GENETIC ANALYSIS OF MORPHOLOGICAL PARAMETERS IN OIL SEED *Brassica*GENOTYPES

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CERTIFICATE

This is to certify that the thesis entitled **"GENETIC ANALYSIS OF MORPHOLOGICAL PARAMETERS IN OIL SEED *Brassica*GENOTYPES"**submitted to the **Department ofGenetics And Plant Breeding**, Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTERS OF SCIENCE (M.S.)** in**GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **FATEMA TUZ ZOHORA**, Registration No. **14-05960** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

June, 2022
Dhaka, Bangladesh

Dr.Md. Harun-Ur-Rashid
Professor
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DEDICATED

TO

MY BELOVED PARENTS

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ABSTRACT

The investigation was started with the selection process of potential populations of *Brassica rapa* L. The present investigation was carried out under field conditions to evaluate morphologicaltraits of 13 genotypes received from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, considering 13traits, using randomized complete block design with three replications during rabi season from November 2020 to February 2021 in research farm of Sher-e-Bangla Agricultural University, Dhaka. The analysis of variance showed significant variation in all the traits. The phenotypic variances were higher than genotypic variances with little differences in all traits. High heritability estimates were observed for days to 50% flowering, days to maturity, number of secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua and yield per plant. Correlation study revealed that seed yield per plant had a highly significant positive correlation with number of secondary branches per plant, length of siliqua, number of siliquae per plant and thousand seed weight at both genotypic and phenotypic level, while days to first flowering, days to 50% flowering and days to 80% maturity showed significant negative correlation with yield at both phenotypic and genotypic level. Path coefficient analysis found that number of secondary branches per plant had the highest positive direct effect followed by plant eight, root length,thousand seed weight and days to 80% maturity had medium level direct effects towards yield, while days to first flowering, days to 50% flowering, shoot length, number of primary branches per plant, number of siliquae per seed, length of siliqua and number of siliquae per plant had negative direct effects.Plant height exhibited lowest (76.15 cm) in G1. The highest number of primary branches per plant (5.80) was recorded in G9. The highest number of secondary branches per plant (6.13) was observed in G6. The highest number of siliquae per plant (155.53) was in G6, the number of seeds per siliqua (24.09) was found highest in G10. The thousand seed weight exhibited the highest (2.82 g) in G10 followed by G6 (2.74 g). The yield per plant was maximum (6.92 g) in G10.Considering the morphological and genetical parameters, the genotypes G1, G6, G9, G10 could be considered as a potential parent for future breeding program.

SOME COMMONLY USED ABBREVIATIONS

Abbreviation	Full word
%	Percentage
°C	Degree Celsius
AEZ	Agro-Ecological Zone
Agric.	Agriculture
Agril.	Agricultural
Agron.	Agronomy
ANOVA	Analysis of Variance
BBS	Bangladesh Bureau of Statistics
BD	Bangladesh
CEC	Cation Exchange Capacity
cm	Centi-meter
CV%	Percentage of Coefficient of Variation
cv.	Cultivar (s)
DAS	Days After Sowing
df	Degrees of Freedom
DM	Dry Matter
EC	Emulsifiable Concentrate
Eco.	Ecology
et al.	And Others
etc.	Etcetera
F_2	The second generation of a cross between two dissimilar homozygous parents
FAO	Food and Agricultural Organization
g	Gram (s)
G	Genotype
GN.	Genotype Number
HI	Harvest Index
hr.	Hour (s)
ICARDA	International Centre for Agricultural Research in Dry Areas
j.	Journal
kg	Kilogram (s)
m	Meter
M.P.	Muriate of Potash
m^2	Square Meter
MOA	Ministry of Agriculture
NARS	National Agricultural Research Institute
No.	Number
NS	Not Significant
ppm	Parts Per Million
R	Residual Effect
RCBD	Randomized Complete Block Design
Res.	Research

SAU	Sher-e-Bangla Agricultural University
Sci.	Science
SE	Standard Error
T.S.P.	Triple Super Phosphate
t/ha	Tonnes per Hectare
Univ.	University
var.	Variety

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CHAPTER I

INTRODUCTION

Oilseed *Brassica* is one of the most important and profitable crops in the world (Rahman *et al*., 2022). *Brassica* is the most important source of edible oil and consists of 380 genera and 3000 species. It is one of the ten most economically important plant families with a wide range of agronomic traits (Rahman *et al*., 2022). In Bangladesh, *Brassica* are economically important and high yielding oil seeds grown from long time that is why it is neededto improve oilseed *Brassica* varieties for successful expansion of cultivation of oilseed crops (Rahman *et al*., 2022). On a global scale, Brassicaceae oilseeds are major contributors to vegetable oil for daily living and nutritional purposes. Among the *Brassica* species, *B. napus*, *B. juncea,* and *B. rapa* are the most common and widely cultivated as oils seed crops (Choudhary *et al.*, 2015; Singh *et al*., 2016). Although *B. napus*, known as rapeseed, has become the main oilseed crop, in late-frost areas like China, Northern Europe, and Canada, short-duration and dwarf stature *B. rapa* cultivars are still used as ideal spring cultivars (Quijada *et al*., 2007).

B. rapa is widely cultivated as an oilseed crop in Bangladesh and India. *B. rapa* is the most common and important oilseed crop in Bangladesh, accounting 70% of total oil crop hectarage (BBS, 2016). It ranks first (66.21% of total oilseed crop cultivated area) with a cultivated area of 6.10 lakh ha, producing 409659.06 MT of oilseeds during the 2021–2022 fiscal year (BBS, 2022).

B. rapa species is more popular among Bangladeshi farmers than *B. napus* and *B. juncea* because of its short generation cycle (75–80 days) and suitability in cropping patterns, e.g. rice (transplanted aman)– mustard–rice (boro) and/or rice (transplanted aman)–mustard–maize (Sultana *et al*., 2021). In Bangladesh, the field-level yield of the existing *B. rapa* cultivars is 1.44 MT ha^{-1}(BBS, 2018), which is still less than half the target of 3 MTha^{-1} (Sultana *et al*., 2021). For this reason, the Bangladesh government has set the oilseed crop improvement research as a national priority.

In Bangladesh, edible oil consumption is increasing every year. According to the US Department of Agriculture (USDA, 2019), Bangladesh's annual edible oil consumption was at 2.85 million MT in 2019, which is 11% higher than the annual

consumption in 2018 (Sultana *et al.,* 2021). According to the USDA data, Bangladesh imported about 2.8 million MT of edible oil in the year 2019–2020 and spent two billion US dollars in the fiscal year 2017–2018 for importing both soybean and palm oil to meet the domestic demand(Rahman *et al*., 2022). Unless measures are taken to increase the domestic production of edible oil, the country will continue to lose billions to the foreign market. Moreover, the winter crops in Bangladesh competes with one another due to the limited planting area. Hence, to reduce the import of oil, the only alternative is to increase the yield potential of oil crops. Furthermore, the nutritional quality of oil favorable for human health and consumption is also a major concern. Based on the above-mentioned concerns, steps should be taken to develop high-yielding and better-quality mustard cultivars to satisfy the country's demand for edible oils.

The genus *Brassica* has been categorized into three groups' viz-rapeseed, mustard, and cole. Therape seed group includes the diploid *B. rapa,* turnip rape (AA, 2n=20) and amphidiploid *B. napus* L, rape (AACC, 2n=38) while the mustard group includes species like *B. juncea* Czern and Coss (AABB, 2n=36); *B. nigra* Koch (BB, 2n=16) and *B. carinata* brown (BBCC, 2n=34). *B. rapa* shows earliness in flowering and maturity, the lower fiber content in the meal, low content of saturated fatty acid in oil, and fewer siliquae shattering of yellow seed, that's why it is more popular than *B. napus*.

Rapeseed oil is required for cooking purposes and body massing, hairdressing, and various types of pickles preparation. It also has several medicinal values. It is considered a high energy food and a carrier for fat-soluble vitamins (A, D, E, and K). Inadequate intake of fat and oil decreases the availability of' fat-soluble vitamins and caused dietary imbalance and food wastage. In a balanced diet, 20-25% of calories arrive from fats and oils, and the average demand of fats and oil is about 37 g/day (Rahman, 1981). The seeds of *B. rapa* contain 42% oil, 25% protein (Khaleque, 1985). However, the oil content of currently cultivated *B. rapa* cultivars in Bangladesh contains high erucic acid (40%– 45%) and high pungency due to high amounts of glucosinolates (300 parts per million or ppm) (Mortuza *et al.,* 2006; Sultana *et al.,* 2021).It is an essential source of raw materials for industrial use, i.e., making soaps, paints, hair oils, lubricants, textile auxiliaries pharmaceuticals, etc. For animal feeding and organic manures, oil cake is used. *B. rapa* is the leading oil

yielding species of *Brassica* in Bangladesh (FAO, 2013). It occupies the first position in respect of area and production (Naznin *et al*., 2015) among Bangladesh's oil crops.

The country is suffering from a colossal shortage in edible oils, and a large portion of total edible oil consumed per year is imported. The use of low yielding indigenous cultivars, improper management practices, and reduction of cultivation area are the top reasons for low yield in this country. There is limited scope for horizontal expansion of its production due to the pressure of other crops. Farmers are interested in cultivating the existing low yielding varieties with low input and management; that's why the increasing yield is difficult. Short duration variety is still prevalent in Bangladesh because it can fit well into the T. Aman – Mustard–Boro rice cropping pattern. There are few improved short-duration varieties of *B. rapa* is available to replace the existing Tori-7. Thus, there should be an attempt to develop short duration and high yielding varieties of rapeseed with more oil percentage in seed, tolerant to biotic and abiotic stress to fulfill the demand of edible oil of the country.

The present study was undertaken with thirteen*Brassica rapa*genotypes to determine the importance of the genotypes from breeding point of view. However, the objectives of the study were-

1. To identify the superior genotypes of mustard considering morphological andphenotypic parameters; and
2. Toestimate correlation and path coefficient of different yield traits of *B. rapa* and select the promising parents for future hybridization program to develop modern mustard genotypes in future.

CHAPTER II

REVIEW OF LITERATURE

Brassica species has achieved much importance by a large number of researchers on various aspects of its utilization and production. *Brassica* species is the most important oil crop in Bangladesh and many countries of the world too. Many studies on the variability, interrelationship, path co-efficient analysis, heritability and genetic advance have been done in many countries. The review of the literature concerning the studies presented under the following heads:

2.1 Genotypic and phenotypic variability

2.2 Heritability and genetic advance

2.3 Correlation analysis; and

2.4 Path co-efficient analysis

2.1 Genotypic and phenotypic variability

For initiating a successful breeding program, genetic variability is a prerequisite to develop high yielding varieties. There are a good number of pieces of literature concerning the variability in the *B*rassica species. Some of those are discussed here.

Dash *et al*. (2007) conducted an experiment on fifty genotypes of toria. Fourteen characters were included in the investigation, to estimate genetic variability, character association, direct and indirect effect on seed yield and genetic divergence for earliness and other yield attributes in toria (*B. rapa* L. var. toria). Analysis of variance revealed considerable variability among 50 toria genotypes for all the fourteen characters under study. For all the characters, PCV was higher than GCV. Secondary branches per plant and leaf area index reflected high estimates of GCV and PCV. High estimates of broad sense heritability coupled with high genetic advance as per cent of mean were observed for secondary branches per plant, leaf area index, and specific leaf weight, reflecting greater contribution of genetic component.

Halder (2013) experimented with studying the variability in eleven advanced lines of *B. rapa*.The phenotypic variance was higher than the genotypic variance for every character. The difference between phenotypic and genotypic variance was minimum in the number of primary branches per plant, length of siliqua, thousand seed weight, seeds per silique, days to 50% flowering and days to 80% flowering.

Naznin *et al.* (2015) evaluated on thirty-three genotypes of *B. rapa* L. to find out their inter-genotypic variability. The environment highly influenced the character such as plant height whereas all other characters influenced the least. The highest phenotypic

and genotypic coefficient of variation was found in the number of secondary branches per plant.

Parveen *et al.* (2015) conducted an experiment to study on genetic variability using 15 rape seed genotypes. The result suggested that the phenotypic variance for all the characters was considerably greater than the genotypic variance indicating little influence of environmental factors on their expression.

