GENETIC VARIABILITY STUDIES OF SESAME (*Sesamum indicum* L.) GENOTYPES

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CERTIFICATE

This is to certify that thesis entitled, "**GENETIC VARIABILITY STUDIES OF SESAME (*Sesamum indicum* L.) GENOTYPES**" 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 (MS) in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **MD. NAZRUL ISLAM**, **Registration No. 26281/00564** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2022
Place: Dhaka, Bangladesh

Prof. Dr. Md. Abdur Rahim
Supervisor

DEDICATED TO
MY
BELOVED PARENTS, WIFE AND DAUGHTERS

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ABSTRACT

A field experiment was conducted forty-three sesame (*Sesamum indicum* L.) genotypes at Sher-e-Bangla Agricultural University, Dhaka, during the period of March 2022 to August 2022 using Rrandomized Complete Block Design (RCBD) with three replications to study the genetic variability and interrelationship for various traits among the genotypes. The results revealed that there was a significant variation among the genotypes for the studied traits. The phenotypic variances were higher than the genotypic variances. High broad base heritability together with high genetic advance in percent of mean was observed for number of secondary branches per plant (90.06%), 1000-seed weight (99.31%) and seed yield per plant (97.89%) while moderate heritability for plant height (59.81%). The significant positive correlation with seed yield per plant was found for plant height (r_g = 0.546, r_p= 0.246), days to 50% flowering (r_g = 0.587, r_p= 0.448), days to 80% maturity (r_g = 0.615, r_p= 0.321), number of primary branch (r_g = 0.650, r_p= 0.344), number of capsules per plant (r_g = 0.775, r_p= 0.275), number of seed per capsule (r_g = 0.320, r_p= 0.240), height of first capsule (r_g = 0.376, r_p= 0.254) and 1000-seed weight (r_g = 0.377, r_p= 0.373). Path co-efficient analysis revealed that plant height (0.856), days to 80% maturity (0.227), number of primary branches per plant (0.467), number of secondary branches per plant (0.441), capsule length (0.258) and number of seeds per capsule (0.213) had the positive direct effect on yield per plant whereas, internode length (-0.799) followed by and number of capsules per plant (-0.370) and days to 50% flowering (-0.198) had the negative direct effect. Considering mean performance, heritability and correlation analysis, the sesame genotypes G6, G12 and G36 for seed yield per plant, and G26, G27 and G37 for early maturity could selected for further improvement.

LIST OF CONTENTS

LIST OF CONTENTS (Cont'd)

LIST OF CONTENTS (Cont'd)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviations
Agriculture	Agr.
Agro-Ecological Zone	AEZ
Anonymous	Anon.
Bangladesh Bureau of Statistics	BBS
Biology	Biol.
Biotechnology	Biotechnol.
Botany	Bot.
Cultivar	Cv.
Dry weight	DW
Editors	Eds.
Emulsifiable concentrate	EC
Entomology	Entomol.
Environments	Environ.
Food and Agriculture Organization	FAO
Fresh weight	FW
International	Intl.
Journal	J.
Least Significant Difference	lsd
Liter	L
Triple super phosphate	TSP
Science	Sci.
Soil Resource Development Institute	SRDI
Technology	Technol.
Serial Number	Sl. No.

CHAPTER I

INTRODUCTION

Sesame (*Sesamum indicum* L.) is a flowering plant of the genus *Sesamum* which belongs to Pedaliaceae family and commonly known as 'Till' in Bangladesh. It is a self-pollinated diploid species with 2n = 26 chromosomes. It is the second most important oil seed crop next to mustard in Bangladesh while one of the major oilseed crop in Ethiopia (Rahman *et al.*, 2007; Girmay, 2018). Sesame is one of the world's oldest oilseed crop and cultivated in Asia for over 5000 years (Bisht *et al.*, 1998). In India, the antiquity of sesame is known from the use of its seed in religious ceremonies (Shah, 2016). It is originated from Africa, then spread to both China and India (Sharaby and Butovchenko, 2019). The crop is highly tolerant to drought, grows well in most of the well-drained soils and various agro climatic regions, and is well adapted to different rotations (Tripathi *et al.*, 2013).

Sesame is very useful crop as its seed contains 42-50% oil (Hosen and Shamsi, 2017; Paul *et al.*, 2019). The oil contains about 42% linoleic acid, 25% protein and 16-18% carbohydrate (Miah *et al.*, 2015; Khan *et al.*, 2009). Moreover, premium quality edible and medicinal oil can be extracted from sesame seed, which can be conserved for a long time. Sesame oilcake is good feed for poultry, fish, cattle, goat and sheep (Khan *et al.*, 2009). Sesame seeds are used in baking, candy making, and some other food industries (Anilakumar *et al.*, 2010). Sesame oil is used in cooking, salad dressing and margarine (Sharaby and Butovchenko, 2019). It also provides ingredients for pharmaceutical and cosmetic industries, and

synergist for insecticides (Salunkhe and Desai, 1986). Sesame oil and foods fried with it have a long shelf life due to the presence of *sesamol* (an antioxidant) (Anilakumar *et al.*, 2010). It poses various health benefits, including prevention of diabetes, reducing blood pressure and lowering the blood cholesterol levels (Devarajan *et al.*, 2016). Besides, this oil is good for digestion, heart health, healthy skin, preventing cancer, lessen anxiety, alleviates anemia, protects from radiation damage to DNA, respiratory health, oral health, as well as bone health (Sultana *et al.*, 2019). Moreover, sesame seeds are considered as a good source of dietary fiber, protein, vitamin B, copper, manganese, calcium, and magnesium (De and De, 2021).

The major sesame growing countries are India, China, Myanmar, Sudan, Uganda, Ethiopia, Nigeria, Tanzania, Pakistan, Korea, Russia, Turkey, Mexico and South America while are India and China are the world's largest producers of sesame. The largest producers of sesame are Myanmar, India, Nigeria and Sudan while Japan followed by China is the largest importer in the world (Sharaby and Butovchenko, 2019; Ayana, 2015).

In 2020, world sesame production was 6172.32 thousand metric tons from 13965.844 thousand ha of land of which 70% was produced in Asia and 25% in Africa (www.fao.org/faostat/). The average sesame yield in Bangladesh is about 944 kg per ha. Currently, about 33,657 ha of land are under sesame cultivation and annual production is about 28,835.78 m tons (www.fao.org/faostat/).

In Bangladesh, sesame is cultivated in both *Kharif* and *Robi* seasons, but two-third sesame is produced in kharif season (Chowdhury and Hassan, 2013). High land with sandy loam is the best suited for sesame cultivation. The average productivity of sesame is still low as compared to other oilseed crops due to the

lack of high yielding cultivars, resistance to major insect pests and shattering problem in Bangladesh. A high harvest (3600 kg/ha) of sesame was reported in Nigeria (Uzo and Ojiake, 1981). In plant breeding, selection is a fundamental part by which genotypes with high productivity in a given environment are selected. Phenotypic selection for high yielding sesame cultivar is difficult due to the complex polygenic nature of trait in sesame. This is because of highly influence of environment on these traits which reduces the progress to be attained through direct selection. Therefore, the genetic improvement through indirect selection for yield could be vital. Consequently, genetic variability studies play a significant role for the improvement in sesame. Every year, huge amount of foreign exchange is being spent to import edible oil. Since sesame is treated as less input intensive crop, hence, breeding improved varieties could be a promising approach (Ashri, 1988). A very little research has been done on improvement of the sesame in Bangladesh. Therefore, development of high yielding and biotic stress (disease) resistance genotypes of sesame is essential. Little is known about the genetic variability of landrace collections of sesame. Therefore, the proposed research will highlight on genetic variability, heritability and genetic advance and interrelationship among different genotypes of sesame.

