CHARACTER ASSOCIATION OF SESAME (*Sesamum indicum* L.)

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CERTIFICATE

*This is to certify that the thesis entitled, '**CHARACTER ASSOCIATION OF SESAME (Sesamum indicum L.)**' submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **SHAIMA SULTAN BUSHRA, Registration number: 20-11082** 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 duly been acknowledged.

Dated: June, 2022
Place: Dhaka, Bangladesh

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Dedicated To
My Venerable Parents,
Shan & Miraz

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The Author

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By

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ABSTRACT

The experiment was conducted in the experimental area of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka during the time period of March to June 2022 to find out the character association of 32 sesame genotypes. Mean performance, variability, correlation matrix, path analysis and genetic diversity analysis on different yield contributing characters and yield of sesame genotypes was estimated. The longest plant (127.87 cm) was found in the genotype of G-3, whereas the shortest plant (93.29 cm) from the genotype of G-1. The highest yield/plant (307.67 g) was found in the genotype of G-27, whereas the lowest yield/plant (83.20 g) was observed from the genotype of G-10. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the yield contributing traits. In correlation study, significant positive association was recorded for yield/plant of sesame genotypes with number of branches/plant (-0.049), number of capsules/plant (0.879), length of capsule (0.355) and number of seeds/capsule (0.554). Path analysis revealed that days to first flowering had negative direct effect (-0.326) on yield/plant. Number of capsules/plant had positive direct effect (0.859) on yield/plant. Number of branches per plant had negative direct effect (-0.077) on yield/plant. Number of seeds/capsule had positive direct effect (0.290) on yield/plant. Weight of 1000 seeds had positive direct effect (0.267) on yield/plant. In genetic diversity, cluster I was the largest cluster comprising of 20 genotypes followedby cluster II with 9 genotypes, cluster III belongs 2 genotypes and cluster IV have 1 genotypes of sesame. Inter cluster distance was maximum (2.761) between clusters II and III, followed by clusters II and I (11.165). In consideration of yield contributing characters and yield G-27 perform better followed by G-24 and G-9.

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LIST OF COMMONLY USED ABBREVIATIONS

Full word	Abbreviations	Full word	Abbreviations
Agro-ecological Zone	AEZ	Journal	J.
Agricultural	Agril.	Kilogram	kg
Agriculture	Agric.	Meter	m
And others	*et al*.	Mean sum of square	MSS
Annals	Ann.	Methods	Meth.
Applied	App.	Meter square	m2
Application	Appl.	Millimeter	mm
Bangladesh Agricultural Research Council	BARC	Muriate of potash	MP
		Number	No.
		Percentage	%
Bangladesh Agricultural Research Institute	BARI	Phenotypic co-efficient of variation	PCV
		Phenotypic variance	δ2p
Bangladesh Bureau of Statistics	BBS	Physiology	Physiol.
		Plant Genetic Resource Centre	PGRC
Biology	Biol.		
Botany	Bot.	Proceeding	Proc.
Centimeter	cm.	Progressive	Progr.
Cooperative	Coop.	Randomized complete block design	RCBD
Days after transplanting	DAT		
		Review	Rev.
Edition	Edn.	Report	Rpt.
Environment	Environ.	Reporter	Rep.
Etcetera	etc.	Research / Resource	Res.
Evolution	Ev.	Sher-e-Bangla Agricultural University	SAU
Food and Agricultural Organization	FAO		
		Serial	Sl.
Genetic advance	GA	Science	Sci.
Genotypic co-efficient of variation	GCV	Society	Soc.
		Soil Resource Development Institute	SRDI
Genotypic variance	δ2g		
Gram	g	Standard error	SE
Hectare	ha.	Technology	Technol.
Heritability in broad sense	h2b	Triple super phosphate	TSP
		That is	i.e.
Horticulture	Hort.	Ton	t
International	Intl.	University	Univ.
Incorporation	Inc.	Vegetable	Veg.

CHAPTER I

INTRODUCTION

One of the most ancient annual oilseed crops cultivated in tropical and temperate regions is Sesame *(Sesamum indicum L.)* (Amoo et al., 2017). It is commonly known as til in Bengali, belongs to the Sesamum genus of the Pedaliaceae family. (Raja *et al*., 2007). It is a self-pollinated diploid plant (2n = 26) with oil-rich seeds (50–60%) and antioxidants (Sharma et al., 2014). The size of the sesame genome, which is around 350 megabytes, has not been extensively studied. In a sesame reference genome with a low amount of repetitive sequences (28.5%), a total of 27,148 genes have been annotated (Wang et al., 2014). The crop is cultivated either as a pure stand or as a mixed crop with *aus* rice, jute, groundnut, millets, and sugarcane. In Bangladesh, sesame occupies a remarkable area under production and contributes second-ranked production after rapeseed and mustard. Although at present about 3, 21,338hectares of land are under sesame cultivation with a production of 19795 metric tons (BBS, 2020). It is widely naturalized in tropical regions around the world and is cultivated for its edible seeds, which grow in pods. World production in 2018 was 6 million metric tons (5,900,000 long tons; 6,600,000 short tons), with Sudan, Myanmar, and India as the largest producers. (FAOSTAT, 2020).

It is important oil seeds crops and is widely cultivated in Africa and Asia. It is the queen of high quality vegatable oils for human consumption as it contains high levels unsaturated fatty acids and antioxidants e.g. sesamol, sesamin, sesamolin and sesaminor (Nupur et al., 2010). Sesame is considered as "the queen of oilseed" crops because of its high nutritional value and health benefits. Sesame seed is used for a wide range of edible products and also for industrial uses (Bedigian, 2011) . It contains 40 to 63 per cent oil, which contains significant amount of oleic and linoleic acids (Abate and Mekbib, 2015). Sesame contains about 41.3–62.7% oil (Uzun et al., 2008), 18–25% protein (Borchani et al., 2010), 20–25% carbohydrate (Tunde-Akintunde et al., 2012) and as a result it is grown in many countries as oil seed crop. It is an important oilseed crop grown in India, China, Korea, Russia, Turkey, Mexico, South America, and several countries of Africa. Sesame seeds are rich in oil, proteins, unsaturated fatty acids, vitamins, minerals,and folic acid (Kapoor *et al*., 2015). Among the sesame producing countries, India and China are the world‟s largest producers followed by the areas found in developing countries Myanmar, Sudan, Ethiopia, Uganda, Nigeria, Tanzania, Pakistan and Paraguay (Sharma, *et al*., 2014). Despite its long history and nutritional value, the crop has low yielding

capacity compared to other oilseed crops, mainly due to its low harvest index, susceptibility to diseases, seed shattering and indeterminate growth habit (Yol and Uzun, 2012). Sesame is considered a self-pollinating crop but varying degrees (5 to 60%) of cross pollination may occur depending on insect activity, environmental conditions and availability of other vegetation (Yermamos, 1980). According to Hamrick and Godt (1989) out-crossing plant species have a tendency to present between 10 and 20% of the genetic variation between populations. Variation is a necessary criterion for selection program aimed at improving some desirable characters in sesame. Sandipan *et al.*, (2010) reported low to moderate GCV and PCV for all the characters evaluated. Adeyemo and Ojo (1993) reported days to flowering, plant height, height of first capsule, number of capsule per plant and seed yield per plant as important characters to be considered in the evaluation of germplasm of sesame. Genetic advance can easily be achieved after selection for a few generations because of the combination of this autogamy and heterogeneity in sesame species. Plant germplasm of a particular crop collected from the local sources provides greater genetic variability and can furnish useful traits to broaden the genetic base of crop species. The success in genetic improvement of the crop andthe development of a species needs the availability and accessibility of genetic variability (Pervaiz *et al*., 2010).

The estimation of character associations could identify the relative importance of independent characters contributing to dependent ones and suggest upon the character(s) that may be useful as indicator for one or more of other characters. In other words, character associations between yield components can be used as the best guide for successful yield improvement by indirect selection. Achievement of such success depends upon sort and accuracy of correlation coefficient estimated as well as plant materials, environmental conditions and their interaction (Sarwar *et al*., 2007). The success of crop improvement programme depends on the selection of parents having high variability, so that desired character combination may be selected to enhance the yield. Heritability provides information on the transmissibility of character from one generation to another. Johnson et al. (1955) advised that heritability estimates along with genetic advance would be more useful in predicting grain yield under phenotypic selection than heritability estimates alone. The information on strength and direction of association of component characters with seed yield and also inter association among them would be very useful in formulating an effective breeding programme for improvement of seed yield (Jogdhande et al., 2017 and Manisha et al., 2018)

No doubt the genetic variability present in the Bangladeshi sesame germplasms needs protection from the continuous genetic erosions. Knowledge of genetic diversity among landraces will help in the selection and breeding of high yielding, good quality cultivars that will increase quality sesame production (Mumtaz *et al*., 2010). Nevertheless, the development of improved plant cultivars is restricted mainly due to narrow genetic pool which results into limited possibility to restructure the sesame crop. The knowledge of genetic diversity will help in the selection and breeding of high yielding, good quality cultivars that will increase production.

Considering the above mentioned facts this research work was under taken with the following objectives:

- To estimate the nature of association of traits; direct and indirect relation among yield and yield contributing characters of sesame germplasms.
- To measure the yield potentiality of sesame genotypes.
- To screen out the suitable genetically diverse parents of sesame germplasms for future breeding program.

CHAPTER II

REVIEW OF LITERATURE

Sesamum indicum , which is widely khown as “Till” in Bangladesh. In Bangladesh and in many countries of the world sesame is a valuable oil seed crop. Though it has precisely high nutritional value it does not get so much attention and very few research report are available on the advancement of this crop. The crop has trivial less attention by the researchers on various aspects because in general it grows with minimum care and management practices. Many studies on the genetic variability, multivariate analysis and character association have been carried out in many countries of the world. The work so far done in Bangladesh is not sufficient and decisive. Notwithstanding, some of the significant instructive works and research findings so far been carried out at home and abroad on this aspect have been reviewed in this chapter under the following sub-headlines:

2.1 Variability, heritability and genetic advance in sesame

Abate and Mekbib (2015), assemble forty nine sesame genotypes from low- altitude areas of Ethiopia and were evaluated for estimation of character association and genetic variability. Morphological data recorded on 14 quantitative traits were analyzed for analysis of variance, phenotypic and genotypic variability, heritability, genetic advance, correlation and path coefficient analysis. Analysis of variance exposed significant difference among the genotypes for each character except for primary branches, suggesting the existence of considerable genetic variation in the studied germplasm with regard to seed yield and its component traits. There is a high variation in mean performance of genotypes for the studied traits. Am-NG-15 is a high yielding genotype but with lowest oil content, whereas Tigray-13 is a low yielding genotype but with highest oilcontent. Hence, a crossing program between these genotypes can result in desirable hybrid that can be used for the ongoing sesame improvement program. Moderate heritability with moderate genetic advance was observed for most of the yield related traits, signifying that these attributes are governed by both additive and non-additive genes action.

Sabiel *et al.* (2015); conducted a study to estimate the extent of genetic variability in genotypes of sesame (*Sesamum indicum* L.) under rainfed conditions in semi-arid zones. Twelve genotypes of sesame were grown for threeconsecutive seasons. Genotypic and

phenotypic variability, genetic advance and heritability in a broad sense were estimated. The highest genotypic coefficient ofvariation was observed for seed yield kg/ha while days to flowering showed highheritability estimate (above 85%) during these seasons. Moreover, the high genetic advance was recorded in 1000-seed weight while all other traits showed low genetic advance. Highly significant differences among genotypes were observed in days to flowering, plant height and 1000-seed weight. Significant differences in seed yield (kg/ha) and biomass yield (kg/ha) and non-significant difference in days to maturity were observed. The high yielding genotypes were Ang-5 (4 locules with black seeds) and Hirehri with seed yields of 365 and 347 kg/ha, respectively.

Tripathi *et al.* (2013); collected total of 100 sesame accessions from diverse ecologies of India were used in a research work and analysis of variance revealed significant difference among genotypes for all the nine characters studied. High heritability combined with high genetic advance was recorded for seed yield/plant, number of secondary branches/plant and 1000 seed weight indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Genetic parameters of variability and heritability of different characters were studied by Revathi *et al*. (2012) in four crosses of sesame. In the present study, variability parameters were observed in two crosses viz., Paiyur 1 × SVPR 1, F_2 of TMV 4 × SVPR 1 and their BC_1F_1s. High genotypic coefficient of variability and phenotypic coefficient of variability were observed for number of branches per plant, number of capsules per plant and seed yield per plant. High heritabilityalong with high genetic advance as per cent of mean for number of branches per plant, number of capsules per plant and seed yield per plant will be useful for further breeding program. Based on *per se* performance, heritability, genetic advance as per cent of mean, F_2 and BC_1F_1 of TMV 4 × SVPR 1 were considered as superior crosses. This cross can be subjected to selection program to obtain high yielding segregates.

The study was carried out by Akbar *et al*. (2011) to evaluate the phenotypic variability in the local sesame genotypes using 16 qualitative and quantitative traits. A total of 105 sesame accessions collected from diverse ecologies of Pakistan were used. A considerable level of variation was recorded for a number of morphologic and agronomic traits, while limited diversity for observed amongthe accessions for characters like stem hairiness, flower color (white with purple shading), seed color and to some extent

phyllody disease.