Iqbal *et al.* (2015) carried out an investigation to study the genetic variability parameters of procured germplasm for various traits viz., days to 50% flowering, days to maturity, plant height (cm), no. of primary branches plant-1 , no. of secondary branches plant-1 , no. of pods plant-1 , thousand seed weight (g) and seed yield ha-1 . The set of 49 genotypes of brown sarson (*Brassicarapa*var. Brown sarson) were grown. PCV was higher than corresponding GCV for all the traits studied. High GCV was observed in seed yield plant-1 , whereas moderate GCV was revealed in no. of primary branches plant-1 and no. of secondary branches plant-1 . High values of heritability have been recorded for 50% flowering, days to maturity, no. of primary branches plant-1, no. of secondary branches plant-1 and seed yield ha-1 (g).

Sikarwar *et al*. (2017) experimented with assessing the genetic variability in 21 diverse genotypes of yellow sarson (*B. rapa*var. yellow sarson) for ten yield and its contributing characters. Analysis of variance for the design of the experiment showed highly significant differences for all the characters. High phenotypic co-efficient of variation and genotypic coefficient of variation were found for the number of secondary branches per plant followed by seed yield per plant, the number of primary branches per plant and number of siliquae on the main raceme. Days to flowering, plant height and length of siliqua showed low PCV and GCV.

Salam *et al.* (2017) carried out a research on experimental materials comprised 30 F1 from a 6×6 diallel crosses to estimate the genetic variability, heritability, genetic advance. Analysis of variance revealed presence of sufficient variability present as per different biometrical analysis except for days to maturity and oil content (%). Relative magnitude of phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation. The high GCV and PCV were observed for only two traits viz. number of branches per plant and harvest index (%). The traits plant height (cm), siliqua length (cm), number of siliquae per plant and seed yield per plant had moderate GCV and PCV. The highest heritability estimates were observed for the traits erucic acid content followed by plant height, branches per plant, seed yield per

plant, siliqua length, days to 50% flowering and harvest index (%). Genetic advance as percentage of mean was observed high for the character number of siliquae per plant, followed by seed yield per plant, days to maturity and plant height.

Rauf and Rahim (2018) evaluated 35 genotypes of *B. napus* based on RCBD with 3 replications. The genotypes were indicated significant amount of variations for the most pf the characters. Comparatively phenotypic variances were higher than the genotypic variances for most of the characters to be studied.

Tripathi *et al.* (2019) did a case study in twenty diverse genotypes of Indian mustard (*B. juncea*) for thirteen characters, revealed high heritability in broad sense for 6 the characters of days to 50% flowering and primary branches per plant,while days to maturity showed moderate heritability with high genetic advance as percent of mean.

Muhammad and Waluyo (2019) arranged an experiment on fifty-seven tested genotypes of*Brassica* species and 3 varieties as check for 24 quantitative characters and found a wide variability in the character of seeds per siliqua, number of siliqua per plant, and fresh weight. High heritability was found in the character of age of seed harvest, number of siliquae per plant, length of siliquas and number of seeds per siliqua indicating an efficient selection for the crop improvement.

Nagoo *et al.* (2021) was carried out an experiment for the estimation of the genetic variability, heritability, genetic advance and correlation analysis in fifty-seven *B. rapa* lines during Rabi 2019-2020 who found all the characters exhibited large amount of variability. Significant differences were observed in the studied genotypes for all 8 characteristics which give an insight into the existence of genetic variation in the available genotypes, indicating a great scope for selection and further improvement of *B. rapa* in terms of quality and quantity.

Mondal *et al*. (2022) studied genetic variability for 20 characters on twenty genotypes of Indian mustard (*B. juncea*). and reported number of siliquae per plant, harvest index (%), seed yield per plant and number of secondary branches had high to moderate GCV and PCV indicating the high amount variation present among the genotypes. The value of PCV is higher than the GCV suggested that the apparent variation is not only due to genotype but also due to the influence of environment.

2.2 Heritability and genetic advance in *B.* species

Heritability and genetic advance from selection are prerequisites for starting a breeding program. Study about related works on the *Brassica* species for heritability and genetic advance are reviewed below:

Czern *et al*. (2003) was conducted an experiment on Indian mustard (*B. juncea)* to estimate genetic variability, correlation and path analysis. The higher estimates of heritability coupled with higher genetic advance was found in yield per plant, siliqua on main branch, and branches per plant indicated that heritability of the trait is mainly due to additive effects and selection is effective for such traits. High heritability accompanied with medium to low genetic advance for plant height, length of main branch, days to flowering is indicative of non-additive gene action and the high heritability is being exhibited due to favorable influence of the environment rather than genotypes.

Fayyaz and Afzal (2014) studied on indigenous lines which was planned with an aim to check locally collected *B. rapa (B. campestris*, L.) accessions for genetic variability, heritability and genetic advance. Observations was done on eight quantitative parameters viz. primary branches, siliqua main raceme-1, main raceme length, siliqua length, siliqua width, plant height, seed silique-1, and thousand seed weight were made. Highly significant differences were observed in all traits except siliqua width, which showed significant variation. The highest heritability coupled with higher genetic advance was noticed in plant height which provided the evidence that this trait was under the control of additive genetic effects, while rest of the traits exhibited variable trends. Hence, it was observed that indigenous accessions have great proportion of genetic variability, which can be manipulated in future breeding programs for utilizing their genetic potential.

Suman (2014) investigated on elite lines of Indian mustard to study the extent of genetic variability by estimation of different parameters such as genotypic and phenotypic coefficients of variation, heritability, and the expected genetic advance for 11 quantitative characters.The characters like days to first flowering, days to 50 % flowering, days to maturity, plant height, siliqua length,number of seeds per siliqua and 1000-seed weight were found less influenced by the environmental factors as indicated by lower differences in magnitudes between GCV and PCV. On the contrary, the characters like number of primary branches, number of siliquae per plant, harvest index and seed yield per plant were much influenced by the environmental factors as evident from higher magnitude of difference 29 between PCV and GCV. High to moderate heritability with low genetic advances for days to

maturity and other quantitative characters suggested the predominant role of non - additive gene action.

Parveen *et al.* (2015) studied on genetic variability and correlation between yield contributing traits using 15 rape seed genotypes. The results indicated that the phenotypic variance for all the characters was considerably higher than the genotypic variance denoting little influence of environmental factors on their expression.

Ali *et al*. (2016) conducted an investigation to study the mean performance, heritability and genetic gain of yield and its components of *B. rapa* L. genotypes. Six genotypes of *B. rapa* were chosen for one or more several important traits for genetic improvement and were crossed in a half diallel design 30 and genetic analyses were conducted based on different generations. The inherent genetic differences among the genotypes were found which might be exploited through selection. The life span of the parent SAU 3 was the lowest but its yield was moderate compared to other parents. In the cross P1×P2, length of siliqua showed high (58.06%) narrow sense heritability with very low genetic gain (0.65). Considering the yield contributing traits in connection with the heritability and genetic gain, it might be concluded that TORI 7 was the ideal parent and the hybrid combination BARI 6 × SAU1 was the ideal hybrid for *Brassica rapa.*

Bibi *et al.* (2016) checked heritability and genetic advance in *B. juncea.* in RCBD with 3 replications. The high heritability along with high genetic advance was noted in plant height, siliqua length and seed yield while days to flowering and maturity, number of branches per plant, number of seeds per siliqua and 1000 seed weight exhibited variable trends.

Sikawar *et al.* (2017) carried out an experiment to assess the genetic variability, heritability and genetic advance in 21 diverse genotypes of yellow sarson (*B. rapa* Var. yellow sarson) for ten yield and its contributing characters. Analysis of variance for the design of the experiment indicated highly significant differences for all the characters. High Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were observed for number 31 of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and number of siliquae on main raceme. Hence, direct selection of these traits will prove effective. Days to flowering, plant height and length of siliqua showed low PCV and GCV. Higher estimates of broad sense heritability were observed for all the characters. High heritability coupled with high genetic advance was observed for number of secondary

branches per plant, seed yield per plant, length of main raceme, number of siliquae on main raceme, number of seeds per siliqua and number of primary branches per plant. High heritability with moderate genetic advance in case of length of siliqua and thousand seed weight whereas, High heritability and low genetic advance was observed for days to flowering and plant height.

Rauf and Rahim (2018) evaluated 35 genotypes of *B. napus* based on RCBD with 3 replications. Seed yield per plant exhibited the highest value of heritability followed by number of siliquae per plant while plant height exhibited the lowest value of heritability.

Gupta *et al.* (2019) estimated heritability and genetic advance in 35 genotypes of *B. rapa* L. High heritability was recorded for all the characters. Genetic advance was also high for number of siliquae per plant and plant height. Number of siliquae per plant showed high heritability with high genetic advance and genetic advance percent of mean.

Aktar *et al,* (2019) estimated variability ranges in 18 *Brassica* genotypes. All traits showed high heritability. High heritability values with high genetic advance in percent of mean was observed for number of branches per plant, number of siliquas per plant, number of seeds per siliqua and yield per plant.

Nagoo *et al.* (2021) was carried out an experiment for the estimation of the genetic variability, heritability, genetic advance and correlation analysis in the set of 57 *B. rapa* lines during rabi 2019-2020 revealed the high amount of PCV and GCV along with high values of broad sense of heritability and genetic advance was found, no. of seeds per siliqua, no. of siliqua per plant followed by seed weight.

Mishra and Nath (2022) carried an experiment consisting of 57 treatments in a RBD with three replications during Rabi 2021-22. High heritability and high genetic advance were observed for number of siliquae on main raceme followed by 1000 seed weight, while high heritability coupled with moderate genetic advance in per cent of mean was recorded for number of primary branches, number of secondary branches, harvest index and seed yield per.

2.3 Correlation analysis

The estimation of correlation is one of the most common and useful statistical techniques in research. For improvement in yield and quality, study of association among its components is important. It contributes to ascertain which of the postulated

components have positive and significant relationship with grain yield and quality traits. Pearson's correlation determines the extent to which values of the two traits are "proportional" to each other. Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables.

Halder *et al*. (2016) studied on eleven advanced lines and three popular check varieties of *B. rapa* L. and reported that the correlation co-efficient analysis had direct and indirect effect of eleven characters on yield per hectare. Yield per hectare was positively and highly significantly correlated with days to first flowering, days to 80% flowering and number of primary branches per plant which indicated that the yield would be higher by improving these characters while would be decreased with the increase of days to 50% flowering and length of siliquae as they were negatively correlated with yield.

Kumar *et al.* (2016) was undertaken an investigation to study the correlation and path coefficient analysis of twelve quantitative traits in 30 Indian mustard (*B.juncea*) germplasm lines. Correlation study revealed that harvest index and total biological yield per plant exerted high significant positive correlation coefficients with seed yield at both genotypic and phenotypic level. Seed yield is negatively correlated with days to 50 % flowering and days to maturity which promotes early flowering and early maturing genotypes.

Dawar *et al.* (2018) was carried out the research activities to determine the selection criteria for yield improvement in selected thirty genotypes of Indian mustard. The 19 correlation coefficient of the seed yield per plant had significant and positive correlation with plant height; number of primary branches, total no. of siliqua per plant and 1000-seed weight at genotypic level.

Tadesse and Alemu (2019) was carried out an experiment in order to evaluate the association of characters and path coefficient analysis on yield contributing traits in Ethiopian mustard. The correlation analysis showed seed yield per plot was highly significant and positively correlated with oil yield, biomass per plot, harvest index, plant height and thousand seed weight both at genotypic and phenotypic level.

Khan *et al.* (2019) was undertaken an investigation to study the correlation and path analysis of thirteen quantitative traits in twelve Indian mustard (*B. juncea*). Correlation study revealed that biological yield per plant and siliqua on main raceme exerted high positive significant genotypic correlation with grain yield per plant and

secondary branches per plant was found negatively correlated with grain yield per plant.

Saiyad *et al.* (2020) was carried out the experiment with sixty diverse genotypes of Indian mustard (*B. juncea*) in order to study correlation and path analysis for seventeen quantitative and qualitative traits who found seed yield per plant was significantly and positively correlated with plant height, number of branches per plant, number of siliquae per plant, seeds per siliqua, length of siliqua, 1000-seed weight, oil content, linolenic acid and erucic acid at genotypic level.

Akoju *et al.* (2020) studied on *B. juncea* revealed genotypic and phenotypic correlation coefficient of seed yield per plant had significant positive correlation with plant height at genotypic level. However, seed yield per plant recorded negative correlation with days to 50% flowering at both levels but was significant at genotypic level.