Objectives:

The proposed research was undertaken with the following objectives:

- to determine the genetic variability among sesame genotypes
- to assess interrelationship among the genotypes based on yield and its contributing traits
- to select suitable parents for the utilization in future hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Sesame (*Sesamum indicum* L.) is a vegetarian oil seed crop so many countries in the world including Bangladesh. In recent years, various oilseeds have been increasingly used for food purposes. Whole seeds, oils, meal and cake by-products are valuable sources of nutritional and bioactive components. Their properties are widely promoted by nutritionists and food producers, and therefore the interest of consumers in new pro-health ingredients is growing rapidly around the world. Some of the important recent research work on sesame carried out at home and abroad on this aspect have been summarized in this chapter:

2.1 Genetic variability

A field experiment was carried out by Kumar *et al.* (2022) using 33 sesame genotypes (including three checks) in RCBD with three replications to evaluate the yield and its contributing traits. The ANOVA revealed significant variations among the genotypes for studied characters. The result showed that the phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were higher for seed yield, number of productive branch and inter-node length. Genetic advance as per cent of mean for seed yield, numbers of productive branches, height of 1st node from ground and internode length. The high positive correlation was found for number of productive branches, number of capsules per plant, number of seeds per capsule and days to maturity with seed yield. Moreover, path analysis showed that number of

productive branches, number of capsules per plant, days to maturity, and number of seeds per capsule had high positive direct effect on seed yield.

Roy *et al.* (2022) reported the high GCV and PCV for number of branches per plant and number of capsules per plant. High heritability coupled with high genetic advance was observed for seed yield per plant, number of branches per plant and capsules per plant which suggested the major role of additive genetic effects for their expression, and better possibilities for utilization of direct selection for those characters. The highest GCV and PCV values were found in number of seeds per capsule. Likewise, the GCV and PCV were also high for days to 50% flowering, stem height from base to first branch, number of capsules per plant, number of seeds per capsules, 1000-seed weight, and oil content.

Kumar *et al.* (2022a) performed an experiment with 500 sesame accessions during *Kharif* 2019 at Jabalpur, India. The PCV values were higher than GCV values. High heritability was observed for all the traits under study. Low genetic advance as percentage of mean was reported in days to flower initiation, days to 50% flowering, days to maturity while medium heritability in oil content (%), plant height, number of seeds per capsule. The high heritability was observed in capsule length, number of capsules per plant, thousand seed weight, number of primary branches per plant, seed yield per plant, number of secondary branches per plant. The results suggested that magnitude of additive genetic effects that will assist in phenotypic selection in early segregating generation.

Srikanth and Ghodke (2022) reported the high GCV and PCV for number of capsules per plant and seed yield per plant. High heritability coupled with high genetic advance as percentage of mean was detected for number of capsules per plant, number of seeds per capsule, 1000-seed weight, and seed yield per plant which suggested the influence of additive genetic effects, as such phenotypic selection would be effective.

Thouseem *et al.* (2022) conducted an experiment with white seeded sesame germplasm using RCBD during 2019-2020 to assess genetic variability, heritability and genetic advance. The ANOVA revealed that there a significant variation in the germplasm for the all the characters. The PCV was higher than the GCV for all the traits. Higher of GCV and PCV was found in seed yield per plant followed by primary branches per plant, number of capsules per leaf axil, and number of capsules per plant. High heritability was recorded for all the characters excluding days to maturity. High genetic advance (GA) as percentage of mean was found in all the studied characters except 1000-seed weight, days to 50% flowering, capsule length (cm), protein content (%), oil content (%) and days to maturity. Moreover, high heritability together with high genetic advance as percentage of mean was found in seed yield per plant, number of capsule leaf per axil, number of capsules per plant, primary branches per plant, number of seeds per capsule and plant height.

A set of 55 sesame germplasm were assessed for 16 quantitative traits by Durge *et al.* (2022). The ANOVA and genetic variability components such as PCV, GCV, heritability and GA as percentage of mean were analyzed. ANOVA revealed a significant variation among genotypes for 12 traits. High PCV GCV were found for seed yield per plant, capsules per plant and number of secondary branches per plant.

High heritability together with moderate to high genetic advance was recorded in plant height, capsules per plant and seed yield per plant.

An experiment was conducted by Ahmed *et al.* (2021) to estimate the genetic behavior of 14 genetically diverse genotypes of sesame during the two summer seasons of 2017 and 2018, for seed yield and their components using a RCBD with 3 replications. The results showed that a significant differences among sesame genotypes for all traits. Number of branches per plant, number of capsules per plant, and seed yield per plant had the highest estimates of PCV and GCV. High heritability coupled with the high genetic advance (as a % of mean) was observed in length of fruiting zone, number of branches per plants, number of capsules per plants, and seed yield per plant.

Thirty sesame genotypes were evaluated by Pavani *et al.* (2020) during *Kharif* 2018 for genetic variability and other related parameters in respect of ten quantitative characters. The ANOVA revealed significant differences among genotypes for all the ten characters studied. High GCV and PCV were observed for the number of capsules per plant whereas moderate for days to 50% flowering, plant height to first capsule, number of branches per plant. Then again, height of the main stem, capsule length, 1000-seed weight, days to maturity, oil content and seed yield per plant showed low GCV and PCV. High heritability and genetic advance as % of mean was found in days to 50 per cent flowering, number of branches per plant and plant height to first capsule.

Fifty diverse sesame genotypes were assessed to study genetic variability by Sultana *et al.* (2019). The results showed that a significant variation in most of the studied characters among the genotypes. They found that phenotypic variances were higher than genotypic variances. The highest GCV was observed in seed yield per plant whereas the highest heritability was exhibited by hundred seed weight followed by days to 80% maturity, pods per plant, number of branches per plant and seed yield per plant.

A field experiment was conducted by Kiruthika *et al.* (2018) to assess the genetic variability on yield and with its attributing traits in sesame genotypes. High heritability was found in all the traits except capsule width and single plant. High genetic advance as % of mean was recorded for all the traits except plant height, capsule width and single plant yield.

Genetic variability of 23 sesame genotypes was examined for 12 agro morphological and biochemical traits by Begum *et al.* (2017). They found high estimates of PCV, GCV, heritability and GA for seed yield, plant height, capsule number and 1000-seed weight.

A field experiment was conducted in Ethiopia with forty-nine sesame genotypes to evaluate for estimation of genetic variability and character association. Data were collected from 14 quantitative traits. The ANOVA shown significant difference among the genotypes for each traits except for primary branches, suggesting the existence of considerable genetic variation in the studied germplasm with regard to

seed yield and yield component traits. A moderate heritability with moderate genetic advance was recorded for yield related traits (Abate and Mekbib 2015).