The field experiment was conducted by Sumathi and Muralidharan (2010) with thirty hybrids produced by line × tester mating design from eleven sesamegenotypes involving five branched and six monostem/shy branching types. Observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, capsule breadth, number of seeds per plant, 100 seed weight, seed yield per plant and oil content. The traits, number of branches per plant, number of capsules per plant and seed yield per plant showed high PCV and GCV estimates. There is scope for selection based on these characters, and the diverse genotypes can provide materials for a sound breeding program. High heritability combined with high genetic advance (as per cent of mean) observed for plant height, number of branches, number of capsules and seed yield per plant showed that these characters were controlled by additive gene effects and phenotypic selection for these characters would likely to be effective.

Thirteen genotypes of sesame (*Sesamum indicum*) were evaluated by Alake *et al*.(2010) in field trials for two years in the field in a randomized complete block design with three replications. The results showed year effect to be highlysignificant for all the characters except 1000-seed weight, and genotype effect was highly significant for all the characters except height of first capsule. Also genotypes x year interactions were significant for number of days to flower and 1000-seed weight. Genotype Packqueno, NCRI-Ben-03L, Yandev and NCRI- Ben-01M had highest seed yield per hectare (0.229; 0.209; 0.204 and 0.206t/ha respectively). Close resemblance between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for all traits except number of days to flower indicating that selection for these traits would be effective. Heritability estimates in general were high for all the nine characters studied except number of days to flower. Most characters showed significant positive correlation with grain yield except 1000-seed weight which showed negative correlation with seed yield. The PCA identified height at maturity (94%), number of capsule per plant (93%), height of flowering (92%), height of first capsule (85%), capsule weight per plant (78%) and number of seeds per capsule (93%) as the characters that contributed significantly to variations found in the sesame genotypes. Highest heritability coupled with high genetic advance was observed for capsule weight per plant, height of first capsule and seed yield per hectare. Thus, these traits could be used as selection criteria for yield improvement in sesame.

The genetic variation was determined by Banerjee and Kole (2006) in a population of 30 advance breeding lines of sesame in Visva-Bharati, Sriniketan, West Bengal, India in summer seasons. Phenotypic and genotypic coefficients ofvariation were high for plant height, branches per plant, capsules per plant, seedsper capsule and seed yield per plant and low for 1000-seed weight. High to moderate estimates of heritability accompanied by high to moderate genetic advance for plant height, branches per plant, capsules per plant, seeds per capsule and seed yield per plant indicated the predominance of additive gene action for the expression of these characters. Plant height, branches per plant, capsules per plant and seeds per capsule exhibited positive and significant genotypic and phenotypic correlations with seed yield.

Genetic variability and correlation were studied by Mothilal (2006) among 20 genetically diverse sesame (*Sesamum indicum*) genotypes kharif in Vridhachalam, Tamil Nadu, India. Biometrical observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches, number of capsules per plant, 1000-seed weight, and seed yield per plant. The phenotypic (PCV) and genotypic (GCV) coefficient of variability wereestimated. Heritability and genetic advance were also calculated. The PCV was invariably higher in magnitude than the GCV. High heritability (h^2) estimate wasobserved for all the characters. High heritability with high genetic advance render the selection effective and it was observed for plant height and number of capsules per plant. The genetic advance as percent of mean was high for number of capsules and number of branches per plant, indicating high additive gene action. The high heritability with low genetic advance for days to 50% flowering, days to maturity, number of branches, 1000-seed weight and seed yield per plant indicated expression of non-additive gene action for these characters.

Ravikant *et al*. (2006) carried out an experiment using 19 elite genotypes in Bihar, India during kharif. Results revealed that three traits (among 11) viz., 1000 seed weight, seed oil content (%) and seed yield per plant were most effective for selection of elite genotypes for high oil yield.Field experiments were conducted by Rasal and Gavhane (2006) in Niphad, India, during kharif season, to determine the flowering pattern and its effect on the yield of 12 sesame. The results revealed that, in sesame, the genotype SMVT 411 produced significantly higher seed yield of 7.86 g/plant, followed by SMVT 406 (7.00 g/plant) and SMVT 408 (5.96 g/plant). The higher seed yield of these genotypes was attributed to maximum percent fruit set, higher number of fruits and higher total number of flowers produced per plant.

Multiple linear regression analysis was conducted by Shim *et al*. (2006) to interpret the relationship between sesame grain yield and its components under early sowing cropping condition. Twenty-one sesame cultivars were used during an experiment in Miryang, Korea republic.

The t test showed that stem length, number of capsules per plant, 1000-seed weight and seed weight per plant gave significant contribution to sesame grain yield, therefore, these variables were assumed to mostly influence the yield components of sesame. Meanwhile, F value showed that stem length, number of capsules per plant and seed weight perplant gave significant contribution to sesame grain yield, while 1000 seedsweight did not significantly show. Based on the results, it is reasonable to assume that high yield potential of sesame under early sowing cropping condition would be obtained by selecting breeding lines with long stem length, number of capsules per plant, and seed weight per plant, which was different result at the late sowing: cropping condition in which days to flowering and maturity were assumed to be more affected factors to the sesame grain yield.

Heterosis for days to 50% flowering, plant height, number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, 1000-seed weight and seed yield per plant was evaluated by Tripathi and Mishra (2005) in 24 crosses derived from a 8×3 line × tester analysis in sesame (*Sesamum indicum*). The eight genotypes crossed with three testers (TMV-5, CO-1 and TC-25) were TKG-55, JLT-7, TNAU-11, KANAK, B-67, SVPR-1, TRS-9 and TKG-22. Heterosis was worked out over mid parent, better parent and standard parent. The study revealed that the hybrids TNAU-11 × TC-25, TKG-55 × CO-1 and JLT-7 × TMV-5 were the most superior for exploitation of seed yield and other contributing characters.

Forty diverse genotypes of sesame were studied by Singh (2005) during kharifto understand the variability and relative contribution of eight quantitative characters (days to 50% flowering, days to maturity, plant height, number of branches, number of capsules per plant, capsule length, capsule width and seeds per capsule) towards the yield. Wide range of variation was recorded for all the characters, except pod length and pod width. Phenotypic coefficient of variationwas higher than the coefficient of variation for all the genotypic characters under study.

Babu *et al*. (2005); carried out an experiment with four lines, three testers and 12hybrids obtained from line × tester mating indicated significant differences among all the 19

sesame genotypes for all the characters. The analysis of geneticparameters revealed a narrow difference between the genotypic and phenotypic coefficients of variation. Estimates of heritability were high for all the characters, while genetic advance as percent of mean was high for seed yield per plant, number of seeds per capsule, number of primaries, number of capsules per plant and 1000-seed weight. Medium genetic advance as per cent of mean was recorded by days to 50% flowering and plant height. Oil content and days to maturity had a low genetic advance as percent of mean. This indicated that simple selection could be effective for improving majority of characters including seed yield per plant.

Variability in seed yield and its components (days to 50% flowering, plant height, branches per plant, capsules per plant, seeds per capsules and 1000-seed weight) was assessed by Ganesan (2005) in approximately 136 determinatesesame germplasm lines at Vriddhachalam, Tamil Nadu, India. The genotypic and phenotypic coefficients of variation were low for most traits. Number of capsules per plant recorded the highest coefficient of variation, indicating that selection for determinate lines with high number of capsules per plant will be effective in increasing economic yield in sesame. High heritability (99.46%) coupled with high genetic advance as percentage of mean (67.55%) was recorded for number of capsules per plant. Plant height (99.51 and 59.66%), number of seeds per capsule (91.95 and 25.73%) and 1000-seed weight (99.31 and 25.96%) also recorded high heritability estimates and moderate level of genetic advance as percentage of mean. These results indicate that additive genesare governing these traits and that phenotypic selection for these traits will be effective.

A study was conducted by Laurentin *et al*. (2004) in Venezuela to investigate the relationship between yield and yield components (plant height, capsulenumber/plant, branch number/plant, total fructification length, capsule length and 1000-seed weight) in eight sesame genotypes (UCLA 83, Fonucla, UCLA 295, UCLA 65, UCLA 37-1, UCLA 249, UCLA 90 and UCLA 1), using different methods. The methods were: genotypic and phenotypic correlation analysis, regression analysis and pathway coefficients. The branch number and total fructification length showed the highest genotypic and phenotypiccorrelation with yield.

Genetic variation and correlation between seed yield and yield parameters (plant height, number of primary branches per plant, number of total branches per plant, distance from the base to the first branch or DB, number of capsules onthe main axis, number of

capsules per plant, capsule length, and number of seedsper capsule) were studied by Sonali and Datta (2004) in 22 sesame genotypes (control and 21 macromutant lines) grown in Kalyani, West Bengal, India. The phenotypic coefficient of variation was greater than the genetic coefficient of variation. High degree of heritability was recorded for plant height, number of seeds per capsule, number of capsules per plant, and DB. High heritability with high genetic advance was registered for number of capsules per plant and DB. After years of preliminary and advanced yield trials, seven advanced sesame genotypes were selected by Iwo *et al*. (2002) for on-station evaluation at NCRI, Badeggi and among four genotypes identified as promising lines were selected with the farmers' variety (Yandev-55) for multi-locational on-farm evaluation in six states. The result obtained showed that two genotypes 530-6-1 and E-8 gave the highest yield across the locations. Also the linear responses of the genotypes indicated E-8 to have average response to environments. This shows that E-8 hasthe potential to grow well under favorable condition. Other genotypes 530-6-1, Type 4 (1), Goza-25 and the check (Yandev 55) have b values less than Unity, which was an indication of better performance under poor environmental conditi

2.2 Correlation of yield and yield contributing traits in sesame

Sabiel *et al*. (2015) conducted a study to estimate the extent of genetic variability in genotypes of sesame (*Sesamum indicum* L.) under rainfed conditions in semi-arid zones. Twelve genotypes of sesame were grown at El Fasher Research Station Farm for three consecutive seasons. They reported that seed yield (kg/ha) was highly significant and positively correlated with biomass (yield kg/ha) (r = 0.81), 1000-seed weight (r = 0.57) and plant height (r = 0.50). However, it was highly significant and negatively correlated with days to flowering (r = -0.22). Therefore, the characters biomass yield kg/ha, 1000-seed weight and plant height were the most contributing characters on sesame seed yield.

The study was carried out by Akbar *et al*. (2011) to evaluate the phenotypic variability in the local sesame genotypes using 16 qualitative and quantitative traits. A total of 105 sesame accessions collected from diverse ecologies of Pakistan were used. The correlation coefficient analysis indicated that plantheight, capsules plant^{-1}, capsule length and 1000-seed weight had the significant positive effect on seed yield. The characters related to maturity, days to flower initiation and days to 50% flowering showed negative correlation with seed yield

Abate and Mekbib (2015) collected forty nine sesame genotypes from low- altitude areas

of Ethiopia and were evaluated by at Werer Agricultural Research Centre, for estimation of genetic variability and character association. Morphological data recorded on 14 quantitative traits were analyzed for analysis of variance, phenotypic and genotypic variability, heritability, genetic advance, correlation and path coefficient analysis. The traits biomass/plant, harvest index and 1000 seed weight exhibited highly significant positive correlation with seed yield/plant.

The field experiment was conducted by Sumathi and Muralidharan (2010) with thirty hybrids produced by line × tester mating design from eleven sesame genotypes involving five branched and six monostem/shy branching types. Observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, capsule breadth, number of seeds per plant, 100 seed weight, seed yield per plant and oil content. Seed yield per plant showed significantly positive correlation with plant height, number of branches per plant, number of capsules per plant, days to 50% flowering, days to maturity and 100 seed weight.

Liu and Zhao (2006), conducted an experiment with fifteen recently developed sesame cultivars/lines and 15 traits were recorded. With the exception of yield per plant, the other 14 traits were grouped into four groups. Canonical correlation analysis was made on the recorded data. Agronomic traits (plant height, capsule axis length and first capsule height) and yield contributing traits (seed per capsule and 1000-seed weight) were found to be most important toseed yield. These two trait groups were positively correlated and, therefore, can be combined for seed yield improvement. Oil content was correlated positively with agronomic traits, yield-contributing traits and volume weight of seed and negatively with seed width and protein content. As no negative correlation existed between oil content and seed yield, it is therefore presumed that the two can be improved simultaneously by indirect selection of seed characters.

Variability studies on yield and a yield component of sesame mutant lines in M_7 generation was carried out by Onginjo and Ayiecho (2009) in two locations for two seasons in Kenya. The objective of the study was to assess performance of the mutant lines developed through induced mutational breeding. Seed yield per plant registered the highest coefficient of correlation (63.8%). In addition, seed yield had positive and significant ($P<0.05$) correlation with biomass yield, harvest index and 1000- seed weight. It showed a weak positive association with plant height, oil content, number of capsules

per plant and number of days to flowering. Biomass yield, harvest index, 1000 seed weight and oil content had positive direct effect on seed yield. Line Mun 096/1/k5/2/4 was superior to the best check cultivar Spssik 116.

