accounted for 55.50% of the total variation among the characters describing 41 advanced populations of *Brassica napus* L. populations is designed. According to the principal axes I and II, a two dimensional chart (Z_1 – Z_2) of the populations. The scatter diagram revealed that there were five apparent clusters. The populations were distantly located from each other (Figure 3).

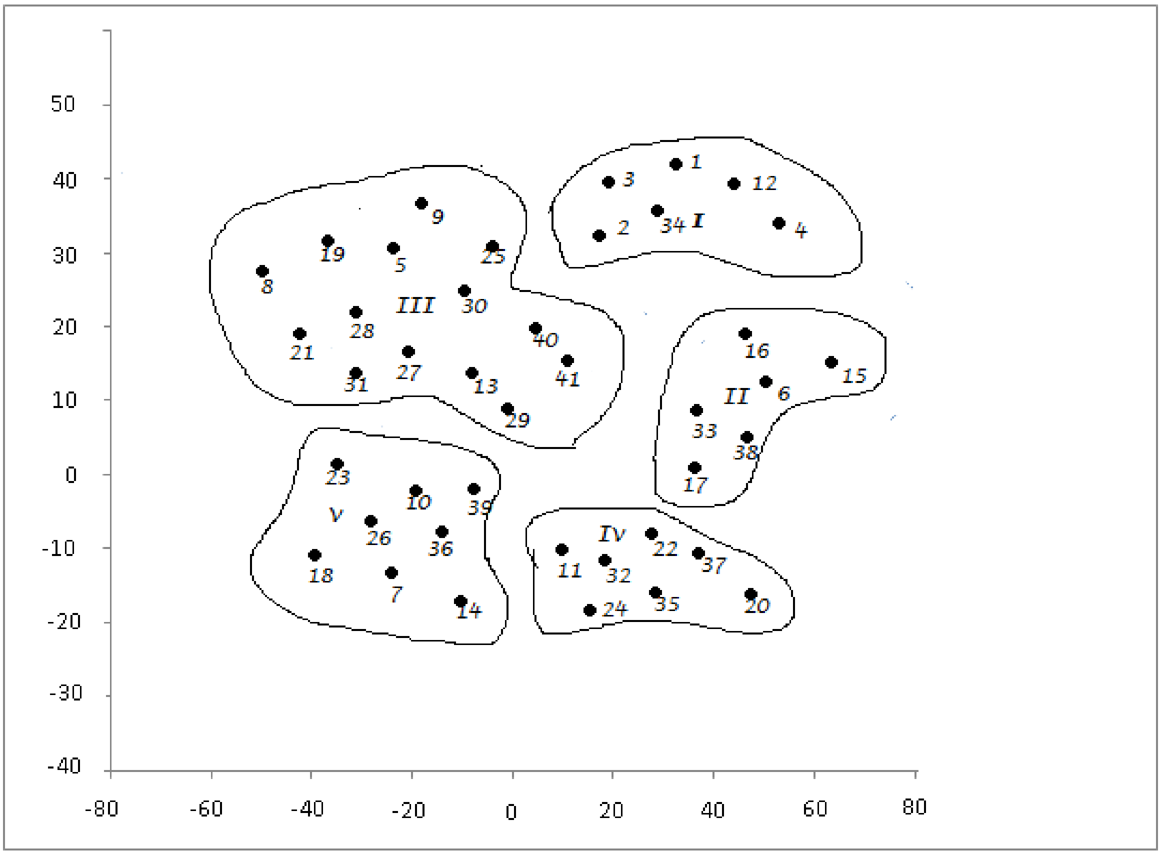

Fig 3. Scattered distribution of 41 *Brassica napus* populations on principal component score superimposed with clustering.

4.6.3 Non-hierarchical clustering

Forty one (41) *B. napus* populations were grouped into five different clusters nonhierarchical clustering (Table 9). These results confirmed the clustering pattern of the populations obtained through principal component analysis.

Mahmud *et al.* (2008) reported four clusters, five clusters in Brassica species reported five clusters in linseed. Cluster III had the highest number of populations (14) followed by V and IV which had 8 and 7 populations, respectively. On the other hand, Cluster I and II had 6 and 6 populations respectively (Table 9).