Sabiel *et al.* (2015) studied 12 sesame (*Sesamum indicum* L.) genotypes of under rainfed conditions to evaluate genetic variability. The highest GCV was found for seed yield whereas days to flowering exhibited high heritability (85%). Furthermore, the high genetic advance was recorded in 1000-seed weight. Highly significant differences among genotypes were found in days to flowering, plant height and 1000-seed weight.

Tripathi *et al.* (2013) conducted a field experiment with 100 sesame germplasm and found high heritability coupled with high genetic advance for seed yield per plant, number of secondary branches per plant and 1000-seed weight suggesting additive gene effect and phenotypic selection for those traits would be rewarding for further breeding.

Revathi *et al.* (2012) studied genetic variability and heritability of different traits in four crosses of sesame (Paiyur 1 × SVPR 1, F_2 of TMV 4 × SVPR 1 and their BC_1F_1s). High GCV and PCV were found in number of branches per plant, number of capsules per plant and seed yield per plant. High heritability couple 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 6 further breeding program.

Akbar *et al.* (2011) to estimate the variability in the local sesame genotypes for 16 traits of 105 sesame accessions in Pakistan. They found a significant level of variation various traits, whereas limited diversity was observed for the characters, including

stem hairiness, flower color (white with purple shading), seed color and to some extent phyllody disease.

A field trials was conducted with 13 genotypes of sesame for two years in a RCBD with three replications. The results displayed year effect to be highly significant for all the characters except 1000-seed weight, and genotype effect was highly significant for all the characters except height of first capsule. Likewise, genotypes × 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. Close resemblance between GCV and PCV was observed for all traits except number of days to flower demonstrating that selection for these traits would be rewarding. High heritability was found for all the nine characters studied except number of days to flower. High heritability together with high genetic advance was recorded for capsule weight per plant, height of first capsule and seed yield per ha (Alake *et al.* 2010)

An experiment was carried out by Sumathi and Muralidharan (2010) with 30 hybrids developed by line × tester mating design from eleven sesame genotypes involving five branched and six monostem/shy branching types. Data 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. They found high PCV and GCV in number of branches per plant, number of capsules per plant and seed yield per plant suggesting a scope for selection for those characters. High heritability coupled with high genetic advance (as % of mean) observed for plant height, number of branches,

number of capsules and seed yield per plant exhibited that those traits were governed by additive gene effects and phenotypic selection would be effective.

Deshmukh *et al.* (1986) conducted an experiment with 25 genotypes of sesame to assess their genetic potential. The result showed that all the genotypes had considerable amount of variations in their mean performance with respect to various characters. The ANOVA showed significant differences among genotypes for all the character studied except for plant height and stem height from base to first branch, indicating high degree of variability in the genotypes. The studies on genotypic coefficient of variation (GCV) and phenotypic coefficient (PCV) values greater than 20% are considered as high, whereas value less than 10% are regarded to be low and values between 10% and 20% to be medium. The PCV value for days to 50 per cent flowering, internodal length, stem height from base to first branch, number of capsules per plant, seeds per capsule, 1000 seed weight, oil content and seed yield are high. Plant height and capsule length had medium PCV. Days to 80% maturity and number of locules per capsules are found to be low.

2.2 Correlation co-efficient and path analysis

Kumar *et al.* (2022b) evaluated 33 sesame genotypes for yield and its attributing traits in RCBD with three replications. The ANOVA showed significant differences among the genotypes for all traits. A significantly high positive correlation was recorded for number of productive branches, number of capsules per plant, number of seeds per capsule and days to maturity with seed yield. Further, path analysis revealed that number of productive branches, number of capsules per plant, days to maturity, number of seeds per capsule had high positive direct effect on seed yield.

Ahmed *et al.* (2021) reported that seed yield per plant had high significant correlation with the length of fruiting zone in both branched genotypes and non-branched genotypes. Furthermore, length of fruiting zone, number of capsules per plant and 1000-seed weight had great positive direct effects on seed yield per plant. Henceforth, these characteristics could be helpful in increasing sesame seed yield.

Saravanan *et al.* (2020) carried out an experiment in the F_2 population of the cross OMT 21 A × JLSC 96 of sesame to evaluate the genetic variability, character association of yield and yield related traits. Their result revealed that yield per plant had a significant positive correlation with the number of capsules per plant followed by 1000-seed weight, plant height and the number of branches per plant. Moreover, path analysis showed that the number of capsules per plant had a high positive direct effect on yield per plant. The phenotypic selection for these traits such as number of capsules per plant, plant height, 1000-seed weight and the number of branches per plant would be effective for crop improvement program.

Sultana *et al.* (2019) conducted a field experiment with 50 sesame genotypes using 3 replications in RCBD. Their results revealed that the genotypic correlation with seed yield per plant showed a significantly strong positive with days to 50% flowering, plant height and number of pods per plant at both the genotypic and phenotypic level in sesame. Furthermore, the path co-efficient analysis showed that pods per plant and seeds per pod were the most important contributing traits to seed yield.

Patil and Lokesha (2018) studied genetic variability, character association and path analysis between yield and its attributing traits in 100-sesame advanced breeding lines. A significant positive association with seed yield per plant for number of capsules per plant, number of branches per plant, capsule length, number of seeds per capsule, capsule weight and test weight had strong and at both genotypic and phenotypic levels. Further, path co-efficient analysis indicated that number of seeds per plant followed by number of capsules per plant were important traits to be considered for realizing the improvement in yield in sesame owe to their positive contribution. Days to maturity and capsule length were negative. Capsule weight influence seed yield negatively through most characters.

Abhijatha *et al.* (2017) conducted an experiment with thirty-three accessions of sesame to asses variability, degree and direction of character association among yield and its contributing traits and the direct and indirect effects of various components on yield. The highest genotypic and phenotypic correlation with seed yield was recorded in number of capsules per plant. Path analysis showed that number of capsules per plant had the highest positive direct effect on seed yield per plant followed by number of seeds per capsule. Number of primary branches per plant and days to maturity had the maximum positive indirect effect on seed yield per plant through number of capsules per plant.

Ramazani (2016) conducted a field experiment with 18 lines sesame to assess genetic variability, character association in a RCBD with three replicates in two years during the 2013 and 2014. The correlation co-efficient analysis showed a significant negative correlation between seed yield and number of capsules per plant and number of seeds

per capsule. Correlation between germination period and seed yield was positive and significant at 5% probability level. The path co-efficient analysis for seed yield as a dependent variable implicated that the number of seeds per capsule had the highest negative direct effect on seed yield. The highest negative indirect effect on seed yield was related to the number of capsules per plant through the number of seeds per capsule. Cluster analysis using Ward's method divided 18 investigated lines into five clusters.

Sabiel *et al.* (2015) conducted an experiment to estimate the genetic variability in genotypes of sesame. They reported that seed yield had a highly significant and positively correlation with biomass (r = 0.81), 1000-seed weight (r = 0.57) and plant height (r = 0.50). Nevertheless, it was highly significant and negatively correlated with days to flowering (r = -0.22). Therefore, the characters biomass yield, 1000-seed weight and plant height were the most contributing characters on sesame seed yield.