Genetic variability and correlation were studied by Mothilal (2006) among 20 genetically diverse sesame (*Sesamum indicum*) genotypes kharif in Vridhachalam, Tamil Nadu, India. Biometrical observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches, number of capsules per plant, 1000-seed weight, and seed yield per plant. Association analysis revealed that seed yield per plant had significantly positive correlation with days to maturity, plant height, number of branches and number of capsules per plant.

Forty diverse genotypes of sesame were studied by Singh (2005) during kharifto understand the variability and relative contribution of eight quantitative characters (days to 50% flowering, days to maturity, plant height, number of primary branches, number of capsules per plant, capsule length, capsule width and seeds per capsule) towards the yield. The seed yield exhibited highly significant and positive correlation with days to maturity, number of capsules perplant, capsule length and seeds per capsule at both genotypic and phenotypic level.

An investigation was carried out in Tamil Nadu, India by Parimala and Mathur (2006) to understand interrelationship and degree of dependence of seed yield onits components and elucidate their relative importance by using a full diallel set of six diverse cultivars of sesame and observations were recorded on seed yield and seven component characters including number of branches per plant, plant height, number of capsules per plant, capsule length, number of seeds per capsule and 1000-seed weight. The correlation coefficients of seed yield with plant height, number of branches per plant and number of capsules per plantwere highly significant and positive while those with number of seeds per capsule and 1000-seed weight were negative.

Correlation and path analysis studies by Siddiqui *et al*. (2005) on the yield and yield components of seven parents (Krishna Z-4-Co-1, TKG 32, TC 25, AHT 123, TKG 105, TKG 117 and RT 161) and 21 F_1 hybrids of sesame were

conducted using the diallel mating design. The seed yield was significantly and positively correlated with days to first flowering, days to 50% flowering, days to maturity, number of branches per plant, plant height, number of capsules per plant, weight of seed per

capsule, length of capsule and 1000-seed weight.

Fourteen sesame parentals and their 40 crosses were evaluated by Kumar and Sundaram (2002) for correlation between yield and yield contributing traits. The genotypic and phenotypic correlations between yield and capsule number, seed weight, primary branches, plant height and oil content, were positive while the associations between yield and days to flowering, capsule length and seeds per capsule were positive but non-significant. Simultaneous improvement of capsulenumber, primary branches and plant height would be possible as they were intercorrelated with each other.

Genetic variation and correlation between seed yield and yield parameters (plant height, number of primary branches per plant, number of total branches per plant, distance from the base to the first branch or DB, number of capsules onthe main axis, number of capsules per plant, capsule length, and number of seedsper capsule) were studied by Sonali and Datta (2004) in 22 sesame genotypes (control and 21 macromutant lines) grown in Kalyani, West Bengal, India. Seed yield was positively correlated with all the yield parameters except DB. The correlation among the yield parameters was mostly positive and significant.

Seed yield and related characteristics of sesame population involving eight determinate and four indeterminate types were studied by Uzun and Cagrgan (2001) by simple correlation coefficients and path coefficient analysis. Observations were recorded for seed yield, number of capsules per plant, number of seeds per capsule, stem height to the first capsule, plant height,fruiting zone length, 1000-seed weight, and number of fruiting branch. Number of capsule per plant was highly correlated with seed yield based on the correlation analysis.

2.3 Characters association for yield and yield contributing traits in sesame

An investigation was carried out in Tamil Nadu, India by Parimala and Mathur (2006) to understand interrelationship and degree of dependence of seed yield onits components and elucidate their relative importance by using a full diallel set of six diverse cultivars of sesame and observations were recorded on seed yield and seven component characters including number of branches per plant, plant height, number of capsules per plant, capsule length, number of seeds per capsule and 1000-seed weight. In path analysis, the highest direct effect on seed yield was exerted by the number of capsules per plant. It was evident that mostof the associations of seed yield with its component characters

were indirectly influenced through the number of capsules per plant. The multiple correlation coefficient between seed yield and all seven characters in equation was very high(R = 0.9754). The step-wise regression analysis revealed that the number of capsules per plant was the most important character having r = 0.9687 and could explain 93.84% of the total variation of seed yield

Fifteen sesame genotypes were grown by Biabani and Pakniyat (2008) in experimental station of Agricultural College, Shiraz University in Badjgah, Iran. Many plant traits were scored in the field. Path coefficient analysis and factor analysis divided the 15 measured variables into five factors. The five factors explained 81% of the total genetic variation in the dependence structure. Factor one was strongly associated with number of capsules in the main stem, length of floral axis, number of capsules per plant and plant height.

The genetic variation was determined by Banerjee and Kole (2006) in a population of 30 advance breeding lines of sesame in Visva-Bharati, Sriniketan, West Bengal, India in summer seasons. The results of path analysis at the genotypic level indicated that branches per plant, capsules per plant and seeds per capsule were the important characters determining seed yield in the studied sesame population.

Thirty-two hybrids and 12 parents were studied by Mothilal and Manoharan (2006) for seed yield and its contributing traits in sesame. Seed yield waspositively and significantly correlated with number of branches, number of capsules on main stem, number of capsules on branches, number of seeds per capsule and 1000-seed weight. Number of branches, number of capsules on branches and number of seeds per capsule showed positive direct effects on seed yield. Selection for these traits will be useful in increasing seed yield in sesame.

Correlation and path analysis studies by Siddiqui *et al*. (2005) on the yield and yield components of seven parents (Krishna Z-4-Co-1, TKG 32, TC 25, AHT 123, TKG 105, TKG 117 and RT 161) and 21 F_1 hybrids of sesame wereconducted using the diallel mating design. Strong positive direct effects were observed for plant height, days to 50% flowering and weight of seed per capsule.The indirect negative effects on yield were observed for days to first flowering, days to maturity, number of branches per plant, number of capsules per plant andlength of capsule.

The study was carried out by Mansouri and Najafabadi (2004) on 32 multi- branched sesame genotypes in Iran. Based on stepwise regression and ordinary path analyses,

number of capsules per plant, number of seeds per capsule, length of main inflorescence and 1000-seed weight had the highest direct effects on yield. Compared with ordinary path analysis, sequential path analysis showed higher values for the direct effects of length of main inflorescence, number of capsules per plant and 1000-seed weight and indirect effects of number ofbranches per plant and length of main inflorescence through number of capsules per plant.

Genetic variation and correlation between seed yield and yield parameters (plant height, number of primary branches per plant, number of total branches per plant, distance from the base to the first branch or DB, number of capsules onthe main axis, number of capsules per plant, capsule length, and number of seedsper capsule) were studied by Sonali and Datta (2004) in 22 sesame genotypes

(control and 21 macromutant lines) grown in Kalyani, West Bengal, India. Path analysis showed that the number of capsules per plant had the greatest positive direct effect on seed yield, followed by capsule length, number of seeds per capsule, and total number of branches per plant. The indirect contribution of these traits on seed yield was also very significant and positive. Plant height, number of primary branches per plant, and number of capsules on the main axis showed direct negative effects on seed yield, and the indirect effects on seed yield via these traits were generally negative. The results suggested the simultaneous selection for number of capsules per plant, capsule length, and number of seeds per capsule for efficient breeding in sesame.

A study was conducted by Laurentin *et al*. (2004) in Venezuela to investigate the relationship between yield and yield components (plant height, capsulenumber/plant, branch number/plant, total fructification length, capsule length and 1000-seed weight) in 8 sesame genotypes (UCLA 83, Fonucla, UCLA 295, UCLA 65, UCLA 37-1, UCLA 249, UCLA 90 and UCLA 1), using different methods. The methods were: genotypic and phenotypic correlation analysis,regression analysis and pathway coefficients. Pathway analysis showed that1000-seed weight and branch number had the most important direct effect on yield, but these variables also showed negative indirect effects on each other.

Seed yield and related characteristics of sesame population involving eight determinate and four indeterminate types were studied by Uzun and Cagrgan (2001) by simple correlation coefficients and path coefficient analysis. Observations were recorded for seed yield, number of capsules per plant, number of seeds per capsule, stem height to the first capsule, plant height,fruiting zone length, 1000-seed weight, and number

of fruiting branch. Plant height had the greatest direct effect on seed yield of determinate growth habit regarding the result of path coefficient analysis, differing from the results of earlier reports on indeterminate sesame types.

2.4 Clustering outline and cluster distance in sesame genotypes

Pandey *et al*. (2015); carried out a study with 37 characters including both quantitative and qualitative traits of sixty genotypes were characterized following IPGRI morphological descriptors for sesame. Multivariate analysis was computed to distinguish the varieties into different groups. Cluster analysis based on morphological and molecular marker classified sesame genotypes into two major groups. Mantel test showed an insignificant correlation between phenotypic and molecular marker information. The genotypes belonging to the same geographical area did not always occupy the same cluster. The results confirmed that both genetic and phenotypic diversity in a combined way could efficiently evaluate the variation present in different sesame accessions in any breeding program.

Tripathi *et al*. (2013); collected total of 100 sesame accessions from diverse ecologies of India were used in a research work and analysis of variance revealed significant difference among genotypes for all the nine characters studied. Genetic divergence using Mahalanobis D^2 statistics was worked out and based on D^2 values the germplasm lines were grouped into eleven different clusters. Clustering was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences. Maximum inter cluster distance was observed between cluster VI and cluster XI (134.72) followed by clusters V and XI (124.23) while, lowest divergence was noticed between cluster IV and V (9.37). Among the nine characters studied, days to 50% flowering contributed highest towards genetic divergence (21.05 %)followed by seed yield per plant (20.85 %). Cluster VI exhibited highest means for days to 50 % flowering (62.5), plant height (119.8), number of primary and secondary branches per plant (10.4, 19.3) and days to maturity (110.5). Cluster XI exhibited lowest means for days to 50 % flowering (46), plant height (81.4), number of primary branches per plant (6.7) and days to maturity (100.5). Greatergenetic divergence was found between clusters VI and XI followed by clusters Vand XI indicating superior and novel recombinants and explore the fullest rangeof variability for the characters and to realize good recombinant can be realized by mating between the lines of these clusters in a definite fashion.

The study was carried out by Akbar *et al*. (2011) to evaluate the phenotypic variability in the local sesame genotypes using 16 qualitative and quantitative traits. A total of 105 sesame accessions collected from diverse ecologies of Pakistan were used. Plant height, days to maturity, capsules plant^{-1} and seed yield plant^{-1} were the major determinants of the genetic diversity in the collection. Cluster analysis places all the accessions into seven groups. Clustering was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences. Elite sesame germplasm has been selected on the basis of best agro-morphological performance from 105 sesame collections. These results have an important suggestion for sesame germplasm agro-morphological assessment, enhancement, categorization and conservation in Pakistan.

The experiment was conducted by Parsaeian *et al*. (2011) to study the genetic variation among eighteen genotypes of sesame (*Sesamum indicum* L.) collected from various agro-climatic regions of Iran along with six exotic genotypes from the Asian countries using both agro-morphological and ISSR marker traits. The results showed significant differences among genotypes for all agro- morphological traits and a relatively high genetic coefficient of variation observed for number of fruiting branches per plant, capsules per plant, plant height and seed yield per plant. Cluster analysis based on these traits grouped thegenotypes into five separate clusters. Larger inter- than intra cluster distances implies the presence of higher genetic variability between the genotypes of different groups. Genotypes of two clusters with a good amount of geneticdivergence and desirable agronomic traits were detected as promising genotypes for hybridization programs. The discordance among diversity patterns and geographical distribution of genotypes found in this investigation implies thatthe parental lines for hybridization should be selected based on genetic diversity rather than the geographical distribution.

Genetic divergence was studied by Kumhar and Solanki (2009) growing 82 genotypes of sesame, *Sesamum indicum* L. at Agricultural Research Station, Mandor, Jodhpur. The hierarchical cluster analysis indicated the presence of considerable genetic divergence among the genotypes. The genotypes were grouped into eight clusters using Ward's minimum variance method. The inter- cluster Euclidean2 distance was maximum between cluster V and VIII followed by cluster V and VII and cluster II and V which indicated that the genotypes included in these clusters will give high heterotic response and thus better segregants. The maximum cluster means were revealed by cluster V for seed yield, plant height and number of capsules/plant, cluster II for number of primary

branches/plant and cluster III for test weight, while cluster VIII showed minimum cluster means for plant height to first capsule, days to 50% flowering and maturity. Among the eight characters studied seed yield contributed the most(38.9%) towards the divergence of genotypes.

The genetics of seven quantitative traits of sesame was studied by Lavanya *et al*. (2006) through a full diallel cross involving six genotypes (TMV-3, TMV-4, TMV-6, CO-1, SVPR-1 and VRI-1) in field experiments conducted in Tamil Nadu, India. Yield characters such as days to 50% flowering, plant height at maturity, number of branches per plant, number of capsules per plant, number ofseeds per capsule, 1000-seed weight and seed yield per plant were observed. Data from the parents and F_1 crosses were analysed using the Hayman method of diallel analysis. The estimates of D were significant for five out of the seven traits studied. The values of H_1 and H_2 as well as the $H_2/4H_1$ indicated that there were unequal frequencies of alleles at all the loci for all the characters studied, excepting 1000-seed weight.Field experiments were conducted by Kumaresan and Nadarajan (2005) in TamilNadu, India to study the stability of yield and its components (days to 50% flowering, number of branches, numbers of capsules and single plant yield) in 64sesame genotypes comprising 48 hybrids and 16 parents. The parents, i.e. TNAU28, TN 8467 and B 203 and the F_1 hybrids, i.e. SI 42 × VRI 1 and B 203 ×SVPR 1, were identified as stable genotypes with high yield. These genotypes can be recommended for varied environments to exploit their high yield potential.