According to the cluster means (Table 10), cluster II showed better performance in case of days to 1st flowering (29.50) followed by cluster I (29.22) suggested that this cluster composed of late flowering populations. cluster I showed better performance in case of plant height (108.09), number of primary branches per plant (3.06) and number of secondary branches per plant (2.56). Thus indicates that population of this cluster could be used for parent in future hybridization program for higher plant height, number of primary branches per plant and number of secondary branches per plant. Cluster I showed better performance in case of number of siliqua per plant (185.78), siliqua length (8.48), number of seeds per siliqua (23.89) and seed yield per plant (8.29) suggested that population of this cluster could be used for parent in future hybridization program for higher seed yield per plant. Cluster IV showed higher 1000 seed weight (3.76) which indicated that population of this cluster could be used for parent in future hybridization program for higher 1000 seed weight. Moreover, Cluster V had lower cluster mean for days to 1st flowering (27.75) and days to 50% flowering (33.21) suggested that this cluster composed of early flowering populations.

4.6.4 Canonical variate analysis (CVA)

Canonical variate analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 11. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the populations of different groups.

Islam *et al* (2016) reported that the inter-cluster distances in *B. rapa* were larger than the intra-cluster distances. Uddin (1995) also reported similar result in mustard.

The highest inter-cluster distance was observed between clusters I and V (9.148), followed by between clusters I and IV (8.612), II and V (7.933), III and V (7.207) and I and II (6.144). In contrast, the lowest inter-cluster distance was observed between cluster II and IV (4.174) (Table 11). However, the maximum inter-cluster distance was observed between the clusters I and V (9.148) indicating populations from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. Dhillor *et al.* (1990) mentioned that maximum inter-cluster distance gave desirable segregants for the development of high yielding varieties with quality of oil for seed yield. On the other hand, the maximum intra-cluster distance was found in cluster I (0.478), which contained of 6 populations, while the minimum distance was found in cluster II (0.348) that comprises 6 populations. The different multivariate analysis was superimposed in Figure 3 from which it could be concluded that different multivariate techniques supplemented and confirmed one another.

A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, showing in the relative position (Figure 3). According to scatter diagram all the populations were apparently distributed into five clusters.

Table 8. Eigen values and percentage of variation in respect of 10 characters in *Brassica napus* L. populations

Principal Component axes	Eigen values	% of total variation accounted for	Cumulative percent
I	4.893	43.27	43.27
II	1.657	12.23	55.50
III	1.536	10.86	66.36
IV	1.012	8.29	74.65
V	0.814	6.42	81.07
VI	0.706	5.76	86.83
VII	0.492	4.64	91.47
VIII	0.406	3.86	95.33
IX	0.057	2.64	97.97
X	0.166	2.03	100.00

Table 9. Distribution of 41 *Brassica napus* L. populations in five different clusters

Cluster	Total no. of line	Population Number	Population Designation
I	6	G_1, G_2, G_3, G_4, G_{12}, G_{34}	Nap-2037, Nap-10020, Nap-10015, Nap-10019, Nap-2013, BARI-8
II	6	G_6, G_{15}, G_{16}, G_{17}, G_{33}, G_{38}	Nap-206, Nap-9901, Nap-0876, Nap-0762, Nap-0017, Nap-2001
III	14	G_5, G_8, G_9, G_{13}, G_{19}, G_{21}, G_{25}, G_{27}, G_{28}, G_{29}, G_{30}, G_{31}, G_{40}, G_{41}	Nap-9906, Nap-9904, Nap-084, Nap-10009, BARI-13, Nap-2066, Nap-10007, Nap-9908, Nap-2037, Nap-94006, Nap-0837, Nap-179, Nap-1007, Nap-2057
IV	7	G_{11}, G_{20}, G_{22}, G_{24}, G_{32}, G_{35}, G_{37}	Nap-0869, Nap-248, Nap-0733-1, Nap-9905, Nap-0885, Nap-10012, Nap-205
V	8	G_7, G_{10}, G_{14}, G_{18}, G_{23}, G_{26}, G_{36}, G_{39}	Nap-108, Nap-2022, Nap-2012, Nap-0865, Nap-0733-2, Nap-0136, Nap-1005, Nap-10014