An experiment with forty-nine sesame genotypes from low-altitude areas of Ethiopia and were evaluated at Werer Agricultural Research Centre, for genetic variability and character association. The traits biomass per plant, harvest index and 1000-seed weight exhibited highly significant positive correlation with seed yield per plant (Abate and Mekbib 2015).

Akbar *et al.* (2011) evaluated 105 sesame accessions to estimate the phenotypic variability in the local sesame genotypes for 16 qualitative and quantitative traits. The correlation co-efficient analysis revealed plant height, capsules per plant, 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 had negative correlation with seed yield.

A high significant positive correlation with grain yield was observed in sesame except 100-seed weight which showed negative correlation with seed yield (Alake *et al.* 2010).

Sumathi and Muralidharan (2010) conducted field experiment with thirty hybrids produced by line × tester mating design from eleven sesame genotypes involving five branched and six monostem/shy branching types. They found that seed yield per plant had 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.

Onginjo and Ayiecho (2009) studied sesame mutant lines in M7 generation in two locations for two seasons in Kenya to assess performance of the mutant. They showed that seed yield per plant registered the highest co-efficient 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 had 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.

CHAPTER III

MATERIALS AND METHODS

This experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University to find out genetic variability, correlation and character association of 43 sesame genotypes. The photographs of various activities done during experimental period are presented in Plate 1-6. The details of materials used in this experiment and the methods used are described below.

3.1 Experimental Location

The location of the experimental site was situated in the 23^0 74' N latitude and 90^0 35' E longitudes. The photograph showing experimental sites in Appendix I.

3.2 Soil and Climatic Condition

The site is located at Sher-e-Bangla Nagar in Dhaka. It's belonging to the 28-AEZ (Agro Ecological Zone) which called Madhupur tract. The pH of the soil was 5.47-5.65 and organic carbon content was 0.85%. The temperature, relative humidity and rainfall during the experiment period was collected from weather station of Bangladesh.

3.3 Experimental Materials

The seeds of sesame genotypes were collected from the Plant Genetic Resource Centre (PGRC) section of Bangladesh Agriculture Research Institute (BARI),

Bangladesh Agricultural Development Corporation (BADC) and various sesame growing regions of Bangladesh (Table 1).

Table 1. List of Forty-three sesame genotypes with their accession number and source of collection

Sl. No.	Genotype	Accession Number	Source of collection
1	G1	BD-10643	PGRC, BARI
2	G2	BD-10645	PGRC, BARI
3	G3	BD-10648	PGRC, BARI
4	G4	BD-10652	PGRC, BARI
5	G5	BD-10654	PGRC, BARI
6	G6	BD-10661	PGRC, BARI
7	G7	BD-11621	PGRC, BARI
8	G8	BD-11622	PGRC, BARI
9	G9	BD-11623	PGRC, BARI
10	G10	BD-11624	PGRC, BARI
11	G11	BD-11625	PGRC, BARI
12	G12	BD-11626	PGRC, BARI
13	G13	BD-11627	PGRC, BARI
14	G14	BD-11628	PGRC, BARI
15	G15	BD-11629	PGRC, BARI
16	G16	BD-11630	PGRC, BARI
17	G17	BD-11631	PGRC, BARI
18	G18	BD-11632	PGRC, BARI
19	G19	BD-11633	PGRC, BARI
20	G20	BD-11634	PGRC, BARI
21	G21	BD-11635	PGRC, BARI
22	G22	BD-11636	PGRC, BARI
23	G23	BD-11637	PGRC, BARI
24	G24	BD-11638	PGRC, BARI
25	G25	BD-11639	PGRC, BARI
26	G26	BD-11640	PGRC, BARI
27	G27	BD-11641	PGRC, BARI
28	G28	BD-11642	PGRC, BARI
29	G29	BD-11643	PGRC, BARI
30	G30	BD-11644	PGRC, BARI
31	G31	BINA Til-2	BADC, PBNA
32	G32	BINA Til-4	BADC, PBNA
33	G33	BARI Til-3	BADC, PBNA
34	G34	BARI Til-4	PGRC, BARI
35	G35	Si/GPB/22/00041	Rajbari
36	G36	Si/GPB/22/00042	Pabna
37	G37	Si/GPB/22/00043	Chuadanga
38	G38	Si/GPB/22/00044	Chuadanga
39	G39	Si/GPB/22/00045	Kurigram

40	G40	Si/GPB/22/00046	Rangpur
41	G41	Si/GPB/22/00047	Moulovibazar
42	G42	Si/GPB/22/00048	Bagura
43	G43	Si/GPB/22/00049	Gazipur

3.4 Land Preparation:

The land was prepared by a number of ploughing and cross ploughing followed by laddering and harrowing using power tiller. The weeds and stubbles were removed from the field. Then the land was again ploughing.

3.5 Application of manure and fertilizer

The chemical fertilizers such as Urea, TSP, MP and gypsum were applied as per Table 2. The entire amount of TSP, MP and Gypsum were applied as basal dose at final land preparation while Urea was splitted into two installments: 50% during final land preparation and rest 50% at flowering initiation stage.

Table 2. The chemical fertilizers used in the experiment

Fertilizer name	Dose/ha
Cowdung	10 tons
Urea	270 kg
TSP	170 kg
MP	100 kg
Zinc sulphate	5 kg
Gypsum	150 kg

(Source: KRISHI PROJUKTI HATBOI (Handbook on Agro-technology), 5th edition. Bangladesh Agricultural Research Institute, **Gazipur** 1701, Bangladesh)

3.6 Experimental design and layout

The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. A total of 215.25 m^2 (20.5 m × 10.5 m) area was used for this experiment. The spacing between lines to line was 40 cm and plant to plant distance was 15 cm. The sesame seeds were sown in lines in the experimental plots on 29 March 2022. The seeds were placed at about 1 cm depth in the soil.

3.7 Intercultural operations

The standard agronomic practices were done to maintain a healthy growth of sesame plants. Malathion-57 EC@ 5 ml/L of water was applied to control hairy caterpillar.

3.8 Crop harvesting

The harvesting was carried out each genotypes individually when 80% of sesame plants were mature.

3.9 Data collection

Data on various morphological traits were recorded from ten randomly selected plants for each genotypes from each replication to study different genetic parameters and inter-relationships among sesame genotypes. The morphological traits were as follows:

i) Plant height (cm)

Plant height was measured in cm from the base of the plant to the tip of the longest inflorescence.

ii) Days to 50% flowering (days)

Days to 50% flowering were recorded for each genotype separately from date of sowing to the date of 50% flowering in each replication.

iii) Days to 80% maturity (days)

Days to 80% maturity data were recorded from the date of sowing to date of pods maturity of 80% plants of each genotype from each replication.

iv) Number of primary branches per plant

Total number of branches developed from the main stem of the plant was considered as the number of secondary branches per plant.

v) Number of secondary branches per plant

Total number of branches developed from the primary branch of the plant was considered as the number of primary branches per plant.

vi) Number of capsule per plant

Total number of capsule of each plant was counted and considered as the number of capsules per plant.

vii) Capsule length (cm)

Capsule length of capsules was measured in cm from the five representative capsules of every plants.

viii) Number of seeds per capsule

Well-filled seeds were counted from five capsules, which was considered as the number of seeds per capsule. The data was collected from every plant and 10 randomly selected plant from every genotype of every replication.

ix) Height of first capsule (cm)

The height of first capsule was measured in cm from the base of the plant to the first growing capsule.

x) Internode length (cm)

Internode length of every plant was measured in cm from the five representative internodes of every plants.

xi) Thousand seed weight (g)

Weight of 1000 seeds was recorded in grams collected from 10 ran domly selected plants of each genotypes and then averaged.

xii) Seed yield per plant (g)

The seed yield per plant was recorded from individual plant in gram. Data was collected from 10 randomly selected plants of each replication and then averaged.