The study was carried out by Mansouri and Najafabadi (2004) on 32 multi- branched sesame genotypes in Iran. Factor analysis indicated that three factors could explain approximately 80% of the total variation. The first factor compared the number of capsules per plant and length of main inflorescence versus distance of first capsule and first branch from the soil surface. The secondfactor had positive effects on capsule length, number of seeds per capsule and 1000-seed weight, whereas the third factor had positive effects on number of capsules and number of branches per plant. Based on path and factors analyses, selection for lower distance of first capsule and first branch from the soil surface (which could be done in early fruit set stages) can yield similar results as the selection for higher number of capsules per plant and main inflorescence length for yield improvement. Selection based on higher number of seeds per capsule and 1000-seed weight (which have less direct effects on seed yield) could be achieved by selection based on longer capsule length. The latter traits could be measured non-destructively. The

nature of the third factor indicated that selection based on number of branches per plant might result in seed yield improvement in sesame.

The above cited review revealed that the importance of a systematic research on sesame genotypes in genetic diversity, correlation among yield contributing characters, path coefficients patents and gene actions of governing characters for improvement of the sesame crop.

CHAPTER III

MATERIALS AND METHODS

The experiment was carried out to find out the character association of 32 sesame genotypes. The particulars of the materials and methods i.e. description of the experimental site, soil and climate condition ofthe experimental plot, materials used, design of the experiment, data collection procedure and procedure of data analysis that used or followed in this experiment has been presented downwards under the following headings:

3.1 Experimental site description

3.1.1 Period of the experiment

The field experiment was conducted during the time period of March to June, 2022.

3.1.2 Description of the site

The present piece of research work was conducted in the experimental area of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka. The location of the site is $23^0 74^/$N latitude and $90^0 35^/$E longitude with an elevation of 8.2 meter from sea level. The photograph showing experimental sites (Appendix).

3.1.3 Condition of the climate

The geographical location of the experimental site was under the subtropical climate and its climatic conditions is characterized by three distinct seasons, namely winter season from the month of November to February and the pre- monsoon period or hot season from the month of March to April and monsoon period from the month of May to October (Edris *et al*., 1979). Particulars of the meteorological data of air temperature, relative humidity, rainfall and sunshine hour during the period of the experiment was collected from the Weather Stationof Bangladesh, Sher-e-Bangla Nagar, Dhaka and details has been presented in Appendix I.

3.1.4 Characteristics of soil of the experimental plot

The soil belonged to "The Modhupur Tract", AEZ-28 (FAO, 1988). Top soilwas silty clay in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH was 5.47-5.65 and had organic carbon 0.45%. The experimental area was flat having available irrigation and drainage system and above flood level. The selected plot was medium high land. The details have been showed in Appendix II.

3.2 Details of the experiment

3.2.1 Experimental materials

In this experiment 32 sesame genotypes (Table 1) were used as experimental materials which were produced in the 2020-2021 cropping season, and the purityand germination percentage were leveled as 95% and 93% respectively. These seeds were collected from Plant Genetic Resources Centre (PGRC) section of Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur.

Table 1. Name of sesame genotypes used in the present study

Serial no	Sesame genotypes	Serial no	Sesame genotypes
G-1	BD-10646	G-17	BD-11629
G-2	BD-10647	G-18	BD-11630
G-3	BD-10648	G-19	BD-11631
G-4	BD-10650	G-20	BD-11632
G-5	BD-10651	G-21	BD-11633
G-6	BD-10652	G-22	BD-11634
G-7	BD-10654	G-23	BD-11635
G-8	BD-10659	G-24	BD-11636
G-9	BD-11621	G-25	BD-11637
G-10	BD-11622	G-26	BD-11638
G-11	BD-11623	G-27	BD-11639
G-12	BD-11624	G-28	BD-11640
G-13	BD-11625	G-29	BD-11641
G-14	BD-11626	G-30	BD-11642
G-15	BD-11627	G-31	BD-11643
G-16	BD-11628	G-32	BD-11644

3.2.2 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experimental plot was 330.75 m^2 withlength 24.5 m and width 13.5 m. Each replication size was 23.5m*4m, and the distance maintained between two blocks and two plots were 0.5 m and 0.5 m, respectively. Each block was divided into 32 plots where 32 sesame genotypes were allotted at random. There were 96 unit plots altogether in the experiment.

3.3. Crop growing

3.3.1 Main field preparation

The experimental land was opened in the 1rd week of March 2022 with a power tiller, and was exposed to the sun for a week after which the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain a good tilth. Stubble and weeds were removed from the field and finally a desirable tilth of soil was obtained for sowing of sesame seeds. Manures and fertilizers as indicated below in 3.3.3 were mixed with the soil of plot.

3.3.2 Sowing seeds

When the land was in proper joe condition furrows were made for sowing the sesame seeds and seeds were sown at 25 March, 2022. Seeds were sown continuous in rows in broadcasting with maintaining 30 cm line to line distance and plant to plant 5 cm (approximate). The seeds were placed at about 1 cm depth in the soil. After sowing, seeds were covered with soil carefully so that no clods were on the seeds and slightly pressed by hand.

3.3.3 Application of fertilizers and manure

The total amount of cowdung were applied after 1st ploughed. The whole amount of TSP, MoP, gypsum, zinc sulphate, boric acid and 50% urea, was applied as basal dose at the time of find land preparation. The rest of urea was applied in installment at 25 DAS (day after sowing). Manures and fertilizers that were applied to the experimental plot presented in Table 2.

Plate 1. A. Seed bed preparation, land preparation and layout of the land; B. Seedlinds.

Plate 2. C. Irrigation to the new plant; D. After gap feeling; E. Plants after flowering

Plate 3. F. After capsule formation; G. Mature capsule before harvesting.

Table 2. Dose and method of application of fertilizers in sesame field

Fertilizers and Manures	Dose/ha	Application (%)	
		Basal	25 DAS
Cowdung	10 tonnes	100	--
Urea	100-125 kg	50	50
TSP	130-150 kg	100	--
MP	40-50 kg	50	25
Gypsum	100-110 kg	100	--
Zinc Sulphate	0-5 kg	100	--
Boric acid	8-10 kg	100	--

Source: BARI, 2020, Krishi Projukti Hatboi, Joydebpur, Gazipur

3.3.4 After care and intercultural operations

After the germination of seeds, various intercultural operations such as weeding, top dressing of fertilizer and plant protection measures were substantiated for better growth and desirable development of the sesame seedlings followed by the recommendation of BARI.

Irrigation

Due to high temperature several time irrigation was given.

Thinning

Thinning was done carefully for better growth of the germinated palnts and it was done manually after 3 weeks of sowing. Care was taken to maintain constant plant population per plot.

Gap Filling

Due to heavy rainfall and water logging condition many seedling was died. Dead, injured and week seedlings were replaced by healthy one from the stock kept on the border line of the experimental plot. The transplanted seedlings were provided shading and watering for 03 days for the establishment of seedlings.

Weeding

Due to heavy rainfall weed growth was so high. Several times weeding was done followed by raining irrigation.

Plant protection, pest and disease management

Caterpillar did several pest infection. The crop was protected from the attack of insect-pest by spraying Malathion-57 EC@ 5ml/liter of water.The insecticide application were made fortnightly as a matter of routine work from seedling emergence to the end of harvest. Also during the final stage of fruiting period the whole field was covered with net to protect sesame capsule from birds and other insects.

3.4 Harvesting, threshing and cleaning

The crop was harvested manually when 80% of plant was mature. Harvesting was done separately depending upon the maturity and bundled separately, properly tagged and brought to threshing floor. Proper care was taken during threshing and cleaning of sesame seeds.

3.5 Data collection

Days to first flowering

Days to first flowering was recorded by calculating the number of days from sowing date to the date of first flowering by keen observation.

Days to 50% flowering

Days were recorded from sowing date to the date of 50% flowering by keen observation of the experimental plot.

Days to 80% maturity

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

Plant height(cm)

It was measured in centimeter (cm) from the base of the plant to the tip of the longest inflorescence. After harvesting the data was collected. Data of 10 plants was collected in every genotypes and from every replications and then averaged.

Number of branches/plant

The total number of branches arisen from the main stem of each plant was counted from plant of each unit plot. Data were recorded as the average of 10 plants selected at random from the inner rows of each plot.

Number of capsule/plant

10 randomly selected plants from each unit plot were taken, numbers of capsule were

counted and their mean values were recorded.

Length of capsule (cm)

This length of pods was taken in centimeter (cm) of the five representative capsules of every plants. This data was collected from every 10 plants of each genotypes of each replication then average them.

Number of seeds/capsule

Seeds per capsule were counted from 10 randomly selected capsules as harvested from each unit plot.

Weight of 1000 seeds (g)

1000 seeds were counted randomly from the total cleaned harvested sesame seeds of each individual plot and then weighed in grams and recorded.

Seed yield/plant (g)

The seed yield of every individual plant was taken in gram. Data was collected in every 10 plants of each replication then averaged.

3.6 Statistical Analysis

The data obtained for different traits of sesame genotypes were statisticallyanalyzed to observe the differences in different sesame genotypes. The mean values of all the characters were calculated and analysis of variance was performed. The significance of the difference among the treatment means was estimated by the Duncan Multiple Range Test (DMRT) at 5% level of probability (Gomez and Gomez, 1984).

3.7 Variability estimation

Genotypic and phenotypic coefficient of variation and heritability were estimated by using the following formulae:

Genotypic and phenotypic variance estimation

Genotypic and phenotypic variances were estimated with the help of thefollowing formula suggested by Johnson *et al.* (1955).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{MS_V - MS_E}{r}$$

Where,

MS_V = genotype mean square

MS_E = error mean square

r = number of replication

Phenotypic variance (σ^2_{ph}) = $\sigma^2_g + \sigma^2_e$

Where,

σ^2_{ph} = phenotypic variance

σ^2_g = genotypic variance

σ^2_e = error variance

Genotypic co-efficient of variation (GCV) andphenotypic co-efficient of variation (PCV) estimation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation(PCV) were calculated following formula as suggested by Burton (1952):

$$\% \text{ Genotypic coefficient of variance} = \frac{\sigma_g}{\bar{x}} \times 100$$

Where,

σ_g = genotypic standard deviation;

$\bar{x}$ = population mean

$$\% \text{ Phenotypic coefficient of variance} = \frac{\sigma ph}{\bar{x}} \times 100$$

Where,

σ_{ph} = phenotypic standard deviation;

$\bar{x}$ = population mean

Heritability estimation

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$\text{Heritability (\%)} = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where,

σ^2_g = genotypic variance and

σ^2_{ph} = phenotypic variance

Genetic advance estimation

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

$$GA = \frac{\sigma^2_g}{\sigma^2_p} \times K.\ \sigma_p$$

Where,

GA = Genetic advance

σ^2_g = genotypic variance

σ^2_{ph} = phenotypic variance

σ_{ph} = phenotypic standard deviation

K = Selection differential which is equal to 2.64 at5% selection intensity

Genetic Advance in percentage of mean estimation

Genetic advance in percentage of mean was calculated by the following formulagiven by Comstock and Robinson (1952):

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{x}} \times 100$$

3.8 Correlation estimation

Simple correlation was estimated for different traits with the following formula(Singh and Chaudhary, 1985):

$$r = \frac{\sum xy - \frac{\sum x.\ \sum y}{N}}{\left[\left\{\sum x^2 - \frac{(\sum x)^2}{N}\right\}\left\{\sum y^2 - \frac{(\sum y)^2}{N}\right\}\right]^{1/2}}$$

Where,

$\sum$ = Summation

x and y are the two variables

N = Number of observations

3.9 Genotypic and phenotypic path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect of independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say x_1, x_2, x_3 yield y, a set of simultaneous equations (three equations in this example) isrequired to be formulated as given below:

$$ryx_1 = Pyx_1 + Pyx_2rx_1x_2 + Pyx_3rx_1x_3ryx_2$$

$$= Pyx_1rx_1x_2 + Pyx_2 + Pyx_3rx_2x_3ryx_3 =$$

$$Pyx_1rx_1x_3 + Pyx_2 rx_2x_3 + Pyx_3$$

Where, r‟s denotes simple correlation co-efficient and P‟s denote path co- efficient (unknown). P‟s in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

Pyx_1 = The direct effect of x_1 on y

$Pyx_1rx_1x_2$ = The indirect effect of x_1 via x_2 on y

$Pyx_1rx_1x_3$ = The indirect effect of x_1 via x_3 on y

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

$$P^2RY = 1 - \sum Piy.riy$$

Where,

$P^2RY = (R^2)$; and hence residual effect, $R = (P^2RY)^{1/2}Piy$

= Direct effect of the character on yield

riy = Correlation of the character with yield

3.10 Genetic divergence analysis

Genetic divergences among the genotypes studied were assessed by using Mahalanobis‟ D^2 statistics and its auxiliary analysis. Both techniques estimate divergences among a set of genotypes on multivariate scale.