Table 10. Cluster means for 10 characters of 41 *Brassica napus* L. populations

Characters	**Cluster**				
	I	**II**	**III**	**IV**	**V**
DFF	29.22	29.50	28.43	28.24	27.75
D50%F	35.39	35.11	33.64	33.29	33.21
PH	108.09	102.67	100.14	97.72	97.61
NPB/P	3.06	2.89	2.76	2.76	2.67
NSB/P	2.56	1.56	1.86	1.81	1.63
NSQ/P	185.78	135.82	130.62	120.09	114.88
SQL	8.48	8.45	8.22	8.29	8.05
NS/SQ	23.89	22.82	23.60	22.90	21.58
1000 SW	3.50	3.61	3.62	3.76	3.63
SY/P	8.29	7.29	6.26	5.52	4.63

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

Table 11. Average intra and inter-cluster distances (D^2) for 41 *Brassica napus* L. populations

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**0.478**	6.144	5.071	8.612	9.148
II		**0.348**	4.976	4.174	7.933
III			**0.394**	5.579	7.207
IV				**0.433**	6.211
V					**0.411**

*Bold figures denotes intra-cluster distance

It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the populations belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster I and V.

Goswami *et al.* (2006) found moderate genetic diversity between parents had the good general combining ability effect and high specific combining ability as well as high mean values in F_2 in Indian mustard. Main and Bahl (1989), reported that the parents separated by D^2 values of moderate magnitude generally showed higher Keeping this in view, it appears that the crosses between the populations belonging cluster I with cluster IV, cluster I with cluster III, cluster I with cluster II, and cluster II with cluster V might produce high heterosis in respect of yield, ear populations, tallness, higher number of siliqua per plant. Also the crosses between populations from cluster I with cluster V might produce high level of segregating population. So the genotypes belonging to cluster I, cluster IV, cluster III, cluster II and cluster V have been selected for future hybridization program.

4.6.5 Contribution of traits towards divergence of the populations

In vector I (Z_I) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were days to 50% flowering (4.893), plant height (1.657), secondary branches per plant (0.814) and siliqua per plant (0.706). In vector II (Z_2), the second axis of differentiation, primary branches per plant, number of seeds per siliqua, siliqua per plant and thousand seeds weight were important because all these characters had positive signs. On the other hand, primary branches per plant, siliqua length, seed per siliqua, thousand seed weight and seed yield per plant in the first axis of differentiation and siliqua length and seed yield per plant in the second axis of differentiation had a minor role in the genetic divergence because they had positive signs. Siliqua length and siliqua per plant in both the vectors had positive signs, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied. But factorial discriminate and Mahalanobis's D^2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

4.7 Selection of populations for future hybridization

Genotypically distant parents are able to produce higher heterosis (Rameeh, 2011) Results of the present studies indicated significant variation among the populations for all the characters studied. Number of siliqua per plant, siliqua length and seed weight per plant contributed the maximum towards yield improvement. Forty one (41) *Brassica napus* L. populations formed five different clusters. PCA and Cluster analysis gave similar results. Generally, diversity was influenced by the morphological characters, but not by the distribution of the populations, which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performance populations G_1 (Nap-2037), G_2 (Nap-10020), G_3 (Nap-10015), G_4 (Nap-10019), G_9 (Nap-084),

G_{13} (Nap-10009), G_{30} (Nap-0837), G_{31} (Nap-179), G_{32} (Nap-0885), G_{34} (BARI-8) and G_{37} (Nap-205) could be considered suitable populations for efficient hybridization in future. Involving of such diverse populations in crossing program could produce desirable segregants. So, more or less divergent populations are recommended to use as parents in future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with 41 *B. napus* populations in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, during the period from November 2018 to March 2019. The experiment was laid out in Randomized Complete Block Design with three replications. Data on various yield attributing characters such as, days to 1st flowering, days to 50% flowering, plant height ,number of primary branch per plant, number of secondary branch per plant, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g) and seed yield per plant (g) were recorded.