3.10 Statistical analysis

The collected data were subjected to statistical analysis for different components. The Analysis of variance was carried out using 'RStudio', an open-source packages (https://www.rstudio.com). Phenotypic and genotypic variance was calculated by the formula proposed by Johnson *et al.* (1955). Heritability and genetic advance were estimated according to Singh and Chaudhury (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were estimated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficients as well as path analysis were also done by 'RStudio'.

Plate 1. Photographs showing the land preparation and sesame seed sowing at the experimental field of SAU

Plate 2. Photograph showing the seedling stage of sesame

Plate 3. Photograph showing the vegetative growth stage of sesame

Plate 4. Photograph showing sesame experimental field at flowering stage

Plate 5. Photograph showing sesame experimental field at maximum flowering stage

Plate 6. Photograph showing sesame experimental field at capsule maturity stage

i) Estimation of genotypic and phenotypic variances:

Genotypic variance

$$\delta^2 g = \frac{MSG - MSE}{r}$$

Where,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = No of replications

Phenotypic variance

$$\delta^2 p = \delta^2 g + \delta^2 e$$

Where,

$\delta^2 g$ = Genotypic variance,

$\delta^2 e$ = Environmental variance = Mean square of error

ii) Estimation of genotypic and phenotypic co-efficient of variation:

$$GCV = \frac{\delta_g \times 100}{\bar{x}}$$

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

Where,

GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

iii) Estimation of heritability:

$$h^2_b(\%) = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where,

h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

iv) Estimation of genetic advance:

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

$$GA = \frac{\delta^2_g}{\delta^2_p} . K . \delta_p$$

Where,

GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity

v) Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

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

vi) Cluster analysis

Cluster analysis was carried out using online tool freely available at http://www.heatmapper.ca/.

CHAPTER IV

RESULT AND DISCUSSION

During the current study forty-three variety of *Sesamum indicum* genotypes were evaluated to find out the inconsistency among these genotypes and also to study the correlation, path co-efficient for seed yield and different yield contributing characters. All these accessions were grown in 2022 in the field of Sher-e-Bangla Agricultural University. The data were recorded on different yield contributing characters and were statistically analyzed and thus obtained results are described below under the following heads:

- Genetic variability study
- Correlation co-efficient of characters
- Path co-efficient analysis

4.1Genetic variability study

4.1.1 Variability among the forty-three genotypes of sesame

The analysis of variance (ANOVA), mean, range, CV%, phenotypic variance, genotypic variance, environmental variance, phenotypic co-efficient of variation, genotypic co-efficient of variation, genetic advance, heritability for different yield related characters of 43 sesame genotypes are summarized in Figure 1, Table 3 and Table 4. The ANOVA showed highly significant variation among the genotypes for all the traits suggesting a wide scope of selection for these characters (Table 4). This substantial variability provides a good opportunity for improving traits of interest in breeding programs.

4.1.1.1 Plant height (cm)

The maximum and minimum plant height was recorded in G12 (154.47 cm) and G33 (115.47 cm), respectively with the mean value of 132.88 cm (Table 3 and Table 4). The phenotypic variance (191.49) was higher than genotypic variance (40.61) suggested that there was influence of environment on the phenotypic expression of the genes controlling plant height (Table 4). The phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were 10.41 and 4.79 respectively. Heritability estimated for plant height was low (21.16%) with low genetic advance (6.03) and low genetic advance in percent of mean (4.54) suggesting that PH was governed by non-additive gene. In the contrary, Durge *et al.* (2022) reported a high heritability coupled with moderate to high genetic advance for plant height, capsules per plant and seed yield per plant.

4.1.1.2 Days to 50% flowering (days)

The minimum days to 50% flowering (DFF) was found in G26 and G27 (50 days) and maximum DFF was found in G40 and G43 (56.67 days) (Table 3). Phenotypic and genotypic variance for DFF was 2.99 and 1.79, respectively (Table 4). The GCV and PCV for days to 50% flowering were 2.46 and 3.18, respectively. The PCV was higher than the GCV indicated phenotypic expression of this trait is influenced by the environment. A moderate heritability (59.81%) was found for DFF with low genetic advance (2.13) and low genetic advance in percent of mean (3.91). The variations in flowers of different sesame genotypes are presented in Plate 7. However, a high heritability coupled with high genetic advance in percent of mean was reported by Pavani *et al.* (2020)

Table 3. Mean performance of 43 sesame genotypes in respect of 12 traits with Duncun's Multiple Range Test (DMRT)