Lavanya *et al*. (2022) investigated with fifty mustard genotypes to study the correlation and path coefficient analysis of twelve yield contributing characters. Correlation analysis revealed that seed yield per plant is positively and significantly correlated with harvest index followed by number of secondary branches per plant and number of siliquae per plant at genotypic level. Whereas days to 50% flowering, plant height, number of primary branches per plant and number of seeds per siliqua had direct negative effects on seed yield per plant both at genotypic and phenotypic levels.

2.4 Path coefficient analysis

Path coefficient analysis calculates the correlations between yield and its contributing components, taking account of the cross correlation, either positive or negative. It is useful to partition the total correlation into direct and indirect effects on different components (Tollenaar *et al.,* 2004). In agriculture, plant breeders seek assistance in identifying traits that are useful as selection criteria to improve crop yield with help of path analysis.

Tahira *et al.* (2011) experimented with ten wide genetic ranged varieties of *B. juncea* to study the characters relationship. The result reported that plant height and siliquae length exhibited a positive direct effect on seed yield per plant. In contrast, a positive indirect effect of primary branches per plant through plant height and seed per

siliquae significantly affected seed yield per plant. Siliqua length contributed a negative indirect effect through plant height, seed per siliquae and thousand-grain weight.

Afrin *et al.* (2011) experimented with 22 *B. napus* L. advanced lines to determine the path co-efficient among the characters. The plant height exhibited the highest positive and direct effect on seed yield per plant, followed by the number of siliquae 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 and reported that 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) experimented with nine genotypes of *B. napus* to evaluate path analysis for yield and yield components and reported that the seeds/siliqua, 1000 seed weight, days to flowering, days to maturity and seeds/plant showed direct positive contribution towards seed yield per plant.

Rashid *et al.* (2015) studied on 40 oleiferous *Brassica* sp. and reported that his path analysis revealed number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, days to maturity and number of siliquae per plant demonstrated positive direct effect and plant height, length of siliqua, number of seeds per siliqua and 1000 seed weight showed negative direct effect on yield/plant.

Parveen *et al*. (2015) conducted an experiment using 15 rapeseed genotypes to determine the path coefficient. Path analysis showed that maximum positive direct effect was found in the case of 1000 seed weight and seeds per siliqua showed the maximum negative direct effect.

Halder *et al.* (2016) studied on eleven advanced lines and three popular check varieties of *B.rapa* L. and showed clearly picture on the inter-relationship through path co-efficient analysis. Plant height showed highest positive and highly significant direct association with the yield per hectare followed by number of primary branches per plant. Highest negative significant direct effect was found in number of siliquae per plant followed by days to maturity. The high direct effect gave the massage that selection of the traits might be effective for yield improvement. Low residual effect

indicated that the considered traits of the study explained almost all the variability towards yield.

CHAPTER III

MATERIALS AND METHODS

The present investigation entitled “Genetic Analysis of Morphological Parameters in Oil Seed*Brassica* Genotypes’’ was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. The detail information regarding the materials and methodology of this experiment is discussed below:

3.1Experimental site

The experimental site was located at 23^0 77’ N latitude and 90^0 37’ E longitudes with an elevation of 13.03 meters from the sea level (www.distancesfrom.com). Agro-

ecological zone of "The Modhupur Tract", AEZ-28 (www.banglapedia.com) belongs the experimental field.

3.2 Soil and climate

The experimental land was clay loam in texture; medium-high with medium fertility level. The pH of the soil was 5.47 to 5.63, and it contains 0.82% organic carbon content (Appendix II). The experimental site was located in the subtropical climatic zone with wet summer and dry winter. Generally, very few rainfalls, moderate temperature and short day length are observed during the Rabi season. 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 Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, provided the healthy and vigorous seeds of thirteengenotypes of *B.rapa were* used as experimental materials. The materials used in the experiment are showed in Table 1.

Table 1. Name of the genotypes used in the study

Sl. NO.	Genotype	Source
1.	Yellow special (80 days)	GEPB, SAU
2.	BARI 12	GEPB, SAU
3.	BARI 14	GEPB, SAU
4.	BARI 6	GEPB, SAU
5.	BARI 15	GEPB, SAU
6.	TORI 7	GEPB, SAU
7.	SS75	GEPB, SAU
8.	BARI 15 × SS75	GEPB, SAU
9.	TORI 7 × BARI 15	GEPB, SAU
10.	BARI 6 × BARI 15	GEPB, SAU

11.	SAU 1 ×BARI 15	GEPB, SAU
12.	BARI 9 × BARI 6	GEPB, SAU
13.	YELLOW SPECIAL	GEPB, SAU

Note: GEPB= Department of Genetics and Plant Breeding and SAU= Sher-e-Bangla Agricultural University

3.4 Methods

The following specific methods have been used to carry out the experiment:

3.4.1 Land preparation

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

3.4.2 Application of manures and fertilizers

Urea, Triple Super Phosphate (TSP), Muriate of potash (MOP), Gypsum, Zinc oxide and Boric acid were applied to the field. The first half amount of urea the total amount of cow dung, TSP, MOP, Gypsum, Zinc Oxide and Boric acid were applied during final land preparation as a basal dose. The rest amount of urea was used as a top dressing after 25 days of sowing. All the manure and fertilizers were applied as per the guidelines following the BARI Technology Handbook published by BARI.

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

Sl. No.	Fertilizers/ manures	Dose		Application procedure
		Applied in the plot	Quantity/ha	
1.	Urea	5.4 kg	250 kg	50% basal and 50% at the time of flower initiation
2.	TSP	3.7 kg	170 kg	As basal
3.	MOP	1.6 kg	75 kg	As basal
4.	Gypsum	3.2 kg	150 kg	As basal
5.	Boric acid	216 g	10 kg	As basal
6.	ZnO	64.8 g	3 kg	As basal
7.	Cow dung	108 kg	5 ton	As basal

3.4.3 Experimental design and layout

After finalizing the land preparation, the field layout was done. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 18 m × 12 m = 216 m^2. Each replication size was 18 m × 3 m, and the distance between replication to replication was 1 m. The spacing between lines to line was 30 cm, and plant to plant was 10 cm.

Plate 1. The view of experimental field during land preparation

Plate 2. The view of experimental field during seed sowing

3.4.4 Seed selection and sowing

Pure and healthy seeds were selected by avoiding unfilled grains. In the experimental field, seeds were sown in lines in the experimental plots on 28 November 2020, maintaining a soil depth at about 1.5 cm. The seeds were veiled with soil carefully after sowing so that no clods were found to suppress the seeds. Seeds germination were started three to four days after sowing.

3.4.5 Irrigation and drainage

Irrigation was given with sprinkler after sowing of seeds to maintain the soil's proper moisture condition to ensure uniform seed germination. Before the flower initiation, second irrigation was given (22 DAS). Third irrigation was given 40 days after sowing when the pod appeared. Fourth irrigation was given 60 days after sowing when seeds appeared in the pod. A sound drainage system was maintained to drain out the excess water. Special care was taken during irrigation.

3.4.6 Intercultural operations, insect and disease control

Different intercultural operations like weeding, thinning, irrigation, top dressing, pest managementetc. were applied in appropriate time to ensure proper growth and development of the plants. A good drainage system was maintained to release the rain water immediately from the experimental field during the growing period.

3.4.6.1 Tagging and tying

When the plants are visible after 1 week of germination, then tagging of each population of all replication was done. The field was bound with rope to protect the plants from leaning by using bamboo. Tagging of each population of all replication was done after a week of sowing.

3.4.6.2 Weeding and thinning

Two times weeding and thinning was done according to the requirement of maintaining uninterrupted growth of the crop. The first weeding was done after 15 days of sowing. Thinning was done at the same time for maintaining 30 cm from line to line and 10 cm from plant to plant. Second weeding was done after 21 days of sowing.

Plate 3. The view of experimental field during growth stage

3.4.6.3 Pesticide application

Aphid infection was found during the siliqua development stage of the crop.High dose of Metasystox-R 25EC@0.05% was used to reduce aphid infestation. Insecticide was applied in the afternoon to protect the beneficial insect.

3.4.7 Crop harvesting

Harvesting was done from 15th to 25th February 2021 based on maturity. When 80% of the plants exhibited maturity symptoms, i.e., the straw colour of siliquae, leaves, stems, desirable seed colour in the matured siliqua, the crop was assessed to attain maturity. Ten plants were selected for morphological analysis at random in each replication. The plants were harvested by uprooting, and then they were appropriately tagged. Data were recorded on different parameters from these plants.

3.4.8 Data collection

For studying various genetic parameters and inter-relationships, twelve characters of ten plants were taken into account such as days to first flowering, days to 50% flowering, days to maturity, plant height, root length, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua, seed coat colour, thousand seed weight and seed yield per plant.

3.4.9 Data collection methods

The data were recorded on ten selected plants on the following traits-

3.4.9.1 Days to first flowering

When the genotype of each row showed the1st flower bloom, days to 1st flowering were counted. Counting should be started from the sowing date to the date of appearance of 1stflower bloom.

3.4.9.2 Days to 50% flowering

When near about 50% of plants had at least one open flower of each line, days to 50% flowering was counted. Counting should be started from the sowing date to the date of 50% flowering of every entry.

3.4.9.3 Days to 80% maturity

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

3.4.9.4 Plant height (cm)

Measurement of plant height was done in centimeter (cm) which was starting from the base of the plant to the tip of the most elongate inflorescence. After harvesting, data of plant height was taken.

3.4.9.5 Root length (cm)

Root length was measured from the portion situated just below the starting point of the shoot to the plant's end portion. It was estimated in centimeter (cm) and data were taken after harvesting the plants.

3.4.9.6 Number of primary branches per plant

The total number of branches derived from the main stem of a plant was considered primary branches and the record was kept after counting.

3.4.9.7 Number of secondary branches per plant

The total number of branches originated from the primary branches of a plant was counted and deliberated as the number of secondary branches per plant.

3.4.9.8 Number of siliquae per plant

The total number of siliquae of each plant was enumerated and considered as the number of siliquae per plant.

3.4.9.9 Length of siliqua (cm)

Five representative siliquae were chosen randomly from each selected plant, and measurement was taken in centimeter from the base to the tip of a siliqua without beak.

3.4.9.10 Number of seeds per siliqua

All siliquae were collected from the sample plants, and five siliquae were selected randomly. The record was kept after counting the seeds from the siliquae.

3.4.9.11 Thousand seed weight (g)

Ten plants of each genotypes were selected. A thousand seeds from each entry were counted and weighed in grams.

3.4.9.12 Seed yield per plant (g)

Seeds produced by a representative plant were weighted in gram and considered as the seed yield per plant.

3.4.10. Statistical analysis

The data obtained for different traits were analyzed statistically by using Statistix 10 software (https://www.statistix.com/free-trial/) to find out the significance of the difference among the genotypes of *B. rapa*. After evaluating all the characters' mean values, analysis of variance was performed by the F-test. The significant differences among the treatments were estimated by the least significant difference (lsd) test at 5% level of probability (Gomez and Gomez, 1984).

3.4.10.1 Analysis of variance

The variance analysis for different characters was carried out utilizing mean data to assess the genetic variability among populations as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using the F test. The model of ANOVA used is presented below:

Sources of variation	**Degrees of Freedom (D.F.)**	**Mean sum of squares (MS)**	**Expected MS**
Replication	(r-1)	Mr	$p\ \sigma_r^2 + \sigma_e^2$
Population	(p-1)	Mp	$r\ \sigma_p^2 + \sigma_e^2$
Error	(p-1) (r-1)	Me	σ_e^2
Total	(rp-1)		

Where , p = number of treatments (population) ;

r = number of replications;

σ_r^2=variance due to replications;

σ_p^2= variance due to treatments (population); and

σ_e^2= variance due to error

To test the significance of the difference between any two-adjusted genotypic mean, the standard error of the mean was computed using the formula:

$$S.\ E = \sqrt{\frac{2Me}{r}\left(1 + \frac{rqu}{q+1}\right)}$$

Where, S. E = Standard error of mean

Me = Mean sum of square for error (Intra block)

r = Number of replications

q = Number of population in each sub-block

u = Weightage factor computed

3.4.10.2 Estimation of Least Significant Differences (LSD)

Least Significant Differences were estimated according to the formula of Gomez and Gomez (1984).

$$LSD_a = t_a\sqrt{\frac{s^2}{r}}$$

Here, α = Level of significance;

t= tabulated t value with concerned df at same level of significance;

s^2= Error Mean Sum of Square; and

r = Number of replication.