The analysis of variance showed significant differences among the populations for all the characters. From the mean performance it was observed that the days to 1st flowering was lowest in G_1 (Nap-2037) and G_{31} (Nap-179) but the highest in G_3 (Nap-10015) and G_4 (Nap-10019) whereas the lowest days to 50% flowering was observed in G_{30} (Nap-0837) and G_{31} (Nap-179) but the highest was in G_4 (Nap-10019). The highest plant height (121.13 cm) and number of siliqua per plant (204.00) were found in G_4 (Nap-10019) whereas the highest number of primary branches per plant (3.67) was observed in G_9 (Nap-084), G_{32} (Nap-0885) and G_{34} (BARI-8). Again, the highest number of secondary branches per plant (3.67) and 1000 seed weight (4.33 g) were found in G_{34} (BARI-8) and G_{37} (Nap-205), respectively. Similarly, the highest siliqua length (9.27 cm) and number of seeds per siliqua (28.33) were observed from G_{13} (Nap-10009) and G_3 (Nap-10015), respectively. The highest amount of yield per plant (8.87 g) was observed in G_2 (Nap-10020).

Days to 50% flowering (90.45) exhibited the highest value of heritability while number of seeds per siliqua (47.71) exhibited the lowest value of heritability.

High heritability with high genetic advance in percent of mean was observed for number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant 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. 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. In case of number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and seed yield per plant showed higher influence of environment for the expression of these characters. On the other hand, days to 1st flowering, days to 50% flowering, plant height, number of siliqua per plant and siliqua length showed least difference phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Correlation coefficient among the characters were studied to determine the association between yield and yield components. The significant positive correlation with seed yield per plant were found in days to 1st flowering (G = 0.389), days to 50% flowering (G = 0.347), plant height (cm) (G= 0.401), number of primary branches per plant (G = 0.334), number of secondary branch (G = 0.359) and siliqua per plant (G = 0.728). In addition, there were non-significant positive correlation with seed yield per plant was also found in siliqua length (G = 0.197), number of seeds per siliqua (G = 0.256) and thousand seed weight (G=0.108).

Path coefficient analysis revealed that days to 1st flowering, days to 50% flowering, plant height ,number of secondary branches per plant, number of siliqua per plant and thousand-seed weight had the positive direct effect on yield per plant, whereas, number of primary branches per plant, length of siliqua and number of seeds per siliqua had the negative direct effect on yield per plant. The path coefficient studies indicated that plant height, number of primary branches per plant, siliqua length (cm) and number of seeds per siliqua were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Genetic diversity among *B. napus* populations was performed through Principal Component Analysis, Cluster Analysis, Canonical Variate Analysis using GENSTAT computer program. The first two components with eigen value were greater than unity contributed a total of 55.50% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the populations were grouped into five different clusters. Cluster I, II, III, IV and V composed of six, six, fourteen, seven, and eight populations respectively. The highest inter-cluster distance was observed between clusters I and V indicating populations from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and IV.

Generally, diversity was influenced by the morphological characters, but not by the distribution of the populations, which indicated the importance of consumer preference and growers suitability.

Considering diversity pattern and other performance populations G_1 (Nap-2037), G_2 (Nap-10020), G_3 (Nap-10015), G_4 (Nap-10019), G_9 (Nap-084), G_{13} (Nap-10009), G_{30} (Nap-0837), G_{31} (Nap-179), G_{32} (Nap-0885), G_{34} (BARI-8) and G_{37} (Nap-205) could be considered suitable populations for efficient hybridization program in future. Involving of such diverse populations in crossing program could produce desirable segregants. So, more or less divergent populations are recommended to use as parents in future hybridization program.