Mahalanobis' D^2 statistics

First the variation among the materials were tested by Wilkin‟s criteria „^‟.

$$„^‟ = \frac{|W|}{|S|} = \frac{|\text{Determination of error matrix}|}{|\text{Determination of error + variety matrix}|}$$

Now, $„v‟_{(stat)} = -m \log_{e^\wedge} = -\{n-(p+q+1)/2\}\log_{e^\wedge}$

Where,

m = n-(p+q+1)/2

p = number of variables or characters

q = number of varieties – 1 (or df for population)n =

df for error + varieties

e = 2.7183

Data were then analysed for D^2 statistics according to Rao (1952). Error varianceand covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Using the pivotal elements the original means of the characters (X_1, X_2---------X_8) were transformed into a set of uncorrelated variables (Y_1, Y_2---------- Y_8).

Now, the genetic divergence between two varieties/lines (suppose Vi and Vj was calculated as –

$$D^2ij = \sum_{k=1}^{8} (Vik - Vjk)^2$$

Where,

D^2ij = Genetic divergence between „i‟ th and „j‟ th genotypes

Vik = Transformed mean of the „i‟ th genotype for „k‟ th character

Vjk = Transformed mean of the „j‟ th genotype for „k‟ th character

The D^2 values between all the studied genotypes were arranged in order of relative distances from each other and were used for clusters formation, assuggested by Rao, 1952.

$$\text{Average intra-cluster } D^2 = \frac{\sum D^2 i}{N}$$

Where,

$\sum D^2 i$ = Sum of distances between all possible combinations (n) of the genotypes included in a cluster.

N = All possible combinations.

CHAPTER IV

RESULT AND DISCUSSION

The present experiment was conducted to study the multivariate analysis and character association of 32 sesame genotypes. Mean performance, variability, correlation matrix, path analysis and genetic diversity analysis on different yield contributing characters and yield of sesame genotypes was estimated. The experimental results obtained have been presented under the following headings and sub-headings:

4.1 Variability study for 10 yield and yield contributing traits of *Sesamum indicum*

4.1.1 Variability among the 32 variety of *Sesamum indicum*

Results of analysis of variance (Appenix IV) of the studied data on different yield components of 32 materials of *Sesamum indicum* genotypes, values of mean, range, CV%, SD and SE summarized in Table-3 and Table-4 showed the values of genotypic variance, phenotypic variance, environmental variance, genotypic co-efficient of variation, phenotypic co-efficient of variation, environmental co-efficient of variation, heritability, genetic advance, genetic advance in percentage of mean ` for different yield related characters. Among the genotypes, almost all characters exhabit highly significant variation indicating wide scope of selection for these characters. This considerable variability provides a good opportunity for improving desirable traits of interest in plant breeding programs.

Table 3. Range, Mean, CV (%) and standard deviation of 50 sesame **genotypes**

Traits	Range		Mean	CV (%)	SD
	Min	Max			
Days to first flowering	31	35.5	33.03	3.54	1.17
Days to 50% flowering	46	50	48.03	2.48	1.19
Days to 80% maturity	77.33	84.33	80.66	2.48	2.00
Plant height (cm)	93.29	127.87	106.15	6.47	6.87
Number of branchs/plant	2.23	6.03	3.76	24.20	0.91
Number of capsules/plant	46.03	149.40	74.54	31.78	23.69
Number of seeds/capsule	60.77	75.67	68.62	5.10	3.5
Length of capsule (cm)	2.41	2.92	2.61	4.60	0.12
1000 seed weight (g)	2.48	3.25	2.91	7.90	0.23
Seed yield per plant (g)	83.20	307.67	151.57	33.32	50.50

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error

Table 4. Genetic parameters for yield contributing characters and yield of different sesame genotypes

	(σ^2g)	(σ^2p)	(σ^2e)	GCV	PCV	ECV	Heritability (%)	Genetic Advance (GA)	(GA) in percentage of mean
Days to first flowering	1.12	1.88	0.77	3.20	4.15	2.65	59.25	1.67	5.07
Days to 50% flowering	1.21	1.86	0.65	2.29	2.84	1.68	65.17	1.83	3.81
Days to 80% maturity	3.79	4.43	0.64	2.41	2.61	0.99	85.59	3.71	4.60
Plant height	46.13	49.47	3.34	6.40	6.63	1.72	93.25	13.51	12.73
Number of branches/plant	0.82	0.87	0.05	24.11	24.79	5.75	94.62	1.82	48.32
Number of capsules/plant	560.85	561.95	1.10	31.77	31.80	1.41	99.80	48.74	65.38
Length of capsule (cm)	0.01	0.01	0.001	4.51	4.70	1.30	92.05	0.23	8.92
Number of seeds/capsule	12.17	12.47	0.30	5.08	5.14	0.80	97.59	7.10	10.34
Weight of 1000 seeds (g)	0.05	0.05	0.001	7.66	7.74	1.12	97.84	0.45	15.60
Yield/plant (g)	2477.78	2693.52	215.73	32.84	34.24	9.69	91.99	98.35	64.88

σ^2g = Genotypic variance, **σ^2p**= Phenotypic variance and **σ^2e** = Environmental variance, GCV = Genotypic co-efficient of variation, PCV = Phenotypic coefficient of variation, ECV = Environmental coefficient of variation.

4.1.1 Days to first Flowering

Mean value for days to first flowering was 33.03. The days to first flowering ranged from 31 to 35.33 days (Table 3). The minimum days to first flowering was found in G-2, G-3 and G-11 (31 days) which was statistically similar to G-5 and G-19 (31.67) and maximum days to first flowering was found in G-12 (35.33 days). Which was statistically similar to (34.67, 34, 34, 35, 34, 34, 34.33, 34.33, 34) to the sesame genotype G-4, G-6, G-13, G-15, G-21, G-22, G-23, G-25, G-28 (Appendix-III). CV% was 3.54(Table 3). Environmental variance and environmental coefficient of variation were 0.77 and 2.65 respectively. Phenotypic and genotypic coefficient of variance for the days to first flowering was observed as 4.15% and 3.20%, respectively (Table 4). The PCV value is higher than GCV are indicate that the variability for the character was influenced by both genotypes and environment. Days to first flowering exhibited moderate heritability (59.25%) with low genetic advance (1.67) and low genetic advance in percentage of mean (5.07%) indicated that this trait was controlled by non-additive gene. Selection for this character will not be effective. Akber *et al.*(2010) found considerable level of variation among morphological traits. Alake et al (2010) reported highly significant genotype effect in terms of plant height in sesame.

4.1.2 Days To 50% Flowering

The mean sum square for days to 50% flowering showed highly significant (Appendix IV) indicating highly significant difference for this trait. The mean value for the days to 50% flowering was 48.03. The range of days to 50% flowering was 46 to 50 days (Table 3). The minimum days to first flowering was found in G-6, G-9, G-16, G-28, G-29 and G-30 (46-days) which was statistically similar to G-3(47). Maximum days to 50% flowering was found in G-25(50 days). It was statistically similar to (49.67, 49.33) to the genotype G-4, G-17 and 49 for G-(7, 10, 12, 18, 20, 22, 31, 32) (Appendix- III). CV% is 2.48 (Table 3). Phenotypic and genotypic variance for the days to 50% flowering was observed as 1.86 and 1.21 respectively. Environmental variance and environmental coefficient of variation were 0.65 and 1.68 respectively (Table 4).The PCV value is higher than GCV value indicate that the variability for the character was influenced by environment. The genotypic co-efficient of variation is 2.29 and phenotypic co-efficient of variation is 2.84. The difference between GCV and PCV was very low. Heritability estimate for this character was moderately high (65.17%) with low genetic advance (1.83) and low genetic advance in percent of mean 3.81, this indicate that selection for this character would not be effective.

4.1.3 Days To 80% maturity

The mean sum square for the days to 80% maturity was highly significant (Appendix IV). This indicates that there are high range of variation among the sesame genotypes for this character. Maximum days to 80% maturity was recorded 84.33 in G-7 which was statistically similar to 83.33 in G-13, 83 in G-1, G-2, G-5, G-23, G-31 and 82 in G-4, G-6, G-17, G-26, G-28. Minimum days recorded was 77.33 in G-9 and it was statistically similar to (77.67, 79.33, 78.67, 78.33, 78.67) to the sesame genotypes G-16, G-3, G-11, G-21, G-25 (Appendix III). The mean value was 80.66 days and CV(%) was 2.48 (Table 3). The genotypic variance was 3.79 and phenotypic variance was 4.43. The phenotypic variance appear to be higher than genotypic variance, indicates that there was significant influence of environment on this trait. Environmental variance and environmental coefficient of variation were 0.64 and 0.99 respectively. The GCV (2.41) value lower than the PCV (2.61) value. The heritability for this character was high (85.59%) and the genetic advance (3.71) and genetic advance in percent of mean (4.60) (Table 4) was low indicate that selection for this character would not be effective. Pathak and Dixit (1986;1992) estimated moderate genetic advance and high heritability for this trait. Salas also recorded high heritability (95.12%) for days to 80% maturity.

4.1.4 Plant height (cm)

The growth performance of a crop is influenced by the height of the plant. The plant height is determined by both the genetic and environmental factors of the plant. The mean sum square for plant height (141.758) was highly significant ($P \leq 0.01$), which indicated genotypic differences present among the genotypes under the study (Appendix-IV). CV(%) was 6.47. The mean value of plant height was 106.15 cm and the minimum and maximum height is 93.29 cm and 127.87 cm respectively(Table 3). The minimum height was recorded in G-1 which is statistically similar with G-2 (96.55 cm) and the maximum height was recorded in G-3(Appendix-III). Plant height refers to phenotypic variance (49.47) was higher than the genotypic variance (46.13) that indicating that high environmental influence on this characters which was supported by narrow difference between phenotypic (6.63%) and genotypic (6.40%) co-efficient of variation (Table 4). The highest difference for this parameter was also suggested a highly significant influence ofenvironment. High heritability (93.25%) in plant height attached with low genetic advance (13.51) and lowest genetic advance in percentage of mean(12.73). Environmental variance and environmental coefficient of variation were 3.34 and 1.72

respectively (Table 4). High estimate of heritability and low genetic advance for plant height suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non additive genetic effects for the control of this character. This indicate that selection for this character would be effective. Pathak and Dixit (1986, 1992) found high heritability for plant height. They also found higher magnitude of genetic advance in percent of mean in case of plant height.

4.1.5 Number of branches per plant

Number of branches per plant varied highly significant among the genotypes (2.516) (Appendix IV). CV(%) was 24.20. The data ranged from 2.23 to 6.03 for number of primary branches per plant with the mean value of 3.76 (Table 3). Minimum number of primary branches per plant was observed in G-14 (2.23) followed by both G-18, G-10 (2.60) whereas the maximum number of branches/plant was observed in G-24 (6.03). Phenotypic variance and genotypic variance were observed as 0.87 and 0.82 respectively (Table 4). The phenotypic variance was slightly higher than genotypic variance suggested that there was little influence of environment on the expression of the genes controlling this trait. The PCV and GCV was 24.79 and 24.11 respectively. Environmental variance and environmental coefficient of variation were 0.05 and 5.75 respectively. Heritability estimated for this trait was high (94.62%) with low genotypic advance (1.82) and moderately high genetic advance in percent of mean (48.32) (Table 4) which revealed that this character was governed by non-additive gene but high genetic advance in percentage of mean which indicated that possibility of predominance of additive gene, so much scope to improve. As a whole, the high heritability was being exhibited due to favorable influence of environment rather than genotypes and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual plants showed quite a reasonable number of branches which were selected for further study in the next generation. Tepora *et al.*(1983) estimated high heritability and high genetic advance in percent of mean for this trait. Chowdhury *et al.*(1987) also found significant differences for number of branches per plant. Reddy (1986) found similar result as my experiment.

4.1.6 Number of capsules/plant

Statistically important differences were measured for different sesame genotypes in terms

of number of pods/plant (Appendix-IV). CV(%) was 31.78. It was revealed that the average number of capsules/plant was observed around 74.54 with the range from 46.03 to 149.40 (Table 3). The maximum number of capsules per plant (149.40) was found in the genotype of G-27 followed by G-24 (125.93) whereas the minimum number of capsules/plant (46.03) was recorded from the genotype of G-1 followed by G-10 (46.53) (Appendix-III.). Number of capsule/plant refers to phenotypic variance (561.95) was slightly higher than the genotypic variance (560.85) that indicating that high environmental influence on this characters which was supported by narrow difference between phenotypic (31.80%) and genotypic (31.77%) co-efficient of variation (Table 4). The highest difference for this parameter was also suggested a highly significant influence of environment. Environmental variance and environmental coefficient of variation were 1.10 and 1.41 respectively. High heritability (99.80%) in number of capsule/plant attached with moderate genetic advance (48.74) and high genetic advance in percentage of mean (65.38) (Table 4). Highest heritability coupled with high genetic advance was observed for capsule weight per plant, height of first capsule and seed yield per hectare. Thus, these traits could be used as selection criteria for yield improvement in sesame. Revathi *et al*. (2012) estimated high genotypic coefficient of variability and phenotypic coefficient of variability for number of capsules per plant.