Genotypes	PH	DFF	DEM	NPBP	NSBP	NCP	CL	NSC	HFC	IL	TSW	SYP
G1	134.44b-f	54.67c-f	99.00b-g	6.33abcd	**7.47ab**	150.93bcdefgh	2.52b	54.40ijklm	59.20bcdefg	8.94bcdefghij	2.09no	14.89cd
G2	140.37a-d	55.33a-d	**102.33a**	5.33cdefghij	5.73defg	181.47abc	2.50b	58.60cdefghijk	46.40ghijklmno	9.17bcdefghij	1.81qr	9.17lm
G3	147.57a-d	55.33a-d	100.67a-d	5.67cdefghi	6.47cd	124.13cdefgh	2.18bcde	54.87hijklm	69.53abc	10.03bcdef	2.48j	2.74s
G4	126.33f-h	53.00f-h	97.67f-i	4.27hij	7.33ab	131.67cdefgh	2.23bcde	65.20abc	42.07klmnop	7.40ghijkl	2.57ij	10.24ijk
G5	140.78a-d	55.67a-d	99.33b-f	4.87defghij	4.53jklmn	139.33cdefgh	2.23bcde	69.40a	47.27ghijklmno	7.86fghijkl	2.20mn	10.99i
G6	130.84b-h	55.00a-e	100.67abcd	5.40cdefghi	7.53ab	208.33ab	2.10bcde	65.80ab	44.07ijklmnop	8.14efghijk	4.12b	18.07a
G7	140.18a-f	54.00d-f	101.33ab	4.40ghij	2.47st	130.53cdefgh	2.18bcde	57.53efghijkl	49.67fghijklmn	8.74bcdefghij	2.60i	10.77i
G8	117.23gh	55.00a-e	99.33bcdef	4.87defghij	5.67defg	126.40cdefgh	1.87bcdef	62.67abcdefg	55.13defghijkl	7.46ghijkl	3.47e	7.42pq
G9	134.97a-h	55.67a-d	98.33defghi	4.80defghij	6.87bc	137.40cdefgh	2.17bcde	64.07abcde	57.47bcdefghi	13.46a	1.30t	12.17gh
G10	128.78c-h	54.67b-f	100.33abcde	4.87defghij	7.53ab	141.47cdefgh	2.15bcde	57.07efghijkl	50.60efghijklmn	8.24cdefghijk	2.31kl	12.05h
G11	131.02b-h	54.00d-f	100.00abcdef	5.00cdefghij	5.33fghij	172.53abcdef	2.16bcde	54.53ijklm	47.13ghijklmno	6.90jkl	4.20b	14.12de
G12	154.47a	56.00a-c	99.67bcdef	6.27abcde	5.53fgh	186.53abc	2.29bc	64.80abcd	63.93abcdef	10.60bcde	4.20b	17.39ab
G13	140.38a-f	54.00d-f	98.67cdefgh	4.87defghij	4.67ijklmn	138.27cdefgh	2.08bcde	61.07bcdefghij	46.00ghijklmno	8.19defghijk	2.36k	9.81kl
G14	136.67a-g	54.33cd-f	100.00abcdef	5.27cdefghij	3.27qrs	117.60defgh	2.39bc	62.47abcdefg	57.87bcdefghi	10.12bcdef	4.32a	12.51gh
G15	123.03e-h	54.00d-f	98.67cdefgh	4.60fghij	5.00ghijkl	146.13bcdefgh	2.22bcde	54.73hijklm	40.67mnop	7.05ijkl	1.54s	7.69op
G16	117.57gh	53.33e-g	99.00bcdefg	4.73defghij	5.13fghijk	101.20h	2.27bcd	44.27o	46.47ghijklmno	8.43bcdefghij	1.98op	8.09op
G17	133.65b-h	54.67b-f	98.33defghi	5.40cdefghi	7.47ab	174.47abcde	2.30bc	61.20bcdefghi	51.80efghijklmn	8.18defghijk	3.02f	15.34c
G18	142.32a-e	54.33c-f	98.67cdefgh	6.07abcdef	5.93def	149.33bcdefgh	2.31bc	52.67klmn	63.53abcdef	9.42bcdefghi	1.98op	10.70ij
G19	123.51e-h	54.67b-f	99.00bcdefg	3.73j	3.53opqr	107.60gh	2.26bcde	51.73klmn	51.67efghijklmn	8.32cdefghijk	2.53ij	8.28no
G20	132.87b-h	54.00d-f	99.33bcdef	5.53cdefghi	7.73a	159.33abcdefgh	2.19bcde	46.60no	44.73hijklmnop	8.78bcdefghij	1.54s	8.31no
G21	150.38ab	54.67b-f	100.00abcdef	5.20cdefghij	3.27qrs	137.80cdefgh	2.13bcde	57.07efghijkl	64.93abcde	8.53bcdefghij	2.31klm	16.65b
G22	126.57d-h	55.00a-e	100.00abcdef	7.53a	6.40cde	219.40a	1.31f	57.00efghijkl	56.73cdefghij	6.81jkl	3.96c	13.82e
G23	124.09e-h	55.00a-e	99.33b-f	4.47f-j	3.53o-r	112.40e-h	1.36f	58.40c-k	55.13d-l	7.20h-l	4.32a	9.91j-l

PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Day of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = Capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm); TSW = Thousand seed weight (g), SYP = Seed yield per plant (g).

Table 3. Contd.

Genotypes	PH	DFF	DEM	NPBP	NSBP	NCP	CL	NSC	HFC	IL	TSW	SYP
G24	122.85efgh	54.33cdef	100.00a-f	5.73b-i	3.27qrs	127.40cdefgh	1.61def	61.87bcdefgh	50.93efghijklmn	7.12ijkl	2.55ij	12.95fg
G25	142.67abcde	54.67bcdef	101.00a-c	5.00c-j	4.40klmn	128.67cdefgh	2.47b	62.87abcdef	58.67bcdefgh	9.75bcdefg	1.75r	14.13de
G26	117.12gh	50.00i	96.33hi	4.67e-j	4.33klmno	129.13cdefgh	1.61ef	58.00defghijk	31.20p	5.87kl	1.90pq	7.42pq
G27	121.44fgh	50.00i	96.67ghi	4.73d-j	5.47fghi	149.13bcdefgh	1.80cdef	62.47abcdefg	34.13op	6.95ijkl	1.87q	5.10r
G28	141.12abcdef	54.00def	98.00efghi	4.47f-j	3.53opqr	169.47abcdefg	4.08a	54.47ijklm	41.87lmnop	8.31cdefghijk	3.12f	10.23ijk
G29	127.33defgh	52.00gh	96.00i	4.40g-j	4.20lmnop	143.73cdefgh	2.43bc	52.53klmn	39.87nop	8.38bcdefghij	1.72r	6.77q
G30	141.25abcdef	54.67bcdef	99.67bcdef	5.73b-i	5.93def	137.87cdefgh	2.36bc	54.73hijklm	58.80bcdefgh	9.63bcdefgh	3.75d	13.74ef
G31	133.59bcdefgh	55.67abcd	100.00abcdef	5.07c-j	3.47pqr	105.20h	2.38bc	53.67klmn	64.87abcde	9.30bcdefghij	2.35k	12.67gh
G32	126.74defgh	54.33cdef	99.67bcdef	4.13ij	2.80rst	143.93cdefgh	2.47b	54.00jklm	42.60jklmnop	5.43l	2.26klm	9.10lmn
G33	115.47h	54.33cdef	98.67cdefgh	6.60abc	3.27qrs	124.20cdefgh	2.37bc	58.60cdefghijk	59.87abcdefg	7.24hijkl	2.81gh	8.10op
G34	135abcdefgh	56.00abc	99.33bcdef	5.87bcdefgh	4.20lmnop	108.60gh	2.43bc	55.53ghijklm	67.60abcd	8.34bcdefghijk	3.08f	14.03e
G35	132.74bcdefgh	56.00abc	101.00abc	5.73bcdefghi	3.53opqr	138.60cdefgh	1.92bcdef	66.47ab	56.53cdefghij	7.15hijkl	3.91c	14.27de
G36	124.87defgh	56.33ab	101.00abc	7.33ab	4.58jklmn	179.27abcd	2.39bc	62.87abcdef	55.53cdefghijkl	10.65bcd	2.21lm	17.24ab
G37	128.87cdefgh	51.33hi	96.00i	4.67efghij	4.73hijklm	109.53fgh	2.32bc	52.73klmn	54.73defghijklm	10.82b	2.59ij	5.90r
G38	144.58abcd	55.67abcd	100.00abcdef	4.60fghij	2.13t	125.07cdefgh	2.25bcde	60.87bcdefghij	73.93a	10.73bc	2.89g	7.67op
G39	131.76bcdefgh	56.00abc	100.00abcdef	6.00abcdefg	5.60efg	150.73bcdefgh	2.20bcde	48.53mno	59.27bcdefg	8.75bcdefghij	2.51ij	12.60gh
G40	137.53abcdef	56.67a	100.00abcdef	4.80defghij	3.87nopq	141.60cdefgh	2.34bc	52.80klmn	49.60fghijklmn	9.23bcdefghij	2.86gh	12.54gh
G41	123.81 efgh	54.67bcdef	99.33bcdef	4.53fghij	3.93mnopq	146.20bcdefgh	2.34bc	53.60klmn	46.93ghijklmno	8.52bcdefghij	2.53ij	8.46mno
G42	144.35abcd	54.00def	100.00abcdef	4.27hij	4.00mnopq	129.47cdefgh	2.45bc	50.47lmno	56.40cdefghijk	9.75bcdefg	2.75h	13.90e
G43	142.65abcde	56.67a	100.00abcdef	6.53abc	5.13fghijk	125.40cdefgh	2.43bc	56.53fghijkl	71.33ab	10.19bcdef	2.35k	15.49c

PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Day of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = Capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm); TSW = Thousand seed weight (g), SYP = Seed yield per plant (g).