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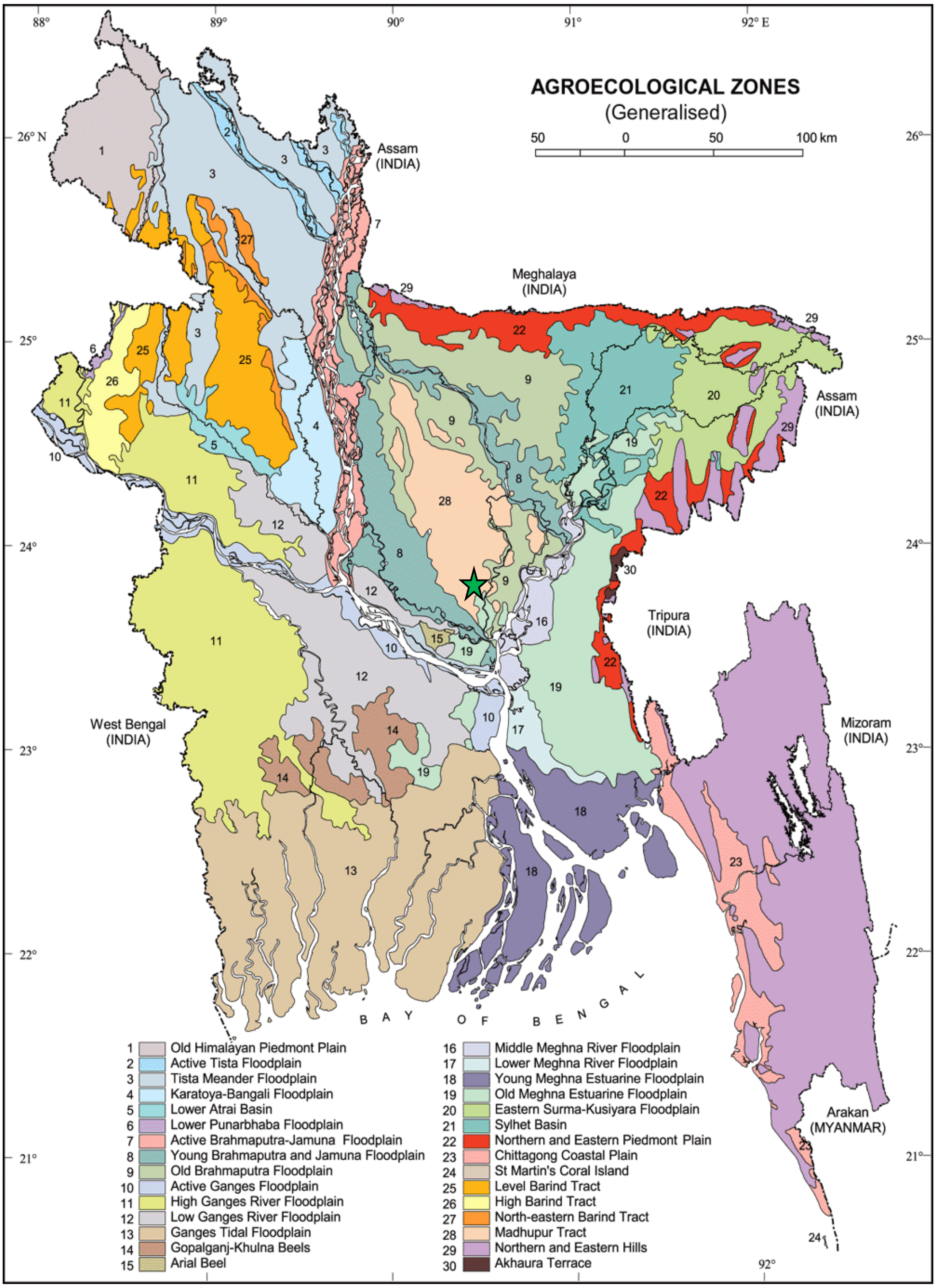
APPENDICES

Appendix I Map showing the experimental site under the study



☆ The experimental site under the study

Appendix II Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

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

Source: Central library, Sher-E-Bangla Agricultural University, Dhaka.