3.4.10.3 Study of variability parameters

Estimation of the variability among the populations for traits related to yield per plant in *B. rapa* L. were narrated below:

3.4.10.3.1 Estimation of genotypic variance and phenotypic variance

To estimate phenotypic and genotypic components of variance, Johnson *et al.* (1955) suggested a formula which is mentioned below:

a. Genotypic variance, $\sigma^2_g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes MSE = Mean sum of square for error, and r = Number of replication.

b. Phenotypic variance, $\sigma^2_p = \sigma^2_g + \sigma^2_e$

Where,

σ^2_p= Phenotypic variance;

σ^2_g= Genotypic variance; and

σ^2_e= Environmental variance = Mean square of error (MSE)

3.4.10.3.2 Estimation of genotypic and phenotypic coefficient of variation

To compute the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters, the following formula was given by Burton, 1952:

$GCV = \frac{\sigma_g}{g} \times 100$

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

Where,

GCV = Genotypic coefficient of variation;

PCV = Phenotypic coefficient of variation;

σ_g= = Genotypic standard deviation;

σ_p= Phenotypic variation; and

$\bar{x}$ = Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) as

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

3.4.10.3.3 Estimation of heritability in broad sense

Singh and Chaudhary (1985) suggested a formula to estimate broad sense heritability which is given below:

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

Where, h_b^2= Heritability in broad sense;

δ_g^2 = Genotypic variance; and

δ_p^2 = Phenotypic variance

Robinson *et al*. (1966) suggested the following categories for heritability estimates in cultivated plants:

Categories: Low: 0-30%; Moderate: 30-60%; and High: >60%.

3.4.10.3.4 Estimation of genetic advance

Allard (1960) suggested the following formula, which was used to estimate the expected genetic advance for different characters under selection:

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

Where, GA =Genetic advance;

σ_g^2= Genotypic variance;

σ_p^2= Phenotypic variance;

σ_p =Phenotypic standard deviation; and

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

Categories: Low (<10%); Moderate (10 – 20%); and High (>20%)

3.4.10.3.5 Estimation of genetic advance in percentage of mean

Following formula was given by Comstock and Robinson (1952) to compute genetic advance in the percentage of mean:

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

Johnson *et al.* (1955) suggested that genetic advance in percent of mean was categorized into following groups:

Categories:

Less than 10% - Low; 10-20% -Moderate; and more than 20% -High.

3.4.10.4 Correlation coefficient analysis

To determine the level of relationship of characters with yield and among the yield parts, the correlation coefficients were computed. Both genotypic and phenotypic correlation coefficients between two characters were determined by utilizing the variance and covariance components, as suggested by Al-Jibouri *et al.* (1958).

$$r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\sigma^2_{gx}}.\sqrt{\sigma^2_{gy}}}$$

$$r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\sigma^2_{px}}.\sqrt{\sigma^2_{py}}}$$

Where,

r_g (xy), r_p (xy) the genotypic and phenotypic correlation coefficients of x and y, respectively.

Cov_{gxy},$Cov_{pxy}$are the genotypic and phenotypic covariance of x and y, respectively.

σ^2_{gx} = = Genotypic variance of the trait x and σ^2_{gy} = Genotypic variance of the trait y.

σ^2_{px} = Phenotypic variance of the trait x and σ^2_{py} = Phenotypic variance of the trait y.

The calculated value of 'r' was compared with table 'r' value with n-2 degrees of freedom at 5% and 1% level of significance, where, n refers to the number of pairs of observation. Thus, the data obtained from various experimental objectives were subjected to pertinent statistical analysis to draw meaningful inference towards the genetic divergence of mustard populations.

3.4.10.5 Path coefficient analysis

According to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), Path coefficient analysis was done

utilizing simple correlation values. In path analysis, the correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

r_{yx_1}=P_{yx_1} + $P_{yx_2}r_{x_1x_2}$ +$P_{yx_3}r_{x_1x_3}$

r_{yx_2}= $P_{yx_1}r_{x_1x_2}$ + P_{yx_2} +$P_{yx_3}r_{x_2x_3}$

r_{yx_3}= $P_{yx1}r_{x_1x_3}$ +$P_{yx_2}r_{x_2x_3}$ +P_{yx_3}

To estimate direct and indirect effect of the correlated characters, say x_1, x_2, x_3yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below: where r's denoted simple correlation coefficient and P's indicate path coefficient (unknown).

P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between $x_1$and y is thus partitioned as follows:

P_{yx_1} = the direct effect ofx_1 on y.

$P_{yx_2}r_{x_1x_2}$ = the indirect effect of x_1 via x_2 on y.

$P_{yx_3}r_{x_1x_3}$= the indirect effect of x_1 via x_3 on y.

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

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

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

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

r_{iy} = Correlation of the character with yield

Categories:

Negligible (0.00 to 0.09);

Low (0.10 to 0.19); Moderate (0.20 to 0.29); High (0.30 to 1.0); and Very High (>1.00).

CHAPTER IV

RESULTS AND DISCUSSION

The present experiment was conducted to assess the genotypic effects and comparative performance among the thirteen advanced populations of *B. rapa* generated through intervarietal crosses and their parent of *B. rapa* to determine the breeding values of the populations. The study was also conducted to determine the phenotypic and genotypic variability, coefficient of variation, heritability, genetic advance, correlation and path coefficient to estimate the direct and indirect effect of yield contributing traits on yield. The data were recorded on different characters such as days to first flowering, days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliquae per plant, no. of seeds per silique, silique length (cm), thousand seed weight (g) and seed yield per plant (g). The data were statistically analyzed, and thus obtained results are described below under the following headings:

4.1 Mean performanceand genetic variability assessment;

4.2 Heritability and Genetic Advance;

4.3 Correlation analysis;

4.4 Path coefficient analysis; and

4.5 Selection

4.1 Mean performance and genetic variability assessment

The success in any crop improvement program depends on the ability of the breeder to define and assemble the required genetic variability, and to select indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather, 1949). Therefore, it is necessary to have prior information on both PCV and GCV, so that the estimate of heritability that helps the breeder to foretell the expected GA possibly by selection for a character can be enumerated.

The results are related to the analysis of variance (ANOVA), mean performance, genotypic, phenotypic, environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) for all the traits. Among the genotypes, almost all characters showed highly significant variation indicating full scope for selection for these characters, i.e., the data revealed substantial variability and thus a high possibility of improvement in most of the traits(Appendix IV). Out of the twelve traits studied, plant height, no. of primary branches per plant, no. of secondary branches per plant are considered as growth attributing characters. Days to 1st flowering, days to 50% flowering and days to maturity were considered as earliness attributes. No. of siliquae per plant, length of siliqua, no. of seeds per siliqua and 1000 seed weight were regarded as reproductive traits. Seed yield per plant was the economic trait.

4.1.1 Days to first flowering

Highly significant variations were observed for the character of days to first flowering at 1% level of significance (Appendix IV). This finding indicates that there was large genotypic difference among the populations. Among all the genotypes, G1 was the earliest genotype in case of days to first flowering (28.00 DAS) and G5 took highest time in case of days to first flowering (37.33 DAS)(Table 3).

The mean value for days to first flowering was 33.03 DAS (Table 3). The phenotypic variance (7.43) was slightly higher than the genotypic variance (5.44). Generally,

quantitative characters are highly influenced by the environment. The GCV and PCV were low 7.06 and 8.25, respectively.

4.1.2 Days to 50% flowering

Highly significant variation was found among the genotypes fordays to 50% flowering ranged from 31.33 to 45.00 DAS with a mean value of 39.36 DAS (Table 3). Among all the genotypes, G1 was the earliest genotype in case of days to 50% flowering (31.33 DAS) and G4 took highest time for flowering (45.00 DAS).

The obtained results expressed that the genotypic variance (17.08) was lower than the phenotypic variance (17.98) indicating environmental factors slightly influenced the expression of this trait (Table 4). The genotypic coefficient of variation and phenotypic coefficient of variationwere 10.50 and 10.77, respectively indicating considerable variability was exist within the genotypes.Akoju *et al*. (2020) found moderate PCV

Table 3. Mean performance of the yield and yield contributing characters of 13 genotypes of *Brassica rapa*

notypes	DFF	DFPF	DM	PH	ShL	RL	NPB	NSB	NSS	LS	NSP	TSW
	28f	31.33h	76.67h	76.15d	66.1d	9.16ef	5.57ab	5.77a	14.28e-g	6.12b	153.93ab	2.15c
	33.33cd	38e	87.33a	91.72bc	82.1bc	9.62d-f	4.80a-d	2.53cd	15.47e-g	5.62d	144.53ab	1.91d
	31de	38e	80de	95.57bc	85.6bc	9.96c-f	4.23cd	1.30fg	13.39g	5.46de	111.03c-e	1.91d
	34.33bc	45a	88.67a	101.62ab	90.38ab	11.23b-e	4.7a-d	2.23de	15.06e-g	5.67cd	133.5a-d	2.25c
	37.33a	41.67 b	84b	93.24bc	84.16bc	9.08f	3.8d	0.00h	20.76b	5.01f	69.5f	1.92d
	29.67ef	33g	78.33fg	88.64c	78.8c	9.84d-f	4.63b-d	6.13a	16.72d-f	6.44a	155.53a	2.74a
	36ab	44.67a	88a	94.5bc	81.12bc	13.38a	3.97d	0.00h	17.2c-e	5.21ef	87.77ef	1.61e
	33cd	39.33de	81cd	93.29bc	81.72bc	11.57a-d	4.23cd	1.50f	20.32bc	5.98bc	104.1de	2.39a
	33cd	41.67b	81.67c	103.09ab	90.3ab	12.78ab	5.8a	0.33h	13.61fg	5.45de	84.47ef	2.34bd
0	33.67bc	40cd	80.67c-e	112a	99.79a	12.21ab	5.23a-c	3.67b	24.09a	5.51de	93.93ef	2.82a
1	34bc	42.33b	79.67d-f	111.68a	99.73a	11.96a-c	4.4cd	1.57ef	19.66b-d	5.44de	124.63b-d	2.03c
2	32c-e	35.33f	79.33ef	89.1c	79.05c	10.05c-f	4.07d	3.03bc	19.09b-d	5.2ef	135.2a-c	1.89d
3	34bc	41.33bc	77.67gh	100.35a-c	86.97bc	13.38a	4.17cd	0.60gh	20.66b	5.47de	104.13de	1.2c-e
n	28.00	31.33	76.67	76.15	66.10	9.08	3.80	0.00	13.39	5.01	69.50	1.61
x	37.33	45.00	88.67	112.00	99.79	13.38	5.80	6.13	24.09	6.44	155.53	2.82
an	33.03	39.36	81.77	96.23	85.13	11.09	4.58	2.21	17.72	5.58	115.56	2.15
	1.15	0.78	0.78	5.75	5.40	1.01	0.53	0.35	1.51	0.16	14.41	0.23
	2.38	1.60	1.62	11.87	11.14	2.08	1.10	0.73	3.13	0.33	29.75	0.47

Here, DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), Shl = Shoot length (cm), RL=Root length (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliquae per plant, LS = Length of siliqua (cm), NSS = Number of seeds per siliqua, TSW = Thousand seed weight (g), YP = Yield per plant (g), Min = Minimum, Max = Maximum, SE = Standard Error, lsd = Least significant difference

(10.51%) and lowest GCV (8.54%) for days to 50% flowering. The study also revealed that, the flowering traits of the genotypes was moderate sensitive and influenced by the environmental temperature fluctuation as well as the expression of the traits was controlled by the additive gene action.

4.1.3 Days to 80% maturity

The average days required to be matured of the siliquae was ranges from 76.67 DAS to 88.67 DAS (Table 3). 88.67 DAS were required for G4 to be matured which was the highest duration for days to pod maturity followed by G7 (88 DAS), however, the lowest days to siliquae maturity was observed inG1 (76.67 DAS) followed by G13 (77.67DAS) (Table 3).