4.1.7 Length of capsule (cm)

It was revealed that the average number of length of capsule was observed around 2.61 with the range from 2.41 to 2.92. CV(%) was 4.60 (Table 3). The length of capsule was observed highest in G-27 (2.92) followed by G-(7, 20) (2.77), G-15 (2.78), G-(19,32) (2.70), G-28 (2.75), G-23 (2.8). Minimum was observed in G-5 (2.41) followed by G-6 (2.46), G-9 (2.44), G-10 (2.48), G-16 (2.47), G-(22, 30) (2.49) (Appendix-III). Length of capsule refers to phenotypic variance (0.01) was same as the genotypic variance (0.01) that indicating that there is not any environmental influence on this characters which was supported by narrow difference between phenotypic (4.70%) and genotypic (4.51%) co-efficient of variation (Table 4). Environmental variance and environmental coefficient of variation were 0.001 and 1.30 respectively. The moderate difference for this parameter was also suggested a moderately significant influence of environment. High heritability (92.05%) in length of capsule attached with low genetic advance (0.23) and high genetic advance in percentage of mean (8.92) (Table 4). The high heritability along with low genetic advance in length of capsule indicated the possible scope for improvement

through selection of the character and breeder may expect reasonable benefit in next generation in respect of this trait. This indicates that the non-additive gene controlling this character. Selection based on this character for future breeding program is not effective. Same result is found by Teddy. El-Hifny *et al.* (1988) found significant difference among genotypes for pod length.

4.1.8 Number of seeds/capsule

Number of seeds per pod reveal highly significant variations (36.808) among the genotypes (Appendix IV). Data revealed that the average number of seeds/capsule was observed around 68.62 with the range from 60.77 to 75.67. CV(%) was 5.10 (Table 3). The number of seeds per capsule was observed highest in G-7 (75.67) followed by G-27 (74.17), G-24 (73.87), G-8 (72.97). Minimum was observed in G-11 (60.77) followed by G-14 (63.9), G-15 (63.8), G-26 (63.23) (Appendix-III). Number of seeds/capsule refers to phenotypic variance (12.47) was slightly higher than the genotypic variance (12.17) that indicating that low environmental influence on this characters which was supported by narrow difference betweenphenotypic (5.14%) and genotypic (5.08%) co-efficient of variation (Table 4). The highest difference for this parameter was also suggested a highly significant influence of environment. Environmental variance and environmental coefficient of variation were 0.30 and 0.80 respectively. Higher heritability (97.59%) in number of seeds/capsule attached with low genetic advance (7.10) and low genetic advance in percentage of mean (10.34) (Table 4). Moderate estimate of heritability and low genetic advance for number of seeds/capsule suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and nonadditive genetic effects for the control of this character. Selection for this character for future breeding program will not be so good Tepora *et al.*(1983) reported high genotypic as well as phenotypic co-efficient of variations for number of seeds per capsule in sesame

4.1.9Weight of 1000 seeds (g)

The perusal of the data pertaining to 100-seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions (0.150) (Appendix-IV). The average weight of 1000 seeds was recorded 2.91 g with a range from 2.48 g to 3.25 g. CV(%) was 7.90 (Table 3). Maximum 100-seed weight (3.25 g) was observed in G-15 followed by G-23 (3.23), G-30 (3.19), G-(24, 31) (3.13), G-(14,

32) (3.12), G-(6 ,12) (3.1), G-17 (3.11). Whereas the minimum was found in G-2 (2.48g) followed by G-16 (2.51), G-11 (2.59), G-5 (2.55), G-22 (2.61) (Appendix-III). Weight of 100 seeds refers to phenotypic variance (0.05) was same as that of the genotypic variance (0.05) that indicating that there was not any environmental influence on this characters which was supported by narrow difference between phenotypic (7.74%) and genotypic (7.66%) co-efficient of variation (Table 4). The highly difference for this parameter was also suggested highly significant influence of environment. Hight heritability (97.84%) in weight of 100 seeds attached with low genetic advance (0.45) and high genetic advance in percentage of mean (15.60). Environmental variance and environmental coefficient of variation were 0.001 and 1.12 respectively (Table 4). The hight heritability along with moderate genetic advance in percentage of mean of this trait indicated that environment control was not predominant for this character. Tripathi *et al*. (2013) reported high heritability combined with high genetic advance for 100 seed weight indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

4.1.10 Yield/plant (g)

Seed yield per plant showed highly significant variations (7649.1) among the genotypes at 1% level of probability (Appendix-IV). The average yield/plant was recorded 151.57 g with a range from 80.20 g to 307.67 g. CV(%) was 33.32 (Table 3). Yield per plant was maximum in G-27 (307.67 g) followed by G-24 (266.8), G-9 (205.4), G-31 (205.67), G-21 (200.93) and minimum for G-10 (83.20g) followed by G-11 (89.43), G-1 (91.5) (Table 3) (Appendix-III). Yield/plant refers to phenotypic variance (2693.52) was higher than the genotypic variance (2477.78) that indicating that high environmental influence on this characters which was supported by narrow difference between phenotypic (34.24%) and genotypic (32.84%) co-efficient of variation (Table 4). The moderate difference for this parameter was also suggested a moderately significant influence of environment. High heritability (91.99%) in yield/plant attached with highest genetic advance (98.35) and high genetic advance in percentageof mean (64.88). Environmental variance and environmental coefficient of variation were 215.73 and 9.69 respectively (Table 4). The high heritability along with highest genetic advance in yield/plant indicated the possible scope for improvement through selection of the character and breeder may expect reasonable benefit in next generation in respect of this trait. Sabiel *et al*. (2015) recorded highest genotypic coefficient ofvariation was observed for seed yield of sesame.

Genetic advance, heritability and selection

Heritability is an index of transmissibility of genes controlling the character. It is also used as a measure of value for selection of a character. During estimation of selection effect for a character heritability associated with genetic advance is more useful than heritability alone. The mode of gene action is also indicated by them.

4.2 Correlation co-efficient

Yield is greatly influenced by various environmental factors and it is a polygenic inheritance character. It is not so effective to select seeds for future breeding based on only yield. For plant breeders correlation co-efficient is very much helpful in selection of yield contributing traits to be given importance by its nature and magnitude. It is possible to improve some other characters along with yield through correlation co-efficient. The genotypic and phenotypic correlation co-efficient of 10 character are presented in (Table 5 and Table 6).

4.2.1 Days to first flowering

The days to first flowering showed highly significant positive relationships with weight of 1000 seeds (g) for both genotypic and phenotypic correlation co-efficient (rg=0.478, rp=0.346) (Table 5 and 6).The correlation was positive and significant so the association between the characters was high. Its reveal that it will be beneficial for the breeders because the improvement of both characters will be beneficial simultaneously. It had negative relationship with length of capsule (rg=-0.031, rp=-0.048). It means that the increase of days to first flowering will decrease the length of capsule. With other characters it showed non-significant positive association.

4.2.2 Days to 50% flowering

Days to 50% flowering showed positive relationship at genotypic correlation co-efficient (rg=0.334) (Table 5) and significant positive phenotypic correlation co-efficient (rp=0.258) (Table 6) with days to 80% maturity. Highly significant genetic correlation indicate that the association of this two character is high. It also showed negative genotypic and phenotypic correlation co-efficient (rg=-0.200, -0.122, -0.017, -0.125 ; rp=-0.157 ,-0.098, -0.016, -0.048) with number of branches/plant, number of capsules/plant, weight of 1000 seeds (g) and yield/plant (g) respectively. It also showed significant positive phenotypic correlation co-efficient with number of seeds/capsule (

rp=0.0231). Positive genetic correlation indicate that increase in one character will cause increase in the other, negative phenotypic significant indicate increase of one character will decrease of other.

4.2.3 Days to 80% maturity

Days to 80% maturity exhibited a significant and positive genotypic and phenotypic correlation with length of capsule (rg=0.397, rp=0.356). It means that the increase of any of these will increase the other. The days to 80% maturity showed non-significant negative genotypic and phenotypic correlation with number of branches/plant (rg=-0.168, rp=-0.164) . This indicates that the increase of one character will decrease the other. The days to 80% maturity showed positive genotypic and phenotypic correlation with plant height, number of capsule/plant, number of seeds/plant, weight of 1000 seeds (g) and seed yield (g). (Table 5 and 6).

4.2.4 Plant height (cm)

Significant positive genotypic and phenotypic association was recorded for plant height of sesame genotypes with weight of 1000 seeds (g) (rg= 0.368, rp=0.363). Significant positive phenotypic relationship was recorded (rp= 0.242, 0.230, 0.235, 0.301) with number of capsules/plant, number of seeds/capsule, length of capsule and yield/plant respectively. On the other hand plant height (cm) showed non-significant negative genotypic and phenotypic association with number of branches/plant (rg=-0.068, rp=-0.062) respectively (Table 5 and 6). Akbar et al. (2011) indicated that plant height had the significant positive effect on seed yield.

4.2.5. Number of branch/plant

Number of branches/plant showed highly significant positive genotypic relationship (rg=0.703, 0.617) with number of capsules/plant and yield/plant (g) respectively. The result indicates that if number of branches/plant increase both of other two characters will be increased. It also showed highly significant positive phenotypic relation with number of capsules/plant, number of seeds/capsule and yield/plant (g) (rp=0.683, 0.250, 0.566) (Table 5 and 6). The result indicates that if number of branches/plant increase the seed yield will be increased.

4.2.6 Number of capsules/plant

Significant positive genotypic association was recorded for number of capsules/plant of sesame genotypes (rg=0.401, 0.879) with number of seeds/capsule and yield/plant (g) respectively. Whereas the non-significant positive genotypic association for length of capsule and weight of 1000 seeds(g) were recorded (rg=0.347, 0.002). Significant positive phenotypic association was recorded for number of capsules/plant (rp=0.397, 0.333, 0.840) with number of seeds/capsule, length of capsule and yield/plant (g) respectively. On the other hand, non-significant positive phenotypic association was observed (rp=0.003) with weight of 1000 seeds(g) (Table 5 and 6). Akbar *et al*. (2011) indicated that capsules plant^{-1} had the significant positive effect on seed yield. Sumathi and Muralidharan (2010) recorded that seed yield per plant showed significantly positive correlation with number of capsules per plant.

4.2.7 Length of capsule

Significant positive genotypic association was recorded for length of capsule of sesame genotypes with days to 80% maturity (0.397), number of seeds/capsules (0.370) and yield/plant (0.355) whereas the non-significant positive association for weight of 1000 seeds (g) (0.027). On the other hand, non-significant negative association was recorded for days to first flowering (-0.031). Length of capsule showed highly significant positive phenotypic association with days to 80% maturity (0.356), number of capsules/plant (0.333), number of seeds/capsules (0.345), weight of 1000 seeds (g) (0.277), yield/plant (0.359) and non –significant negative association with days to first flowering (-0.048) (Table 5 and 6). Akbar *et al*.(2011) indicated that capsule length had the significant positive effect on seed yield.

4.2.8 Number of seeds/capsule

Significant positive phenotypic association was recorded for number of seeds/capsule of sesame genotypes with days to 50% flowering (0.231), plant height (0.230), number of branches/plant (0.250), number of capsules/plant (0.397), length of capsule (0.345) and yield/plant(g) (0.0.523), while the non significant positive association for weight of 1000 seeds(g) was recorded (0. 027). Significant positive genotypic association was recorded for length of capsule (0.370) and yield/plant(g) (0.554) (Table 5 and 6). This indicates the increase in number of seeds/capsule will increase yield/plant(g).

Table 5. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of sesame

Characters	Days to first flowering	Days to 50% flowering	Days to 80% maturity	Plant height	Number of branches/ plant	Number of capsules/ plant	Numbr of seeds/ capsule	Length of capsule (cm)	Weight of 1000 seeds (g)	Yield/ plant (g)
Days to first flowering	1**									
Days to 50% flowering	0.158	1**								
Days to 80% maturity	0.049	0.334	1**							
Plant height	0.203	0.077	0.032	1**						
Number of branches/plant	0.181	-0.200	-0.168	-0.068	1**					
Number of capsules/plant	0.154	-0.122	0.052	0.250	0.703**	1**				
Number of seeds/capsule	0.011	0.273	0.208	0.253	0.258	0.401*	1**			
Length of capsule	-0.031	0.246	0.397*	0.237	0.028	0.347	0.370*	1**		
Weight of 1000 seeds (g)	0.478**	-0.017	0.056	0.368*	0.043	0.002	0.027	0.282	1**	
Yield/plant (g)	0.183	-0.125	0.082	0.310	0.617**	0.879**	0.554**	0.355*	0.208	1**

Here, * indicates significant at 5% level of significance

** indicate significant at 1% level of significance

Table 6. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of sesame

Characters	Days to first flowering	Days to 50% flowering	Days to 80% maturity	Plant height	Number of branches/ plant	Number of capsules/ plant	Number of seeds/ capsule	Length of capsule (cm)	Weight of 1000 seeds (g)	Yield/ plant (g)
Days to first flowering	1**									
Days to 50% flowering	0.090	1**								
Days to 80% maturity	0.042	0.258*	1**							
Plant height	0.164	0.058	0.035	1**						
Number of branches/plant	0.134	-0.157	-0.164	-0.062	1**					
Number of capsules/plant	0.123	-0.098	0.045	0.242*	0.683**	1**				
Number of seeds/capsule	-0.016	0.231*	0.184	0.230*	0.250*	0.397**	1**			
Length of capsule	-0.048	0.195	0.356**	0.235*	0.017	0.333**	0.345**	1**		
Weight of 1000 seeds (g)	0.346**	-0.016	0.052	0.363**	0.035	0.003	0.027	0.277**	1**	
Yield/plant (g)	0.116	-0.048	0.092	0.301**	0.566**	0.840**	0.523**	0.359**	0.198	1**

Here, * indicates significant at 5% level of significance
** indicate significant at 1% level of significance

4.2.9 Weight of 1000 seeds (g)

Significant positive genotypic association was recorded for weight of 1000 seeds(g) of sesame genotypes with days to first flowering (0.478) and plant height (0.368) whereas the non significant positive association for days to 80% maturity (0.056), number of branches/plant (0.043), number of capsules/plant (0.002), number of seeds/capsule (0.027), length of capsule (0.282) and yield/plant (0.208). On the other hand, non significant negative genotypic association was observed with days to 50% flowering (-0.017). Highly significant positive phenotypic association was recorded for weight of 1000 seeds(g) with days to first flowering (0.346), plant height (0.363), length of capsule (0.277) (Table 5 and 6**)**. Abate and Mekbib (2015) 1000 seed weight exhibited highly significant positive correlation with seed yield/plant. Akbar *et al*. (2011) indicated that 1000-seed weight had the significant positive effect on seed yield. Sumathi and Muralidharan (2010) recorded that seed yield per plant showed significantly positive correlation with 100 seed weight.