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

Month	**Air temperature (ºc)**		**Relative humidity (%)**	**Rainfall (mm) (total)**	**Sunshine (hr)**
	Maximum	**Minimum**			
November, 2018	31	18.0	99	227	**5.8**
December, 2018	32.4	16.3	69	0	**7.9**
January, 2019	29.1	13.0	79	0	**3.9**
February, 2019	**28.1**	**11.1**	**72**	**1**	**5.7**

Source: Bangladesh Meteorological Department (Climate and Weather Division), Agargoan, Dhaka – 1212

Appendix IV. Mean performance for 10 different characters in 41 populations of *Brassica napus*

Populations		DFF	D50%F	PH	NPB/P	NSB/P	NSQ/P	SQL	NS/SQ	1000 SW	SY/P
G_{1}	Nap-2037	26.00	32.33	97.37	3.00	2.67	164.67	7.73	24.67	3.00	8.07
G_{2}	Nap-10020	28.33	34.00	103.07	3.33	2.00	171.67	8.37	27.00	4.00	8.87
G_{3}	Nap-10015	32.00	36.00	114.93	3.00	2.33	186.33	9.21	28.33	3.33	8.07
G_{4}	Nap-10019	32.00	39.00	121.13	3.00	2.33	204.00	8.07	18.67	4.00	8.60
G_{5}	Nap-9906	28.33	32.33	101.27	2.67	1.67	132.00	8.20	24.67	3.67	6.00
G_{6}	Nap-206	30.00	37.00	107.20	3.00	2.67	163.67	9.03	26.33	4.00	7.20
G_{7}	Nap-108	27.00	32.33	96.33	3.00	1.67	110.67	7.93	20.67	3.33	4.20
G_{8}	Nap-9904	28.33	33.00	99.60	2.67	2.00	144.00	8.77	25.33	3.33	6.13
G_{9}	Nap-084	28.33	32.33	97.83	3.67	3.33	123.00	8.37	22.67	3.33	6.27
G_{10}	Nap-2022	28.33	32.67	120.13	3.33	2.00	152.67	7.93	19.00	3.67	5.00
G_{11}	Nap-0869	27.67	32.67	100.23	2.00	1.67	113.00	9.03	25.33	4.00	5.60
G_{12}	Nap-2013	29.67	38.67	111.13	2.33	2.33	185.00	9.17	22.67	3.00	7.80
G_{13}	Nap-10009	28.33	33.33	104.60	2.67	1.33	127.33	9.27	27.33	3.33	6.27
G_{14}	Nap-2012	28.00	38.00	116.53	2.67	2.00	151.00	7.73	22.00	3.00	4.67
G_{15}	Nap-9901	29.67	36.00	110.53	2.67	1.00	136.00	8.50	22.90	3.33	6.87
G_{16}	Nap-0876	30.00	36.67	101.67	2.67	1.33	118.33	7.77	20.00	3.33	7.60
G_{17}	Nap-0762	28.67	34.00	98.20	3.00	1.00	113.00	8.47	21.67	3.67	7.33
G_{18}	Nap-0865	28.00	32.00	85.07	2.67	1.00	88.00	7.83	21.00	3.33	4.40
G_{19}	BARI-13	29.00	34.00	101.40	2.67	1.67	105.33	8.43	23.33	3.67	5.93
G_{20}	Nap-248	28.33	34.00	95.12	2.67	2.33	102.33	8.47	22.67	3.67	5.67
G_{21}	Nap-2066	29.67	33.33	96.41	3.00	2.33	133.67	8.03	24.67	3.67	6.53
G_{22}	Nap-0733-1	28.33	31.67	94.10	2.00	1.33	104.33	8.27	21.00	3.67	5.53
G_{23}	Nap-0733-2	27.00	32.00	81.47	2.00	1.67	102.33	7.67	23.67	4.00	4.67
G_{24}	Nap-9905	27.00	32.33	98.27	3.00	1.33	108.33	8.43	21.00	3.67	5.27
G_{25}	Nap-10007	30.00	36.67	109.33	2.67	2.00	145.67	7.87	24.67	3.33	6.60
G_{26}	Nap-0136	27.33	33.00	102.60	2.33	1.33	122.67	8.83	24.33	4.00	5.13
G_{27}	Nap-9908	28.33	34.67	101.55	2.33	1.00	144.00	8.37	23.67	4.00	6.20
G_{28}	Nap-2037	28.67	35.00	108.00	2.33	2.00	133.00	6.98	21.00	3.67	6.07
G_{29}	Nap-94006	29.00	36.00	101.73	2.00	1.67	144.33	8.70	26.67	3.67	5.80
G_{30}	Nap-0837	27.33	31.00	98.93	3.00	2.33	117.00	8.27	23.67	3.67	6.47
G_{31}	Nap-179	26.00	31.00	95.30	3.33	1.33	123.33	7.85	24.33	3.67	6.67
G_{32}	Nap-0885	28.33	33.33	99.67	3.67	2.33	148.33	7.07	24.33	3.67	5.73
G_{33}	Nap-0017	28.00	32.00	102.13	3.00	1.33	159.33	8.73	25.33	3.67	7.73
G_{34}	BARI-8	27.33	32.33	100.93	3.67	3.67	203.00	8.33	22.00	3.67	8.33
G_{35}	Nap-10012	29.33	37.00	102.73	3.33	2.33	150.67	8.73	26.33	3.33	5.73
G_{36}	Nap-1005	29.00	33.33	95.60	2.33	1.67	94.33	8.63	21.67	4.00	4.33
G_{37}	Nap-205	28.67	32.00	93.93	2.67	1.33	113.67	8.03	19.67	4.33	5.13
G_{38}	Nap-2001	30.67	35.00	96.27	3.00	2.00	124.60	8.18	20.67	3.67	7.00
G_{39}	Nap-10014	27.33	32.33	83.13	3.00	1.67	97.33	7.87	20.33	3.67	4.67
G_{40}	Nap-1007	28.67	33.67	94.13	2.67	1.67	132.67	7.33	20.33	3.67	6.60
G_{41}	Nap-2057	28.00	34.67	91.87	3.00	1.67	123.33	8.60	18.00	4.00	6.13
SE(±)		0.174	0.188	1.032	0.106	0.112	5.701	0.082	0.499	0.081	0.285
CV(%)		3.91	3.54	6.56	12.27	13.34	7.12	6.38	13.89	14.32	9.08