4.1.4 Plant height (cm)

Plant height was observed highest in G10 (112 cm) with highest shoot length (99.79 cm) and lowest in G1 (66.1cm) (Table 3). The mean value was recorded as 96.23 cm and mean of sum of square was 283.40 indicating significant differences among the populations for this trait (Appendix III). The lowest plant height was found in G1 (66.1cm) which showed least leaning than the other populations. Genotypic and phenotypic variance was observed 69.59 and 15.95, respectively for plant height with large environmental influence. Ara et al. (2010) found the highest difference between genotypic and phenotypic variance in plant height. Naznin *et al.* (2015) also found the similar results.

4.1.5 Shoot length (cm)

G10 had highest shoot length (99.79cm) and G1 had lowest shoot length (66.1cm). Moderate heritability (59.00%) along with moderate genetic advance (12.55) and moderate genetic advance in percent of the mean (14.74%) (Table 4) was recorded indicating the presence of non-additive gene action. So, improvement through selection may not be possible for this trait.

4.1.6Root length (cm)

G13 had highest root length (13.38cm) and G5 had lowest root length (9.08cm). Moderate heritability (56.04%) along with low genetic advance (2.15) and moderate genetic advance

in percent of the mean (19.40%) (Table 4) was recorded indicating the presence of non-additive gene action. So, improvement through selection may not be possible for this trait.

4.1.7Number of primary branches per plant

Maximum number of primary branches per plant were found in G9 (5.80) and minimum number of primary branches per plant were found in G5 (3.80) followed by G7(3.97), G12 (4.07), G13 (4.17), G3 (4.23), G8 (4.23), G11 (4.4) and G6 (4.63) with mean value 4.58(Table 3).The genotypic and phenotypic variance was recorded as 0.24 and 0.67, respectively.

4.1.8Number of secondary branches per plant

Maximum number of secondary branches per plant was found in G6 (6.13) and G5 and G7 had no secondary branches. The mean sum of square for number of secondary branches per plant was 12.14. The genotypic and phenotypic variance was recorded as 3.99 and 4.18, respectively.

4.1.9 Number of seeds per siliqua

Number of seeds per siliqua ranged from 13.39 to24.09 in different populations. The maximum number of seeds per siliqua was recorded in population G10 (24.09), however, minimum number of seeds per siliqua exhibited in population G3 (13.39) (Table 3). The mean observed for this trait was 17.72.The genotypic variance was (9.83) and phenotypic variance was (13.27) respectively.

4.1.10Length of siliqua (cm)

The siliqua length was 5.58 cm and ranged from 6.44 cm to 5.01 cm. The G6 had long length of 6.44 cm. The siliqua was shorter G5 in (5.01cm) (Table 3). The mean sum of square was significant (0.46) which indicated considerable amount of variation for this trait in the populations (Appendix IV). The genotypic and phenotypic variance for siliqua length were seen as value of 0.14 and 0.18 respectively. Siliqua length exhibited low GCV (6.75%) and PCV (7.60%) values.

4.1.11Number of siliquae per plant

Number of siliquaeper plant ranged from 69.50 to 155.53 in different populations. The maximum number of siliquaeper plant was recorded in population G6 (155.53), however, minimum number of siliquaeper plant exhibited in population G5 (69.5) (Table 3). The mean observed for this trait was 115.56. Number of siliquae per plant was found maximum in G6 (155.53) indicated higher yield than the others. So, selection for this trait of this population will be effective.

4.1.12 Thousand seed weight (g)

The genotypeG10 was exhibited maximum thousand seed weight (2.82 g). Whereas, the G7 was recorded minimum seed weight of (1.62 g). The mean found for this trait was (2.15 g) (Table 3).

4.1.13Yield per Plant (g)

The maximum yield was recorded by the genotype G10 (6.92 g). The lowest yield was recorded by the genotype G5 (3.80g) (Table 3).Yield per plant exhibited moderate estimates of PCV (19.18%) and GCV (16.81%) in (Table 4).

4.2 Heritability and Genetic Advance

4.2.1 Days to first flowering

High heritability (73.22%) coupled with low genetic advance (4.11) and moderate (12.45) genetic advance in percentage of mean were noted for this character rendering them unfit for improvement through simple selection due to prevalence of non-additive gene action (Table 4).

4.2.2 Days to 50% flowering

The high heritability of 94.96% with the low genetic advance of 8.30 and high (21.08) genetic advance in percentage of mean were noted for the character indicating that the character is governed by non-additive gene action and selection may not be rewarding for such trait (Table 4). Saifullah (2010) found high heritability (88.86%) and low genetic advance (2.06) for the trait in *B. rapa.*

Table 4. Estimation of some genetic parameters of the yield and yield contributing characters of 13 genotypes of *B. rapa*

Characters	δ^2_p	δ^2_g	δ^2_e	PCV (%)	GCV (%)	ECV (%)	h^2b	GA	GA (%)
DFF	7.43	5.44	1.99	8.25	7.06	1.19	73.22	4.11	12.45
DFPF	17.98	17.08	0.91	10.77	10.50	0.27	94.96	8.30	21.08
DM	16.64	15.72	0.92	4.99	4.85	0.14	94.45	7.94	9.71
PH	127.52	77.94	49.59	11.74	9.17	2.56	61.12	14.22	14.77
ShL	106.63	62.91	43.72	12.13	9.32	2.81	59.00	12.55	14.74
RL	3.47	1.95	1.53	16.80	12.58	4.22	56.04	2.15	19.40
NPB	0.67	0.24	0.43	17.88	10.79	7.09	36.44	0.62	13.42
NSB	4.17	3.99	0.19	92.64	90.53	2.11	95.50	4.02	182.25
NSS	13.27	9.83	3.44	20.56	17.69	2.86	74.08	5.56	31.37
LS	0.18	0.14	0.04	7.60	6.75	0.84	79.04	0.69	12.37
NSP	983.64	672.01	311.63	27.14	22.43	4.71	68.32	44.14	38.20
TSW	0.17	0.10	0.08	19.32	14.44	4.88	55.88	0.48	22.24
YP	1.03	0.79	0.24	19.18	16.81	2.36	76.87	1.61	30.37

Here, DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), Shl = Shoot length (cm), RL=Root length (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliquae per plant, LS = Length of siliqua (cm), NSS = Number of seeds per siliqua, TSW = Thousand seed weight (g), YP = Yield per plant (g),δ^2_p =Phenotypic variance, δ^2_g= Genotypic variance, δ^2_e= Environmental variance, PCV= Phenotypic co-efficient of variation, GCV= Genotypic co-efficient of variation, ECV = Environmental co-efficient of variation, h^2b =Heritability, GA= Genetic advance, GA% = Genetic advance as percentage of mean

4.2.3 Days to 80% maturity

High heritability (94.45%) with low genetic advance (7.94) and low genetic advance in percentage of the mean (9.71%) indicated the presence of non-additive gene action and selection for such trait might not be recommended (Table 4). Jahan *et al.* (2014) found high heritability along with low genetic advance in percent of the mean for days to maturity in *B. rapa.*

4.2.4 Plant height (cm)

High heritability (61.12%), moderate genetic advance (14.22) along with moderate genetic advance in percentage of the mean (14.77%) were noted for the character indicating 66 the presence of non-additive gene action and selection for such traits may be restricted for improvement of the crop (Table 4). Afrin *et al.* (2011) showed high heritability with the high genetic advance in the percentage of the mean for this character.

4.2.5 Shoot length (cm)

Moderate heritability (59.00%) along with moderate genetic advance (12.55) and moderate genetic advance in percent of the mean (14.74%) (Table 4) was recorded indicating the presence of non-additive gene action. So, improvement through selection may not be possible for this trait.

4.2.6 Root length (cm)

Moderate heritability (56.04%) along with low genetic advance (2.15) and moderate genetic advance in percentage of the mean (19.40%) was recorded indicating the presence of non-additive gene action. So, improvement through selection may not be possible for this trait (Table 4).

4.2.7 Number of primary branches per plant

Moderate heritability (36.44%) along with low genetic advance (0.62) and moderate genetic advance in percentage of the mean (13.42%) was recorded indicating the presence of non-additive gene action which is responsible for the ineffectiveness of the selection for this trait (Table 4). Sultana (2015) reported high heritability (97.43%) and low genetic advance (1.25) for this trait in *B. napus*.

4.2.8 Number of secondary branches per plant

The high heritability of 95.50% with the low genetic advance of 4.02 and very high genetic advance in percentage of the mean (182.25) was recorded indicating that non-additive gene effect was present, making selection ineffective for this trait (Table 4). Sultana (2015) found high heritability (98.70%) and low genetic advance (1.78) for this trait in *B. napus*.

4.2.9 Length of siliqua (cm)

Moderate heritability of 79.04%, low genetic advance 0.69 and moderate genetic advance in percentage of mean of 12.37% were observed for this trait. Moderate heritability in association with low genetic advance suggesting that non-additive gene effect was present and selection may not be recommended for this trait (Table 4). Moderate heritability (73.12%) with low genetic advance (0.55) and low genetic advance in percentage of mean (10.77%) were found by Afrin *et al.* (2016) in *B. rapa* for length of siliqua.

4.2.10 Number of seeds per siliqua

High heritability (74.08%) with high genetic advance (44.14) and high genetic advance in percentage of the mean (38.20%)were observed for this trait (Table 4). Low heritability (61.65%) along with moderate genetic advance (2.37) and low genetic advance in the percentage of the mean (13.80%) were found by Afrin *et al.* (2016) for the trait in.High heritability values along with high genetic advance in percentage of mean for seeds per siliqua was reported by Mahmud (2008) which was similar to the result.

4.2.11 Number of siliquae per plant

High heritability (74.08%), low genetic advance (5.56) and high genetic advance in percentage of mean (31.37) were noted for the character indicated that the heritability is due to non-additive gene effect and selection may be ineffective for the trait (Table 4). Moderate heritability (63.18%) with high genetic advance (31.32) and reasonable genetic advance in percentage of mean (33.59%) were found by Afrin *et al.* (2016) for number of siliquae per plant. Naznin *et al.* (2015) showed high heritability (93.16%) with high genetic advance in percentage of mean (37.74%) for number of siliquae/plant which was similar to this finding.

4.2.12 Thousand seed weight (g)

Moderate heritability (55.88%) in conjunction with low genetic advance (0.48) was noted for this trait, and high genetic advance in percentage of the mean (22.24%) was also observed. Moderate heritability with low genetic advance suggested that nonadditive gene action governs the character. Thus, for crop improvement, selection may be rewarding for this trait (Table 4). Saifullah (2010) reported high heritability (65.03%) along with low genetic advance (0.31) for this trait.

4.2.13Yield per plant (g)

High heritability (76.87%) combined to low genetic advance (1.61) and high (30.37%) genetic advance in percentage of the mean indicated the presence of non-additive gene action which makes the selection ineffective for the trait (Table 4).

4.3 Correlation analysis

In all breeding programs a specific trait can be improved by indirect selection via other characters. A proper understanding of different characters with the target trait and among the different characters themselves is needed for the estimation of correlation of yield with their related characters. Two types of correlation viz., positive correlation which indicating the change of the two traits be in the same direction (increase or decrease) while the negative correlation which means the increase in the first trait combined with a decrease in the second trait (or reverse).The phenotypic and genotypic correlation demonstrated the extent of association among different characters, hence, it assists to base selection procedure to a required balance, when two opposite characters affecting the main characters are being selected. As yield is a complex trait, governed by many genes, the influence of each character on yield could be determined through correlation analysis in order to estimate the extent and nature of relationship prevailing among yield and yield related characters. Therefore, the correlation coefficient values of twelve selected traits in *B. rapa* genotypes are evaluated and estimated results revealed that genotypic correlations were greater than the phenotypic correlation coefficients. Research findings are illustrated in Table 5.