Table 4. Estimation of genetic variability for yield contributing characters related to yield of sesame genotypes

Parameters	Range		MS	Mean	CV (%)	σ^2p	σ^2g	σ^2e	PCV	GCV	h^2_b	GA	GA (% mean)
	Max	Min											
PH	154.47	115.47	272.52*	132.88	9.25	191.49	40.51	150.98	10.41	4.79	21.16	6.03	4.54
DFF	56.67	50.00	6.58**	54.50	2.01	2.99	1.79	1.20	3.18	2.46	59.81	2.13	3.91
DEM	102.33	96.00	5.29**	99.20	1.58	2.28	1.50	0.89	1.52	1.24	65.95	2.05	2.07
NPBP	7.53	3.73	2.12**	5.22	19.37	1.39	0.37	1.02	22.58	11.60	26.40	0.65	12.27
NSBP	7.73	2.13	9.45**	4.24	10.14	2.48	2.23	0.25	32.14	30.50	90.06	2.92	59.63
NCP	219.40	101.20	2070.7**	142.03	27.44	1703.13	183.78	1519.35	29.05	9.54	10.79	9.17	6.46
CL	4.08	1.31	0.49**	2.23	18.20	0.27	0.11	0.16	23.43	14.76	39.69	0.43	19.16
NSC	69.40	44.27	91.98**	57.43	7.68	43.64	24.17	19.48	11.50	8.56	55.37	7.53	13.12
HFC	73.93	31.20	285.34**	53.18	16.66	147.41	68.96	78.46	22.83	15.61	46.78	11.70	22.00
IL	13.46	5.43	6.79**	8.61	17.86	3.83	1.47	2.36	22.76	14.11	38.45	1.55	18.02
TSW	4.32	1.30	2.04**	2.67	2.56	0.69	0.66	0.03	30.92	30.81	99.31	1.69	63.25
SYP	18.07	2.74	38.30**	13.60	4.65	12.95	12.67	0.27	32.01	31.66	97.89	7.26	64.54

*, ** indicate significant at 5% and 1% level of probability, respectively.

PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Day of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm), TSW = Thousand seed weight (g) and SYP = Seed yield per plant (g); σ^2p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic co-efficient of variation, GCV = Genotypic co-efficient of variation, h^2_b = Broad sense heritability, GA = Genetic advance, GA (% mean) = Genetic advance in percent of mean.

4.1.1.3 Days to 80% maturity (days)

The maximum days to 80% maturity (DEM) was recorded G2 (102.33 days) and minimum days recorded was G37 (96.00) days (Table 3). The genotypic variance (1.50) was lower than phenotypic variance was 2.28. Which indicates that there is significant influence of environment on this trait. The GCV (1.24) was lower than the PCV (1.52). The heritability for DEM was high (65.95%) and the genetic advance (2.05) and genetic advance in percent of mean (2.07) was low indicating that the phenotypic selection for DEM would not be effective. Thouseem *et al.* (2022) reported that low heritability for days to maturity in sesame.

4.1.1.4 Number of primary branches per plant

The minimum number of primary branches per plant (NPBP) was observed in G19 (3.73) followed by G32 (4.13) whereas the maximum was observed in G22 (7.53) with the mean value of 5.22 (Table 3 and Table 4). In table 4 the phenotypic variance (1.39) was higher than genotypic variance (0.37) suggested that there was influence of environment on the phenotypic expression of NPBP. The PCV and GCV were 22.58 and 11.60, respectively. Heritability estimated for NPBP was low (26.40%) with low genotypic advance (0.65) and low genetic advance in percent of mean (12.27) indicating this character was governed by non-additive gene (Table 4). Kumar *et al.* (2022) also reported high heritability in case of number of primary branches per plant in sesame.

Plate 7. Photograph showing variations in flowers of different sesame genotypes

4.1.1.5 Number of secondary branches per plant

The lowest NSBP was observed in G38 (2.13) whereas the highest was observed in G20 (7.73) followed by G10, G17, G1 and G4 with the mean value of 4.24 (Table 3 and Table 4). The phenotypic variance (2.48) was slightly higher than genotypic variance (2.23) suggested that there was little influence of environment on the expression of the genes controlling this trait (table 4). The PCV and GCV were 32.14 and 30.50, respectively. High heritability estimated (90.06%) was recorder for NSBP with low genetic advance (2.92) and high genetic advance in percent of mean (59.63) 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 this trait via phenotypic selection. Roy *et al.* (2022) also reported high heritability coupled with high genetic advance for number of branches per plant of sesame.