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NSQ/P = Number of siliqua per plant, SQL = Siliqua length (cm), NS/SQ = Number of seeds per siliqua, 1000 SW = 1000 seed weight (g), SY/P = Seed yield per plant

Appendix V. Principal component score for 41 *Brassica napus* populations

Population no.	**Z1**	**Z2**
G_1	36.22	40.20
G_2	18.96	32.37
G_3	19.10	39.92
G_4	55.26	34.22
G_5	-26.22	30.2
G_6	30.36	12.36
G_7	-25.2	-13.25
G_8	-51.42	28.57
G_9	-18.27	37.48
G_{10}	19.75	-2.2
G_{11}	10.15	-10.24
G_{12}	44.22	39.57
G_{13}	-8.33	13.26
G_{14}	-10.26	-18.78
G_{15}	64.78	5.24
G_{16}	44.4	19.62
G_{17}	37.22	1
G_{18}	-40.12	-11.14
G_{19}	-38.2	31.2
G_{20}	46.42	-16.42
G_{21}	-43.44	19.8
G_{22}	27.55	-19.13
G_{23}	-37.44	1.56
G_{24}	16.44	-19.12
G_{25}	-5.73	31.04
G_{26}	-27.45	-7.24
G_{27}	-20.66	16.12
G_{28}	-32.24	21.22
G_{29}	-2.44	9.24
G_{30}	-10.14	25.04
G_{31}	-32.12	1305
G_{32}	18.92	-19.1
G_{33}	38.34	9.26
G_{34}	30.66	35.2
G_{35}	29.17	-2.2
G_{36}	-17.24	-8
G_{37}	38.67	-1.14
G_{38}	45	5.24
G_{39}	-8.24	-2.27
G_{40}	6.14	20.1
G_{41}	12.33	5.28