4.2.10 Yield/plant (g)

Highly significant positive genotypic association was recorded for yield/plant(g) of sesame genotypes with number of branches/plant (0.617), number of capsules/plant (0.879), length of capsule (0.355) and number of seeds/capsule (0.554), whereas the non-significant positive association for weight of 1000 seeds (0.208). On the other hand, non-significant negative genotypic association was recorded for days to 50% flowering (-0.125) (Table 7). Highly significant phenotypic relationship was recorded for yield/plant (g) with plant height (cm) (0.301), number of branches/plant (0.566), number of capsules/plant (0.840), number of seeds/capsule (0.523), length of capsule (0.359). Whereas non-significant negative relation was for days to 50% flowering (-0.048) (Table 5 and 6). Sabiel *et al*. (2015) reported that seed yield (kg/ha) was highly significant and positively correlated with biomass (yield kg/ha) (r = 0.81), 1000-seed weight (r = 0.57) andplant height (r = 0.50). However, it was highly significant and negatively correlated with days to flowering (r = -0.22). Mothilal (2006) reported that seed yield per plant had significantly positive correlation with days to maturity, plant height, number of branches and number of capsules per plant.

4.2 Path co-efficient analysis

Seed yield is the most essential goal of plant breeding. By using path co-efficient analysis we can estimate various direct and indirect effect of yield on various yield contributing characters. Here yield is considered as dependent character and days to first flowering, days to 50% flowering, days to 80% maturity, plant height, number of branches/plant, number of capsules/plant, number of seeds/capsule, length of capsule and weight of 1000 seeds (g) were treated as causes or independent character. Path co-efficient analysis denotes the components of correlation co-efficient within various traits into the direct and indirect effects and indicates the relationship in more meaningful way. The results of the path co-efficient analysis are presented in Table 7.

4.3.1 Yield/plant *vs* days to first flowering

Path co-efficient analysis revealed that, days to first flowering had negative direct effect (-0.049) with yield per plant. This trait showed indirect positive effect on yield per plant through days to 80% maturity (0.001), number of capsules/plant (0.132), number of seeds/capsule (0.003), length of capsule (0.003) and weight of 1000 seeds (g) (0.127). On the other hand, it showed indirect negative effect with days to 50% flowering (-0.013), plant height (-0.008), number of branches/plant (-0.014). Finally, it made positive non-significant correlation with seed yield (0.183) (Table 7). Siddiqui *et al.*(2005) recorded indirect negative effects on yield for days to first flowering.

4.3.2 Yield/plant *vs* days to 50% flowering

There were negative direct effect (-0.081) to days to 50% flowering with seed yield/plant measured by genotypic co-efficient of correlation. This trait showed indirect negative effect on yield with through plant height (-0.003), number of capsules/plant (-0.103), length of capsule (-0.025), weight of 1000 seeds (g) (-0.004). Whereas it showed indirect positive effect with days to 80% maturity (0.007), number of branches per plant (0.015), number of seeds/capsule (0.080). Finally, it made negative non-significant correlation with seed yield (-0.125) (Table 7).

4.3.3 Yield/plant *vs* days to 80% maturity

Days to 80% maturity had direct positive effect (0.021) on seed yield per plant. This trait showed indirect negative effect on yield with through, days to first flowering (-0.002), days to 50% flowering (-0.027), plant height (-0.001), length of capsule (-0.025). Moreover it showed indirect positive effect with number of branches/plant (0.013),

number of capsules/plant (0.045), number of seeds/capsule (0.060), weight of 1000 seeds (g) (0.015). Finally, it made positive non-significant correlation with seed yield/plant (0.082) (Table 7).

4.3.4 Yield/plant *vs* plant height

Path analysis revealed that plant height had negative direct effect (-0.042) on yield/plant (Table 7). It showed negligible positive indirect effect through days to 80% maturity, number of branches/plant, number of capsules/plant, number of seeds/capsule, length of capsule, weight of 1000 seeds (g). While it showed negligible negative indirect effect through days to first flowering, days to 50% flowering. Finally, it made positive non-significant correlation with seed yield/plant (0.312) (Table 7)

4.3.5 Yield/plant *vs* number of branches/plant

Path analysis revealed that number of branches per plant had negative direct effect (-0.077) on yield/plant (Table 7). It showed negligible positive indirect effect through days to 50% flowering, plant height, number of capsules/plant, number of seeds/capsule, weight of 1000 seeds (g). While it showed negligible negative indirect effect through days to first flowering and days to 80% maturity. Finally, it made positive highly significant correlation with seed yield/plant (0.617) (Table 7).

4.3.6 Yield/plant vs number of capsules/plant

Path analysis revealed that number of capsules/plant had positive direct effect (0.859) on yield/plant (Table 7). It showed negligible positive indirect effect through days to 50% flowering, days to 80% maturity, number of seeds/capsule, weight of 1000 seeds (g). And negligible negative indirect effect through days to first flowering, plant height, number of branches/plant, length of capsule. Finally, it made positive highly significant correlation with seed yield/plant (0.879) (Table 7).

4.3.7 Yield/plant vs number of seeds/capsule

Path analysis revealed that number of seeds/capsule had positive direct effect (0.290) on yield/plant (Table 8). It showed negligible positive indirect effect through days to 80% maturity, number of capsules/plant and weight of 1000 seeds (g). And showed negative indirect effect through days to first flowering, days to 50% flowering, plant height, number of branches/plant, length of capsule. Finally, it made highly significant positive correlation with seed yield/plant (0.554) (Table 7). Banerjee and Kole (2006)

reported that seeds/capsule were the important characters determining seed yield in the studied sesame population.

4.3.8 Yield/plant vs length of capsule (cm)

Path analysis revealed that length of capsule had negative direct effect (-0.103) on yield/plant (Table 7). It showed negligible positive indirect effect through days to first flowering, days to 80% maturity, plant height, number of capsules/plant, number of seeds/capsule, weight of 1000 seeds (g). While length of capsule showed negative indirect effect through days to 50% flowering, plant height, number of branches/plant. Finally, it made positive significant correlation with seed yield/plant (0.355) (Table 6). Siddiqui et al. (2005) recorded indirect negative effects on yield for length of capsule.

4.3.9 Yield/plant vs weight of 1000 seeds (g)

Path analysis revealed that weight of 1000 seeds had positive direct effect (0.267) on yield/plant (Table 8). It showed negligible positive indirect effect through days to 50% flowering, days to 80% maturity, plant height, number of capsules/plant, number of seeds/capsule. Weight of 1000 seeds showed negative indirect effect through days tofirst flowering, plant height (cm), number of branches/plant, length of capsule. Finally, it made positive correlation with seed yield/plant (0.208) (Table 7). Parimala and Mathur (2006) reported the highest direct effect on seed yield was exertedby the number of capsules per plant. Mansouri and Najafabadi (2004) recorded higher values for the direct effects of number of capsules per plant and 1000- seed weight and indirect effects of number of branches per plant through numberof capsules per plant.

Table 7. Path co-efficients for growth parameters, yield contributing characters and yield of different sesame genotypes

Characters	Days to first flowering	Days to 50% flowering	Days to 80% maturity	Plant height	Number of branches / plant	Number of capsules /plant	Number of seeds/ capsule	Length of capsule	Weight of 1000 seeds (g)	Yield/ plant (g)
Days to first flowering	**-0.049**	-0.013	0.001	-0.008	-0.014	0.132	0.003	0.003	0.127	0.183
Days to 50% flowering	-0.008	**-0.081**	0.007	-0.003	0.015	-0.103	0.080	-0.025	-0.004	-0.125
Days to 80% maturity	-0.002	-0.027	**0.021**	-0.001	0.013	0.045	0.060	-0.041	0.015	0.082
Plant height	-0.010	-0.006	0.001	**-0.042**	0.005	0.215	0.073	0.024	0.098	0.310
Number of branches/plant	-0.009	0.016	-0.003	0.003	**-0.077**	0.604	0.074	-0.003	0.011	0.617**
Number of capsules/plant	-0.008	0.010	0.001	-0.010	-0.054	**0.859**	0.116	-0.036	0.001	0.879**
Number of seeds/capsule	-0.001	-0.022	0.004	-0.011	-0.020	0.344	**0.290**	-0.038	0.007	0.554**
Length of capsule	0.001	-0.020	0.008	-0.010	-0.002	0.298	0.107	**-0.103**	0.075	0.355*
Weight of 1000 seeds (g)	-0.023	0.001	0.001	-0.015	-0.003	0.002	0.008	-0.029	**0.267**	0.208

Residual effect = 0.1236

4.4 Genetic diversity analysis

Study of genetic diversity among 32 genotypes of sesame evaluated through Mahalanobis' D^2 statistics and which has been discussed below:

Mahalanobis D^2 statistics was used to measure the degree of diversification among the genotypes. Using this technique, grouping of genotypes was done in four clusters where genotypes grouped together were less divergent than theones placed in different clusters. The clusters separated by greatest statistical distance exhibited maximum divergence. Composition of different clusters with their corresponding genotypes and their source are shown in Table 8. Cluster I was the largest cluster comprising of 20 genotypes followed by cluster II with 9 genotypes, cluster III belongs 2 genotypes and cluster IV have genotypes of sesame (Table 8)

Table 8. Clustering pattern of 32 sesame genotypes by Tocher's method

Cluster	Members	Genotypes No.
I	20	G8, G17, G31, G30, G20, G6, G14, G1, G15, G25, G18, G10, G5, G16, G29, G12, G2, G11, G26, G21
II	9	G4, G19, G22, G3, G28, G13, G23 G32, G9
III	2	G24, G27
IV	1	G7

Table 9. Average intra (bold) and inter-cluster D^2 and D values of 4clusters for 32 sesame genotypes formed by Torcher's method

Cluster	I	II	III	IV
I	**0.573**	1.494	6.990	0.865
II	1.494	**0.398**	2.761	1.060
III	6.990	2.761	**0.860**	5.378
IV	0.865	1.060	5.378	**0.0000**

Table 10. The nearest and farthest clusters from each cluster between D^2 values in sesame

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	IV (0.865)	III (6.990)
2	II	IV (1.060)	III (2.761)
3	III	II (2.761)	I (6.990)
4	IV	I(0.865)	III (5.378)

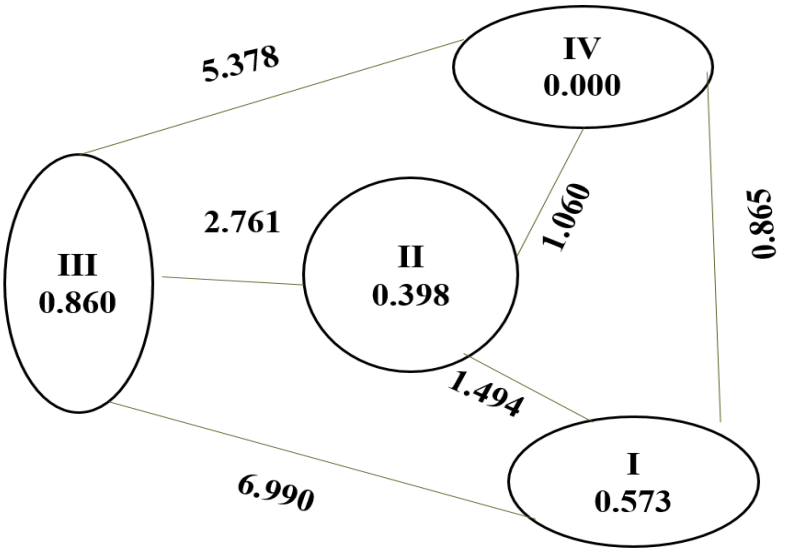

Figure 1. Intra and inter cluster distance between different cluster

Cluster distances denoted by the average inter and intra-cluster distances are the approximate measure of the cluster divergence (Table 9 and 10). Inter cluster distance was maximum (2.761) between clusters II and III, followed by clusters I and II (11.165). The intra and inter cluster distance presented in Figure 1. The results revealed that genotypes chosen for hybridization from clusters with highest distances would give high heterotic F_1 and broad spectrum of variability in segregating generations.