Table 5. Correlation coefficient among the yield and yield contributing characters of 13 genotypes of *Brassica rapa*

Traits		DFF	DFPF	DM	PH	ShL	RL	NPB	NSB	NSS
DFPF	G	0.897**								
	P	0.806**								
DM	G	0.692**	0.659**							
	P	0.544**	0.621**							
PH	G	0.599**	0.776**	0.171^{NS}						
	P	0.432**	0.591**	0.155^{NS}						
ShL	G	0.589**	0.740**	0.173^{NS}	0.992**					
	P	0.406**	0.539**	0.147^{NS}	0.989**					
RL	G	0.438**	0.703**	0.103^{NS}	0.689**	0.591**				
	P	0.368**	0.595**	0.122^{NS}	0.579**	0.452**				
NPB	G	-0.720**	-0.347*	-0.217^{NS}	-0.053^{NS}	-0.049^{NS}	-0.056^{NS}			
	P	-0.269^{NS}	-0.203^{NS}	-0.147^{NS}	0.102^{NS}	0.092^{NS}	0.106^{NS}			
NSB	G	-0.858**	-0.821**	-0.435**	-0.488**	-0.445**	-0.562**	0.526**		
	P	-0.686**	-0.779**	-0.424**	-0.356*	-0.315*	-0.414**	0.343*		
NSS	G	0.479**	0.189^{NS}	-0.177^{NS}	0.495**	0.506**	0.256^{NS}	-0.514**	-0.101^{NS}	
	P	0.410**	0.214^{NS}	-0.153^{NS}	0.331*	0.310*	0.288^{NS}	-0.206^{NS}	-0.110^{NS}	
LS	G	-0.791**	-0.622**	-0.371*	-0.430**	-0.427**	-0.295^{NS}	0.534**	0.807**	-0.315*
	P	-0.658**	-0.562**	-0.321*	-0.318*	-0.316*	-0.175^{NS}	0.299^{NS}	0.690**	-0.171^{NS}
NSP	G	-0.827**	-0.703**	-0.241^{NS}	-0.634**	-0.598**	-0.609**	0.244^{NS}	0.835**	-0.385*
	P	-0.591**	-0.575**	-0.199^{NS}	-0.230^{NS}	-0.194^{NS}	-0.319*	0.223^{NS}	0.736**	-0.372*
TSW	G	-0.424**	-0.306^{NS}	-0.380*	0.307^{NS}	0.326*	0.090^{NS}	0.782**	0.626**	0.218^{NS}
	P	-0.269^{NS}	-0.233^{NS}	-0.272^{NS}	0.133^{NS}	0.158^{NS}	-0.066^{NS}	0.318*	0.484**	0.264^{NS}
YP	G	-0.569**	-0.431**	-0.529**	0.081^{NS}	0.048^{NS}	0.243^{NS}	0.748**	0.766**	0.305^{NS}
	P	-0.397*	-0.372*	-0.460**	0.070^{NS}	0.062^{NS}	0.078^{NS}	0.310*	0.664**	0.266^{NS}

Here, *= significant at 5% level of probability, **= significant at 1% level of probability, NS= non-significant

DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), Shl = Shoot length (cm), RL=Root length (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliquae per plant, LS = Length of siliqua (cm), NSS = Number of seeds per siliqua, TSW = Thousand seed weight (g), YP = Yield per plant (g)

4.3.1 Days to first flowering

Days to first flowering is significant and positively correlated with days to 50% flowering (G=0.897, P=0.806), days to 80% maturity (G=0.692, P=0.544) plant height (G=0.599, P=0.432), shoot length (G=0.589, P=0.406), root length (G=0.438, P=0.368) and number of seeds per siliqua (G=0.479, P=0.410) at both genotypic and phenotypic levels (Table 5). Jamali *et al.* (2016) reported that days to first flowering had highly significant and positive correlation with days to 50% flowering, plant height, siliqua per plant and seed yield while he reported negative association with secondary branches per plant. However, significant and negative correlation was found with days to first flowering with number of secondary branches per plant (G=-0.858, P=-0.686), length of siliqua (G=-0.791, P=-0.658) and number of siliquae per plant (G=-0.827, P=-0.591) at both genotypic and phenotypic levels, while number of primary branches per plant (G=-0.720) and 1000 seed weight (G=-0.424) showed negative correlation with days to first flowering at genotypic levels (Table 5).

4.3.2 Day to 50% flowering

Days to 50% flowering is significant and positively correlated with days to first flowering (G=0.897, P=0.806), days to80% maturity (G=0.659, P=0.621) plant height (G=0.776, P=0.591), shoot length (G=0.740, P=0.539) and root length (G=0.703, P=0.595) at both genotypic and phenotypic levels(Table 5). Maurya *et al.* (2012, Jamali *et al.* (2016) and Tadesse and Alemu (2019), also reported that days to first flowering had highly significant and positive correlation with days to 50% flowering, plant height, siliqua per plant and seed yield while he reported negative association with secondary branches per plant. Days to 50% flowering positive but non-significant correlation with number of seedper siliquae (G=0.189, P=0.214) was found at both genotypic and phenotypic level. However, significant and negative correlation was found with days to 50% flowering with length of siliqua(G=-0.622, P=-0.562) and number ofsiliquae per plant (G=-0.703,P=-0.575) at both genotypic and phenotypic levels (Table 5) while yield per plant (G=-0.431) showed negative correlation with days to 50% flowering at genotypic levels.

4.3.3 Days to 80% maturity

Both at genotypic and phenotypic levels, days to maturity was highly significant and positively correlated with days to first flowering (G=0.692, P=0.544), days to 50% flowering (G=0.659, P=0.621), whereas plant height (G=0.171, P=0.155), shoot length (G=0.173, P=0.147) and root length (G=0.103, P=0.122) showed positive direction but non-significant association at both levels towards days to maturity (Table 5). Mekonnen *et al.* (2014), Naznin *et al.* (2015) and Kumari *et al.* (2017) suggested that days to siliqua maturity had positive and non-significant association with seed yield per plant. Tadesse and Alemu (2019) reported that all the traits were positively and strongly correlated with siliqua maturity both at genotypic and phenotypic levels. On the contrary, negative association with strong significance was observed in number of secondary branches per plant (G=-0.435, P=-0.424), length of siliqua (G=-0.371, P=-0.321) and yield per plant (G=-0.529, P=-0.460) (Table 5). Prakash (2014) found days to siliqua maturity was negatively correlated with secondary branches per plant, seeds per siliqua, 1000 seed weight and yield per plant.

4.3.4 Plant height (cm)

Plant height was significant and positively correlated with days to first flowering (G=0.599, P=0.432),days to 50% flowering (G=0.776, P=0.591), shoot length (G=0.992, P=0.989) and root length (G=0.689, P=0.579) at both genotypic and phenotypic levels where, number of siliquae per seed (G=0.495) was strongly significant and positively associated at only genotypic level (Table 5). However, days to maturity (G=0.171, P=0.155), 1000 seed weight (G=0.307, P=0.133) and yield per plant (G=0.081, P=0.070) were positively but non-significantly associated with plant height at both genotypic and phenotypic levels where, number of primary branches per plant (P=0.102) was non-significant and positively associated at only phenotypic level (Table 5). Number of secondary branches per plant (G=-0.488), length of siliqua (G=-0.430) and number of siliquae per plant (G=-0.634) was negatively correlated with plant height at genotypiclevels. On the contrary, number of primary branches per plant (G=-0.053) at genotypic level and number of siliquae per plant (P=-0.230) at phenotypic level were non-significantly negatively associated with plant height (Table 5). Kumar *et al*. (2016) and Siddique *et al.* (2017) estimated that plant height was negatively associated with days to flowering, primary branches, secondary branches, number of seeds per siliqua, siliqua length and harvest index at genotypic level while negative

correlation with number of siliquae per plant, 1000 seed weight and harvest index at phenotypic level.

4.3.5 Shoot length (cm)

Shoot length was significant and positively correlated with root length (G=0.591, P=0.452) at both genotypic and phenotypic levels where, number of siliquae per seed (G=0.506) was strongly significant and positively associated at only genotypic level (Table 5). However,yield per plant (G=0.048, P=0.062) were positively but non-significantly associated with shoot length at both genotypic and phenotypic levels where, number of primary branches per plant (P=0.092) and 1000 seed weight (P=0.158) were non-significant and positively associated at only phenotypic level (Table 5). Number of secondary branches per plant (G=-0.445), length of siliqua (G=-0.427) and number of siliquae per plant (G=-0.598) was negatively correlated with shoot length at genotypic levels. On the contrary, number of primary branches per plant (G=-0.049) at genotypic level and number of siliquae per plant (P=-0.149) at phenotypic level were non-significantly negatively associated with shoot length (Table 5).

4.3.6 Root length (cm)

Root length was significant and negatively correlated with number of secondary branches per plant (G=-0.562, P=-0.414) at both genotypic and phenotypic levels where, number ofseeds per plant (G=-0.609) was significant and negatively associated at only genotypic level (Table 5). However,number of siliquae per plant (G=0.256, P=0.288), yield per plant (G=0.243, P=0.078) were positively but non-significantly associated with root length at both genotypic and phenotypic levels where, length of siliqua (G=-0.295, P=-0.175) was non-significant and negatively associated at both level (Table 5). Number of primary branches per plant (P=0.106) was non-significant and positive correlation at phenotypic level and1000 seed weight (G=0.090) was non-significant and positive correlated with root length at genotypic levels(Table 5).

4.3.7 Number of primary branches per plant

Among all the traits, number of secondary branches per plant (G=0.526), length of siliqua (G=0.534), thousand seed weight (G=0.782) and yield per plant (G=0.748) showed positive

correlation with number of primary branches per plant atgenotypic levels (Table 5). Gangapur *et al*. (2009), Naznin *et al.* (2015) and Singh *et al.* (2017) reported that primary branches had positive relationship with number of siliquae per plant, yield per plant and 1000 seed weight at both index. On the other hand, number of siliquae per plant (G=0.299, P=0.244) had non-significant correlation with number of primary branches per plant at both levels where, number of seeds per siliqua (P=-0.514) showed negative correlation at genotypic level andnegative non-significant at phenotypic level (Table 5). Kumar *et al*. (2017) revealed that seed yield and 1000 seed weight had non-significant negative association with number of primary branches per plant.

4.3.8 Number of secondary branches per plant

Number of secondary branches per plant showed a highly significant and positive correlation with the length of siliqua (G=0.807, P=0.690),number of siliquae per plant (G=0.835, P=0.736), 1000 seed weight (G=0.626, P=0.484) and yield per plant (G=0.766, P=0.664) at both genotypic and phenotypic levels(Table 5). It also presented that non-significant and negative correlation with number of seeds per siliqua, (G=-0.101, P=-0.110). Naznin (2013) found a significant and positive relation with yield, while Akter (2010) found a negative correlation with the yield.

4.3.9 Number of seeds per siliqua

Number of seeds per siliqua showed a highly significant and positive correlation with days to first flowering (G=0.479, P=0.410) and non-significant and positive correlation with the 1000 seed weight (G=0.218, P=0.264) and yield per plant (G=0.305, P=0.266) at both genotypic and phenotypic levels (Table 5). It also showed that non-significant and negative correlation with length of siliqua (P=-0.171) at phenotypic level (Table 5). Significant and negative correlation between the number of seeds per siliqua and yield were found by Naznin (2013).

4.3.10 Length of siliqua

Length of siliqua showed a highly significant and positive correlation with number of siliquae per plant (G=0.769, P=0.527), 1000 seed weight (G=0.672, P=0.557) and seed yield per plant (G=0.692, P=0.506) at both genotypic and phenotypic levels (Table 5). Saifullah (2010) showed a significant and positive correlation of length of siliqua with yield.

4.3.11 Number of siliquae per plant

Number of siliquaeper plant showed non-significant and positive correlation with 1000 seed weight (G=0.219, P=0.076) at both genotypic and phenotypic levels (Table 5). It also showed significant and positive correlation with yield per plant (G=0.457, P=0.339) at both genotypic and phenotypic level. Uddin *et al*. (2013) found that at both phenotypic and genotypic level yield had a highly significant and positive correlation with the number of siliquae per plant.

4.3.12 Thousand seed weight

Thousand seed weight showed a highly significant and positive correlation with seed yield per plant (G=0.801, P=0.673) at both genotypic and phenotypic levels (Table 5). Akter (2010) reported a significant and positive correlation of thousand seed weight with yield per plant at the genotypic level.

4.4 Path coefficient analysis

Simple correlation does not consider the complex relationships between the various traits related to the dependent variable. Correlation coefficients show relationships among independent variables and the linear relationship between these variables. But it is not sufficient to describe these relationships when the causal relationship among variables is needed. It has been suggested that yield components have either a direct or an indirect effect on yield per plant. Therefore, it was essential to determine the effects of yield components on yield per plant. Consequently, path coefficient analysis is the most common statistical method used for this purpose.