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted in the experimental area of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka during the time period of March to June 2022 to find out the multivariate analysis and character association of 32 sesame genotypes. In this experiment 32 sesame genotypes were used as experimental materials. The experiment was laid out inRandomized Complete Block Design (RCBD) with three replications. Meanperformance, variability, correlation matrix, path analysis and genetic diversity analysis on different yield contributing characters and yield of sesame genotypeswas estimated.

The highest days to starting of flowering (35.5) was found in the genotype of G-12, whereas the lowest days (31) was found from the genotype of G-2. The highest days to starting of maturity (84.33) was found in the genotype of G-7 while the lowest days to starting maturity (77.33) from the genotype of G-9. The longest plant (127.87 cm) was found in the genotype of G-3 , whereas the shortest plant (93.31 cm) from the genotype of G-1. The maximum number of capsules/plant (149.40) was found in the genotype of G-27, whereas the minimum number ofcapsules/plant (46.03) was recorded from the genotype of G-1. The longest capsule (2.92 cm) was observed in the genotype of G-27, while the shortest capsule (2.41 cm) from the genotype of G-5. The maximum number of seeds/capsule (75.67) was found in the genotype of G-7 whereas the minimum number (60.77) was recorded from the genotypes of G-11. The highest weight of 1000 seeds (3.25 g) was observed in the genotype of G-15,while the lowest weight of 1000 seeds (2.48 g) was observed from the genotype of G-2. The highest yield/plant (360.67g) was found in the genotype of G27 whereas the lowest yield/plant (83.20 g) was observed from the genotype of G-10. In consideration of days to starting of flowering refers to phenotypic variance (1.88) was higher than the genotypic variance (1.12) supported by narrow difference between phenotypic (4.15) and genotypic (3.20) co-efficient of variation with moderate heritability (59.25%) in days to starting of flowering attached with low genetic advance (1.67) and high genetic advance in percentageof mean (5.07).

In correlation study, significant positive association was recorded for yield/plant of sesame genotypes with number of branches/plant (0.617),number of capsules/plant

(0.879), length of capsule (0.355) and number of seeds/capsule (0.554), whereas the non significant positive association for weight of 1000 seeds (0.208). On the other hand, non-significant negative association was recorded for days to 50% of flowering (-0.303) and non significant positive association was observed with days to 80% of maturity (0.082), days to first flowering (0.183) and plant height (0.310).

Path analysis revealed that days to first flowering had negative directeffect (-0.0.49) on yield/plant. Days to 50% flowering had negative direct effect (-0.081) on yield/plant. Days to 80% maturity had positive direct effect (0.021) on yield/plant. Plant height had negative direct effect (-0.042) on yield/plant. Number of branches per plant had negative direct effect (-0.077) on yield/plant. Number of capsules/plant had positive direct effect (0.859) on yield/plant. Length of capsules had negative direct effect (- 0.103) on yield/plant. Number of seeds/capsule had positive direct effect (0.290) on yield/plant. Weight of 1000 seeds had positive direct effect (0.267) on yield/plant.

In genetic diversity, cluster I was the largest cluster comprising of 20 genotypes followed by cluster II with 9 genotypes, cluster III had 2 genotypes and cluster IV had 1 genotypes of sesame. Inter cluster distance was maximum (2.761) between clusters II and III, followed by clusters II and I (1.494).

In consideration of yield contributing characters and yield G-27 perform better followed by G-24, G-9. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the yield contributing traits indicating that high environmental influence on the studied characters. Correlation analysis revealed that the characters; days to 80% maturity, number of capsules/plant, number of seeds/capsule, weight of 1000 seeds(g) had highly positive correlation with yield per plant.

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APPENDICES

Appendix I. Monthly record of air temperature, relative humidity and rainfall of the experimental site during the period from March to June 2022

Month (2022)	*Air temperature (°c)		*Relative humidity (%)	Total Rainfall (mm)
	Maximum	Minimum		
March	36	14	67	30
April	37	19.6	54	11
May	33.4	23.2	67	78
June	35.2	25.7	72	194

* Monthly average,

* Source: Bangladesh Meteorological Department (Climate and weather division) Agargoan, Dhaka – 1212

Appendix II. Characteristics of soil of experimental field

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Experimental field, SAU, Dhaka
AEZ	Madhupur Tract (28)
General Soil Type	Shallow 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

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

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka (2022).

Appendix III . Mean performance of different characters of 32 *Sesame* genotypes

Genotypes	DFF	D50%F	D80%M	PH	BPP	CPP	SPC	CL	HSW	SYP
G1	32.33	48	83	93.29	3.07	46.03	66.23	2.67	2.96	91.5
G2	31	48.67	83	96.55	3.57	70.63	70.8	2.64	2.48	133.23
G3	31	47	79.33	99.15	5.07	85.53	66.87	2.68	2.84	161.17
G4	34.67	49.67	82	97.47	4.5	92.4	70.33	2.59	2.69	185.77
G5	31.67	48	83	100.53	3.1	57.83	68.97	2.41	2.55	103.77
G6	33.33	46	82	99.93	3.6	56.97	65.53	2.46	3.1	115.8
G7	32	49	84.33	116.66	2.83	71.67	75.67	2.77	2.8	154.17
G8	33	48	78	101.67	3.8	48.97	72.97	2.6	2.95	128.6
G9	34	46	77.33	101.27	5.2	108.47	66.57	2.44	2.91	205.4
G10	33	49	80	100.73	2.6	46.53	66.33	2.48	2.63	83.2
G11	31	48	78.67	101.81	4.23	67.9	60.77	2.57	2.59	89.43
G12	35.33	49	81.67	115.81	4.23	78.63	67.13	2.55	3.1	140.5
G13	34	48.67	83.33	103.84	3.47	100.47	69.47	2.65	2.76	178.3
G14	32	47.33	79.67	104.63	2.23	52.87	63.9	2.58	3.12	103.9
G15	35	48	80.67	102.58	3.17	54.87	63.8	2.78	3.25	117.97
G16	33	46	77.67	105.1	3.47	64.07	67.5	2.47	2.51	121.43

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), BPP = Branch per plant, CPP = Capsule per plant, SPC = Seeds per capsule, PL = Pod length (cm), HSW = 1000 seed weight (g) and SYP = Seed yield per plant (g).

Appendix III. *Continued*.

Genotypes	DFF	D50%F	D80%M	PH	BPP	CPP	SPC	CL	HSW	SYP
G17	33.67	49.33	82	105.11	3.4	50.03	70.97	2.59	3.11	106.5
G18	32.33	49	78	103.54	2.6	56.43	64.57	2.55	2.7	99.57
G19	31.67	48.67	80.33	104.5	4.83	88.77	71.3	2.7	2.9	192.3
G20	32	49	80.67	106.15	3.3	60.4	69.93	2.77	3.07	128.83
G21	34	48	78.33	105.04	4.27	80.27	69.63	2.56	3.08	200.93
G22	34	49	79.67	108.7	5.17	86.4	69.6	2.49	2.61	154.07
G23	34.33	48.67	83	106.65	4.63	89.3	72.23	2.8	3.23	182.7
G24	33	47.67	79.33	109.4	6.03	125.93	73.87	2.57	3.13	266.8
G25	34.33	50	78.67	109.14	3.13	67.37	71.97	2.65	3.05	133.07
G26	33.67	48	82	109.94	3.33	79.27	63.23	2.56	3.09	147.93
G27	32.67	47.33	82.67	111.74	4.77	149.4	74.17	2.92	2.92	307.67
G28	34	46	82	112.33	3.73	85.8	66.3	2.75	2.85	162.53
G29	32	46	78	111.13	2.9	70.63	71.87	2.56	2.88	176.03
G30	33.33	46	79.67	112.02	4.37	56.6	66.9	2.49	3.19	117.23
G31	33	49	83	112.63	2.87	49.6	67.43	2.56	3.13	205.67
G32	32.67	49	80	127.87	2.93	85.4	69.07	2.7	3.12	154.43

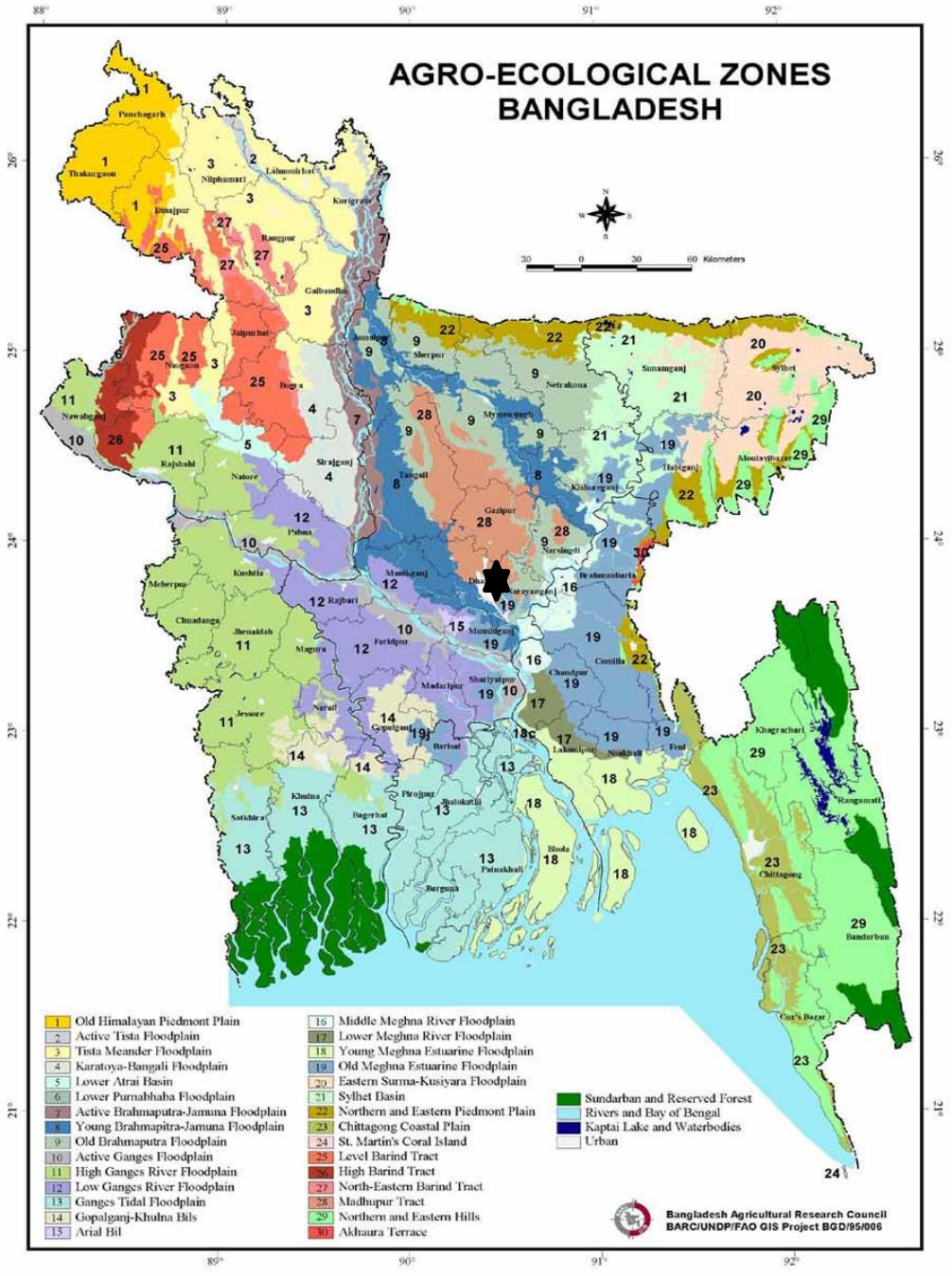
DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), BPP = Branch per plant, CPP = Capsule per plant, SPC = Seeds per capsule, PL = Pod length (cm), HSW = 1000 seed weight (g) and SYP = Seed yield per plant (g)

Appendix IV. Analysis of variance (ANOVA) for growth parameters, yield contributing characters and yield of different sesamegenotypes

Characters	Degrees of freedom (df)			Mean Sum of Squares (MSS)		
	Replication	Genotypes	Error	Replication	Genotypes	Error
Days to first flowering	2	31	62	0.875	4.115***	0.767
Days to 50% flowering	2	31	62	5.906	4.287***	0.648
Days to 80% maturity	2	31	62	0.875	12.010***	0.638
Plant height	2	31	62	2.036	141.758***	3.341
Number of branches/plant	2	31	62	0.463	2.516***	0.047
Number of capsules/plant	2	31	62	5.930	1683.66***	1.10
Length of capsule (cm)	2	31	62	0.010	0.042***	0.001
Number of seeds/capsule	2	31	62	2.155	36.808***	0.301
Weight of 1000 seeds (g)	2	31	62	0.017	0.150***	0.001
Yield/plant (g)	2	31	62	529.7	7649.1***	215.7

***: Significant at 0.001 level of probability.

Appendix V. Map showing the experimental site under the study



The experimental sight under study