Correlation coefficients exhibit a linear association between variables. Seed yield per plant is considered as a dependent variable and its attributes as independent variables such as days to first flowering, days to 50% flowering, days to 80% maturity, plant height, root length, shoot length,number of primary branches per plant,number of secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua, and thousand seed weight. Partitioning of genotypic correlations into direct and indirect effects of important characters by path coefficient analysis of *B. rapa* is presented in Table 6. Residual effects of their independent variables have been denoted as 'R' which have influenced on seed yield per plant to a medium extent.

4.4.1 Days to first flowering

Path coefficient analysis revealed that days to first flowering had a negative direct effect (-0.262) on seed yield per plant (Table 6). Days to first flowering had a positive indirect effect on seed yield per plant through days to 80% maturity (0.103), plant height (0.703), root length (0.465), number of primary branches per plant (0.803), length of siliqua (0.487) and number of seeds per siliqua (0.757) while negative indirect effect was found via days to 50% flowering (-0.228), shoot length (-0.509), number of secondary branches per plant (-2.233), number of siliquae per plant (-0.425) and 1000 seed weight (-0.230). It had significant negative genotypic correlation (-0.569) with seed yield per plant (Table 6).

4.4.2 Days to 50% flowering

Days to 50% flowering had a negative direct effect (-0.254) on seed yield per plant. Days to 50% flowering had a positive indirect effect on seed yield per plant through days to 80% maturity (0.098), plant height (0.911), root length (0.747), number of primary branches per plant (0.388), length of siliqua (0.383) and number of siliquae per plant (0.643) while the negative indirect effect was found via days to first flowering (-0.235), shoot length (-0.639), number of secondary branches per plant (- 2.139), number of seeds per siliqua (-0.167) and 1000 seed weight (-0.166). It had significant negative genotypic correlation (-0.431) with seed yield per plant (Table 6).

4.4.3 Days to 80% maturity

Days to maturity had a positive direct effect (0.149) on seed yield per plant. Days to maturity had a positive indirect effect on seed yield per plant via plant height (0.201), root length (0.109), number of primary branches per plant (0.242),number of seeds per siliqua (0.157), length of siliqua (0.228) and number of siliquae per plant (0.221) while the negative indirect effect via days to first flowering (-0.182), days to 50% flowering (-0.167), shoot length (-0.149), number of secondary branches per plant (-1.133) and 1000 seed weight (-0.206). It had a highly significant negative genotypic correlation (0.529) with seed yield per plant (Table 6).

Table 6. Partitioning of genotypic and phenotypic correlation with seed yield per plant into direct and indirect component of 13 genotypes of *Brassica rapa*

haracters	DFF	DFPF	DM	PH	ShL	RL	NPB	NSB	NSS	LS	NSP	TSW	G co w
FF	**-0.262**	-0.228	0.103	0.703	-0.509	0.465	0.803	-2.233	-0.425	0.487	0.757	-0.230	-0
FPF	-0.235	**-0.254**	0.098	0.911	-0.639	0.747	0.388	-2.139	-0.167	0.383	0.643	-0.166	-0
M	-0.182	-0.167	**0.149**	0.201	-0.149	0.109	0.242	-1.133	0.157	0.228	0.221	-0.206	-0
H	-0.157	-0.197	0.025	**1.174**	-0.856	0.732	0.059	-1.272	-0.439	0.265	0.580	0.167	0.
hL	-0.155	-0.188	0.026	1.165	**-0.863**	0.628	0.055	-1.158	-0.449	0.263	0.548	0.177	0.
L	-0.115	-0.178	0.015	0.809	-0.510	**1.063**	0.063	-1.464	-0.227	0.182	0.558	0.049	0.
PB	0.189	0.088	-0.032	-0.062	0.042	-0.060	**-1.116**	1.371	0.456	-0.329	-0.223	0.424	0.
SB	0.225	0.208	-0.065	-0.574	0.384	-0.598	-0.587	**2.604**	0.089	-0.497	-0.764	0.340	0.
SS	-0.126	-0.048	-0.026	0.581	-0.437	0.272	0.574	-0.263	**-0.887**	0.194	0.352	0.118	0.
S	0.207	0.158	-0.055	-0.505	0.368	-0.314	-0.596	2.103	0.279	**-0.615**	-0.704	0.365	0.
SP	0.217	0.178	-0.036	-0.744	0.517	-0.648	-0.272	2.174	0.341	-0.473	**-0.915**	0.119	0.
SW	0.111	0.078	-0.056	0.361	-0.282	0.096	-0.872	1.631	-0.193	-0.414	-0.200	**0.543**	0.

Residual effect (R): 0.025

Here, *= significant at 5% level of probability, **= significant at 1% level of probability, NS= non-significant

DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), Shl = Shoot length (cm), RL=Root length (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliquae per plant, LS = Length of siliqua (cm), NSS = Number of seeds per siliqua, TSW = Thousand seed weight (g), YP = Yield per plant

4.4.4 Plant height (cm)

Plant height had a positive direct effect (1.174) on seed yield per plant.Plant height had a positive indirect effect on seed yield per plant via days to 80% maturity (0.025), root length (0.732), number of primary branches per plant (0.059),length of siliqua (0.265), number of siliquae per plant (0.580) and 1000 seed weight (0.167) while the negative indirect effect through days to first flowering (-0.157), days to 50% flowering (-0.197), shoot length (-0.856), number of secondary branches per plant (- 1.272) and number of seeds per siliqua (0.439). It had a non-significant positive genotypic correlation (0.081) with seed yield per plant (Table 6).

4.4.5 Shoot length (cm)

Shoot length had a direct negative effect (-0.863) on seed yield per plant. Shoot length had a positive indirect effect on seed yield per plant via days to 80% maturity (0.026), plant height (1.165), root length (0.628), number of primary branches per plant (0.055), length of siliqua (0.263), number of siliqua per plant (0.548) and 1000 seed weight (0.177) while the negative indirect effect on seed yield per plant through days to first flowering (-0.155), days to 50% flowering (- 0.188), number of secondary branches per plant (-1.158) and number of seeds per siliqua (-0.449). It had a non-significant positive genotypic correlation (0.048) with seed yield per plant.

4.4.6 Root length (cm)

Root length had a direct positive effect (1.063) on seed yield per plant. Root length had a positive indirect effect on seed yield per plant via days to 80% maturity (0.015), plant height (0.809), number of primary branches per plant (0.063), number of siliquae per plant (0.558), length of siliqua (0.182), number of siliqua per plant (0.558) and 1000 seed weight (0.049) while the negative indirect effect on seed yield per plant through days to first flowering (-0.115), days to 50% flowering (- 0.178), shoot length (-0.510), number of secondary branches per plant (-1.464) and number of seeds per siliqua (-0.227). It had a non-significant positive genotypic correlation (0.243) with seed yield per plant (Table 6).

4.4.7 Number of primary branches per plant

Number of primary branches per plant had a negative direct effect (-1.116) on seed yield per plant. Number of primary branches had a positive indirect effect on seed yield per plant via days to first flowering (0.189), days to 50% flowering (0.088), shoot length (0.042), number of secondary branches per plant (1.371), number of seeds per siliqua (0.456) and 1000 seed weight (0.424) while the negative indirect effect on seed yield per plant via days to maturity (-0.032), plant height (-0.062), root length (-0.060), length of siliqua (-0.329) and number of siliquae per plant (-0.223). It had significant positive genotypic correlation (0.748) with seed yield per plant (Table 6).

4.4.8 Number of secondary branches per plant

Number of secondary branches had a positive direct effect (2.604) on seed yield per plant. umber of secondary branches per plant had a high positive indirect effect on yield observed by Naznin *et al.* (2015). Number of secondary branches had a positive indirect effect on seed yield per plant through days to first flowering (0.225), days to 50% flowering (0.208), shoot length (0.384), number of seeds per siliqua (0.089) and 1000 seed weight (0.340) while the negative indirect effect on seed yield per plant via days to 80% maturity (-0.065) plant height (-0.574), root length (-0.598), number of primary branches per plant (-0.587), number of siliquae per plant (-0.764), length of silique (-0.497). It had significant positive genotypic correlation (0.766) with seed yield per plant (Table 6).

4.4.9 Number of seeds per siliqua

Number of seeds per siliqua had a negative direct effect (-0.887) on seed yield per plant (Table 6). Number of seeds per siliqua had a positive indirect effect on seed yield per plant through plant height (0.581), root length (0.272), number of primary branches per plant (0.574), length of siliqua (0.194), number of siliquae per plant (0.352) and 1000 seed weight (0.118) while the negative indirect effect on seed yield per plant via days to first flowering (-0.126), days to 50% flowering (-0.048), days to 80% maturity (-0.026), shoot length (-0.437) and number of secondary branches per plant (-0.263). It had non-significant positive genotypic correlation (0.305) with seed yield per plant (Table 6).

4.4.10 Length of silique (cm)

Length of silique had a negative direct effect (-0.615) on seed yield per plant (Table 6). Length of siliqua had a positive indirect effect on seed yield per plant through days to first flowering (0.207), days to 50% flowering (0.158), shoot length (0.368), number of secondary branches per plant (2.103), number of seeds per siliqua (0.279) and 1000 seed weight (0.365) while the negative indirect effect on seed yield per plant via days to 80% maturity (-0.055), plant height (-0.505), root length (- 0.314), number of primary branches per plant (-0.596) and number of siliquae per plant (- 0.704) . It had a highly significant positive genotypic correlation (0.692) with seed yield per plant. Islam *et al.* (2016) observed a positive indirect effect of plant height towards yield (Table 6).

4.4.11 Number of siliquae per plant

Number of siliquae per plant had a negative direct effect (-0.915) on seed yield per plant (Table 6). Number of siliquae per plant had a positive indirect effect on seed yield per plant via days to first flowering (0.217), days to 50% flowering (0.178), shoot length (0.517), number of secondary branches per plant (2.174),number of seeds per siliqua (0.341) and 1000 seed weight (0.119) while the negative indirect effect on seed yield per plant via days to 80% maturity (-0.036), plant height (-0.744), root length (-0.648), number of primary branches per plant (-0.272) and length of siliqua (-0.473). It had a highly significant positive genotypic correlation (0.457) with seed yield per plant. Islam *et al.* (2016) observed a negative indirect effect on the number of siliquae per plant (Table 6).

4.4.12 Thousand seed weight (g)

Thousand seed weight had a positive direct effect (0.543) on seed yield per plant (Table 6). 1000 seed weight had a positive indirect effect on seed yield per plant via days to first flowering (0.111), days to 50% flowering (0.078), plant height (0.361), root length (0.096) and number of secondary branches per plant (1.631) while the negative indirect effect on seed yield per plant via days to 80% maturity (-0.056), shoot length (-0.282),number of primary branches per plant (-0.872), number of seeds per siliqua (-0.193),length of siliqua (-0.414),number of siliquae per plant (0.200). It had a highly significant positive genotypic correlation (0.801) with seed yield per plant (Table 6). Negative indirect effect for thousand seed weight on yield per plant was reported by Naznin *et al.* (2015).

4.4.13 Residual Effects:

The magnitude of residual effect (0.025) indicated that traits included in the path analysis explained about 97.5% of the variation in yield. However, the remaining variation in yield (2.5%) can be attained by incorporating other yield related traits in the path analysis as far as studies involving association of traits is concerned. Naznin *et al.* (2015) found residual effect 0.45 in case of yield per plant. Islam *et al.* (2016) found 0.430 in case of yield per plant.

4.5 SELECTION:

Yellow special (80 days)

Moderate seed yield per plant (6.32g) was found in Yellow special (80 days)with highest number of primary branches per plant (5.57), the highest number of secondary branches per plant (5.77), moderate length of siliqua (6.12),moderate thousand seed weight (2.15 g), moderate number of seeds per siliqua (14.28) and a moderate number of siliquae per plant (153.93). Yellow special (80 days)took lowest days to 80% maturity at 76.67 days.

BARI 6 × BARI 15

The highest seed yield per plant (6.92) was found in BARI 6×BARI 15with moderate number of siliquae per plant (93.93), highest thousand seed weight (2.82g), a moderate number of primary branches perplant (5.23), highestthousand seed weight (2.82g), moderate number of secondary branches per plant (3.67), highest number of seed per siliqua (24.09), highest plant height (112) and moderate days to 80% maturity at 80.67 days.

TORI 7

Moderate seed yield per plant (6.62g) was found in TORI 7with highest number of siliquae per plant (155.53), longest length of siliqua (6.44cm), highest number of secondary branches per plant (6.13), moderate number of seeds per siliqua (16.72), a moderate thousand seed weight (2.74g) and moderate days to 80% maturity at 78.33 days.

CHAPTER V

SUMMARY AND CONCLUSION

The genetic variability is the raw material in breeding industry on which selection acts to evolve superior populations. The genetic variability that exists in the available populations provides ample scope for selecting the best lines for future trial. Yield being a complex quantitative character, direct selection for yield might not result in successful advancement. Therefore, it was necessary to partition the noticed variability into heritable and non-heritable

components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic gain.

The present study was investigated to study the nature and magnitude of genetic variability, the pattern of character association among the characters and the direct and indirect effects of component characters on yield per plant among the populations of *B. rapa* L. The material for the present study comprised of 13 genotypes collected from Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, were evaluated using RCBD design for 12 quantitative characters at Sher-e-Bangla Agricultural University, Dhaka during the period of November, 2020 to February, 2021.

The study exhibited wide range of variability for most of the characters studied. The lowest days to 50% flowering (31.33 days) was found in G1 followed by G6 (33 days). The lowest days to maturity (76.67 days) were observed in G1 followed by G13 (77.67 days). Plant height exhibited lowest (76.15cm) in G1. The highest number of primary branches per plant (5.80) was recorded in G9. The highest number of secondary branches per plant (6.13) was observed in G6. The highest number of siliquae per plant (155.53) was in G6. The lowest length of siliqua (5.01cm) was recorded in G5 followed by G12 (5.2cm)and the highest length of siliqua (6.44cm) was remarked in G6. The number of seeds per siliqua (24.09) was found highest in G10. The thousand seed weight exhibited the highest (2.82g) in G10 followed by G6 (2.74g). The yield per plant was maximum (6.92g) in G10. So, these populations for these traits can be used for future trial.

The phenotypic variance of the materials was considerably lower than the genotypic variance for all the characters studied. Number of primary branches per plant, number of secondary branches per plant, length of siliqua and thousand seed weight showed least difference between genotypic and phenotypic variance which indicated low environmental influence on these characters. Hence, selection will be beneficial for these traits. Days to 50% flowering, days to 80% maturity, plant height, number of siliquae per plant, number of seeds per siliqua and yield per plant showed much difference between genotypic and phenotypic variance suggesting high environmental influence on the expression of these characters. Therefore, selection will not be beneficial for these traits.

The genotypic co efficient of variation were lower than the phenotypic coefficient of variation for all traits under study, which gives an idea about the presence of variations among genotypes were not only genetic variations but also environmental influences are responsible for variations. Normally, the quantitative traits were more influenced by the environmental factors. The phenotypic coefficient of variation values were ranging from 4.99% to 92.64% while the genotypic coefficient of variation values ranged from 4.85% to 90.53%. According to this classification, high genotypic coefficient and phenotypic coefficient of variations were found for NSB (90.53% and 92.64%), NSP (22.43% and 27.14%) respectively while medium phenotypic and genotypic coefficient values were showed from DFPH (10.77% and 10.50%), RL (16.80% and 12.58%), NPB (17.88% and 10.79%), TSW (19.32% and 14.44%) and YP (19.18% and 16.81%) and for DFF (7.06% and 8.25%), DM (4.85% to 4.99%) and LS (6.75% to 7.60%) were low. So, the information of genotypic and phenotypic coefficient of variations in mustard in this experiment showed the genotypic variation for almost all traitsindicating the presence of variability in mustard genotypes.

High values for heritability and genetic advance for various traits designates good genetic potential for selection and for use in future trial.In the present investigations, the value heritability for different traits were found (36.44% to 94.96%), on the other hand genetic advance as a percentage of the mean were observed a wide range 9.71% to 182.25%. High heritability estimates were observed for days to 50% flowering (94.96%), days to80% maturity (94.45%), number of secondary branches per plant (95.50%), number of siliquaeper plant (68.32%), length of siliqua (79.04%), number of seeds per siliqua (74.08%), yield per plant (76.87%). Plant height (14.22) and number of siliquae per plant (44.14) recorded moderate genetic gain and selection based on these characters may result in development of high yielding populations. High heritability coupled with moderate genetic advance was found in plant height and number of siliquae per plant. Significant genotypic and phenotypic positive association with seed yield per plant were observed in number of primary branches per plant and number of secondary branches per plant through the correlation analysis.

Path coefficient analysis at genotypic level found that the thousand seed weight had the highest direct effect followed by length of siliqua. number of primary branches per plant, number of secondary branches per plant, and number of siliquae per plant had medium level

direct effects towards yield, while days to first flowering, days to 50% flowering, days to 80% maturity had negative direct effects. On the contrary, path coefficient analysis at phenotypic level observed that number of secondary branches per plant had the maximum direct effect followed by the plant height, root length, thousand seed weight and days to 80% maturity, whereas days to first flowering, days to 50% flowering, shoot length, number of primary branches per plant, number of seeds per siliqua, length of siliqua, number of siliquae per plant had negative direct effects towards yield.

Selection was carried out among the populations of *B. rapa* L. for most promising populations with having high yield short duration. Yellow special (80 days) took lowest time to mature followed by TORI 7, BARI 9×BARI 6 and SAU 1×BARI 15. Higher seed yield per plant was observed in BARI 6×BARI 15 followed by, TORI 7, Yellow special (80 days), SAU 1×BARI 15, YELLOW SPECIAL and BARI 15×SS75. According to their yield and yield contributing characters, Yellow special, BARI 6×BARI 15 and TORI 7 are selected as superior genotypes. So, these population possessed excellent potential for use in future trial.

CHAPTER VI

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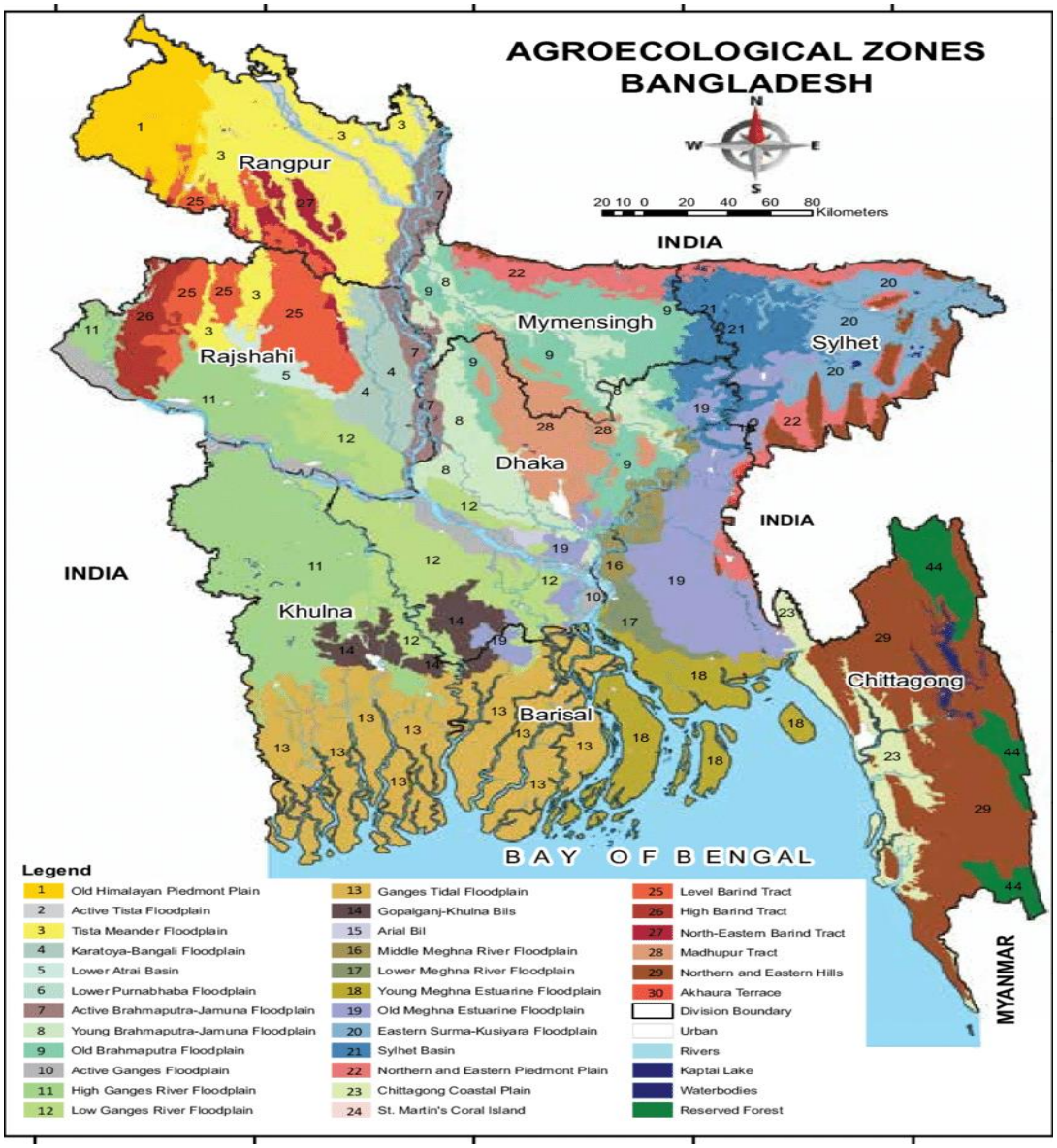
APPENDICES

Appendix I. Map showing the experimental site of the study.



Legend showing the research site

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

A. Morphological characteristics of the experimental field

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

Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

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

C. Chemical composition of the soil:

Soil characters	Value
Organic matter	1.44%
Potassium	0.15 meq/100 g soil
Calcium	1.00 meq/100 g soil
Magnesium	1.00 meq/100 g soil
Total nitrogen	0.072
Phosphorus	22.08 µg/g soil
Sulphur	25.98 µg/g soil
Boron	0.48 µg/g soil
Copper	3.54 µg/g soil
Iron	262.6 µg/g soil
Manganese	164 µg/g soil
Zinc	3.32 µg/g soil

Source: Soil Resources Development Institute (SRDI), Khamarbari, Dhaka

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2020 to February, 2021

Month	Air Temperature (℃)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2021	29.6	19.2	65	32.4	240
December, 2021	26.4	14.1	61	12.5	248

January, 2022	25.4	12.7	58	8.7	263.5
February, 2022	28.7	15.5	53	28.4	252

Source: Bangladesh Meteorological Department (Climate division), Agargaon Dhaka-1212

Appendix IV. Analysis of variance and CV% of 13 genotypes of *Brassica rapa*

Source of variance	DF	Mean sum of square									
		DFF	DFPF	DM	PH	ShL	RL	NPB	NSB	NSS	L
Replication	2	2.79	3.79	7.92	114.06	85.84	2.00	0.18	0.27	4.03	0
Genotype	12	18.30**	52.14**	48.08**	283.40**	232.45**	7.37**	1.16*	12.14**	32.92**	0
Error	24	1.99	0.91	0.92	49.59	43.72	1.53	0.43	0.19	3.44	0
CV (%)		4.27	2.42	1.17	7.32	7.77	11.14	14.25	19.66	10.47	3

Here, CV = Co-efficient of variation, DF = Degrees of freedom, DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), Shl = Shoot length (cm), RL=Root length (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliquae per plant, LS = Length of siliquae (cm), NSS = Number of seeds per siliqua, TSW = Thousand seed weight (g), YP = Yield per plant (g)

** Significant at 1% level of significance * Significant at 5% level of significance, NS = Non significance

Appendix V: Maximum, minimum, mean and CV of twelve parameters of *Brasssica rapa* L.

	Maximum	Minimum	Mean	CV (%)
DFF	28.00	37.33	33.03	4.27
DFPF	31.33	45.00	39.36	2.42
DM	76.67	88.67	81.77	1.17
PH	76.15	112.00	96.23	7.32

ShL	66.10	99.79	85.13	7.77
RL	9.08	13.38	11.09	11.14
NPB	3.80	5.80	4.58	14.25
NSB	0.00	6.13	2.21	19.66
NSS	13.39	24.09	17.72	10.47
LS	5.01	6.44	5.58	3.48
NSP	69.05	155.53	115.56	15.28
TSW	1.61	2.82	2.15	12.83
YP	3.80	6.92	5.29	9.22