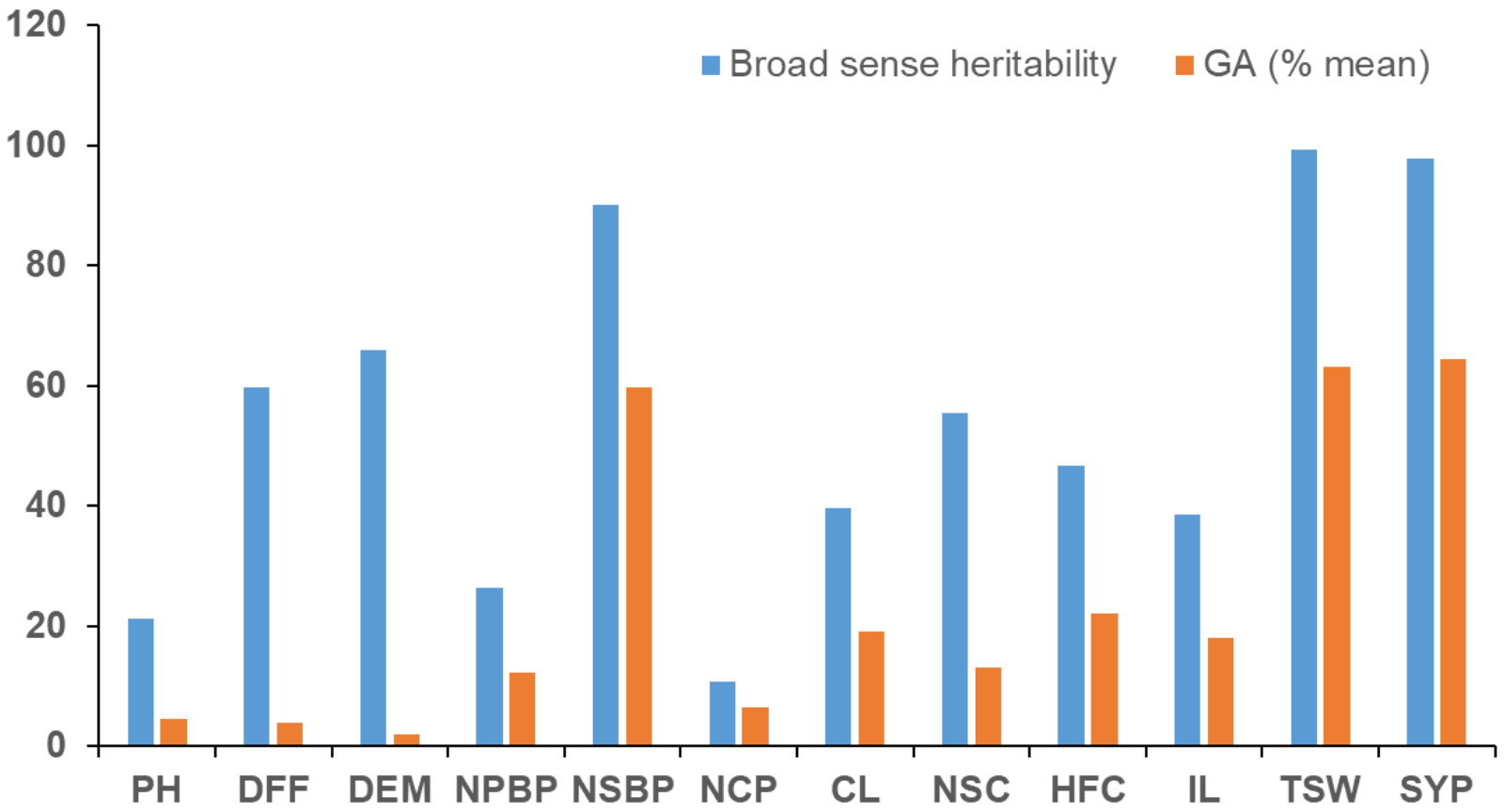

Figure 1. Broad sense heritability (%) and genetic advance of yield and its contributing traits in sesame. PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Day of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm), TSW = Thousand seed weight (g) and SYP = Seed yield per plant (g)

4.1.1.6 Number of capsules per plant

The highest number of capsules per plant (NCP) found in G22 (219.40) while the lowest was observed in G31 (105.20) (Table 3). The NCP showed the highest phenotypic variance (1703.13) and highest genotypic variance (183.78) which indicates large environmental influence over genotypes. The PCV (29.05) was higher than the GCV (9.54) suggesting that the presence of adequate variation between the genotypes (Table 4). The heritability estimates for this trait was low (10.79%) with low genetic advance (9.17) and low genetic advance in percent of mean (6.46) suggesting non-additive gene effects for this trait. However, Paramasivam and Prasad (1981) reported opposite to our result as high heritability estimates for number of capsule per plant in sesame.

4.1.1.7 Capsules length (cm)

The highest capsule length (CL) was observed in G28 (4.08 cm) and the lowest in G22 (1.31 cm) (Table 3). The phenotypic and genotypic variances for this trait were 0.27 and 0.11, respectively. The PCV and GCV were 23.43 and 14.76, respectively for CL indicating that moderate variation exists among sesame genotypes for this trait (Table 4). Variations in capsule length of sesame genotypes are presented in Plate 8. The moderate heritability (39.69%) was observed for CL with low genetic advance (0.43) and low genetic advance in percent of mean is (19.16) suggesting that the non-additive genes controlling this trait. Therefore, phenotypic selection based for CL would not be effective. Kumar *et al.* (2022) showed an opposite result as high heritability for capsule length of sesame.

Plate 8. Photograph showing variations in capsules of various sesame genotypes

4.1.1.8 Number of seeds per capsule

The maximum number of seeds per capsule (NSC) was recorded in G5 (69.40) while the minimum in G16 (44.27) (Table 3). The phenotypic and genotypic variances for NSC were 43.64 and 24.17, respectively. The phenotypic variance was much higher than the genotypic variance indicating a great influence of environment on the phenotypic expression of this trait. The PCV (11.50) was also higher than the GCV (8.56) for NSC suggesting a moderate variation among the sesame genotypes (Table 4). This character also showed a moderate heritability (55.37%) with low genetic advance (7.53) and low genetic advance in percent of mean (13.12). The result revealed that the non-additive effect plays an important role for the phenotypic expression. Thus, phenotypic selection for this character will not be so rewarding. Srikanth and Ghodke (2022) reported high heritability coupled with high genetic advance as percentage of mean for number of seeds per capsule in sesame.

4.1.1.9 Height of first capsule (cm)

The maximum values for height of first capsule (HFC) was found in G38 (73.93 cm) whereas the minimum was in G26 (31.20 cm) with the mean vale of 53.18 cm (Table 3). The phenotypic and genotypic variances for HFC were 68.96 and 78.46, respectively and the PCV and GCV were 22.83 and 15.61, respectively and the moderate heritability (46.78%) was found for HFC with low genetic advance (11.70) and moderate genetic advance in percent of mean (22.00). Pavani *et al.* (2020) found high heritability and high genetic advance for HFC in sesame.

4.1.1.10 Internode length (cm)

The highest internode length (IL) was recorded in G9 (13.46 cm) whereas the lowest was in G32 (5.43 cm) with the mean vale of 8.61 cm (Table 3). The phenotypic and genotypic variances were 3.83 and 1.47, respectively the PCV and GCV were 22.76 and 14.11, respectively (Table 4). The moderate heritability (38.45%) was found for internode length with low genetic advance (1.55) and low genetic advance in percent of mean (18.02). Nevertheless, high genetic advance in per cent of mean was observed by Kumar *et al.* (2022) in sesame.

4.1.1.11 Thousand seed weight (g)

The highest thousand seed weight (TSW) was found in G14 (4.32) and G23 (4.32) whereas the lowest in G29 (0.72) with the 2.67 g mean value (Table 3). There was a little difference between genotypic (0.66) and phenotypic (0.69) variances suggesting that environmental factors have less effect on the phenotypic expression of TSW. The PCV and GCV were 30.92 and 30.81, respectively (Table 4). There was also a very little difference between PCV and GCV, indicating little environmental influence on this trait. A very high heritability (99.31%) with low genetic advance (1.69) and high genetic advance in percent of mean (63.25). It is suggesting that the phenotypic selection for TSW would be rewarded. A similar result was also reported by Srikanth and Ghodke (2022) and Kumar *et al.* (2022) for TSW in sesame.

4.1.1.12 Seed yield per plant (g)

The maximum seed yield per plant (SYP) was found in G6 (18.07 g) while the minimum in G3 (2.74) with the 13.60 g mean value (Table 3). The phenotypic variances and genotypic variances for this trait were 12.95 and 12.67, respectively for SYP and the PCV and GCV were 32.01 and 31.66, respectively. The less differences between genotypic and phenotypic variances as well as PCV and GCV indicated that there is less influence of environmental influences on this trait. The variation found in seed is presented in Plate 9. The SYP showed a very high heritability (97.89%) with low genetic advance (7.26) and high genetic advance in percent of mean (64.54) (Table 4). Thus suggesting that the major role of additive genetic effects and less environmental influence for the phenotypic expression of this trait and the phenotype selection would be rewarded for SYP. Roy *et al.* (2022), and Srikanth and Ghodke (2022) also reported high heritability coupled with high genetic advance for seed yield per plant in sesame.

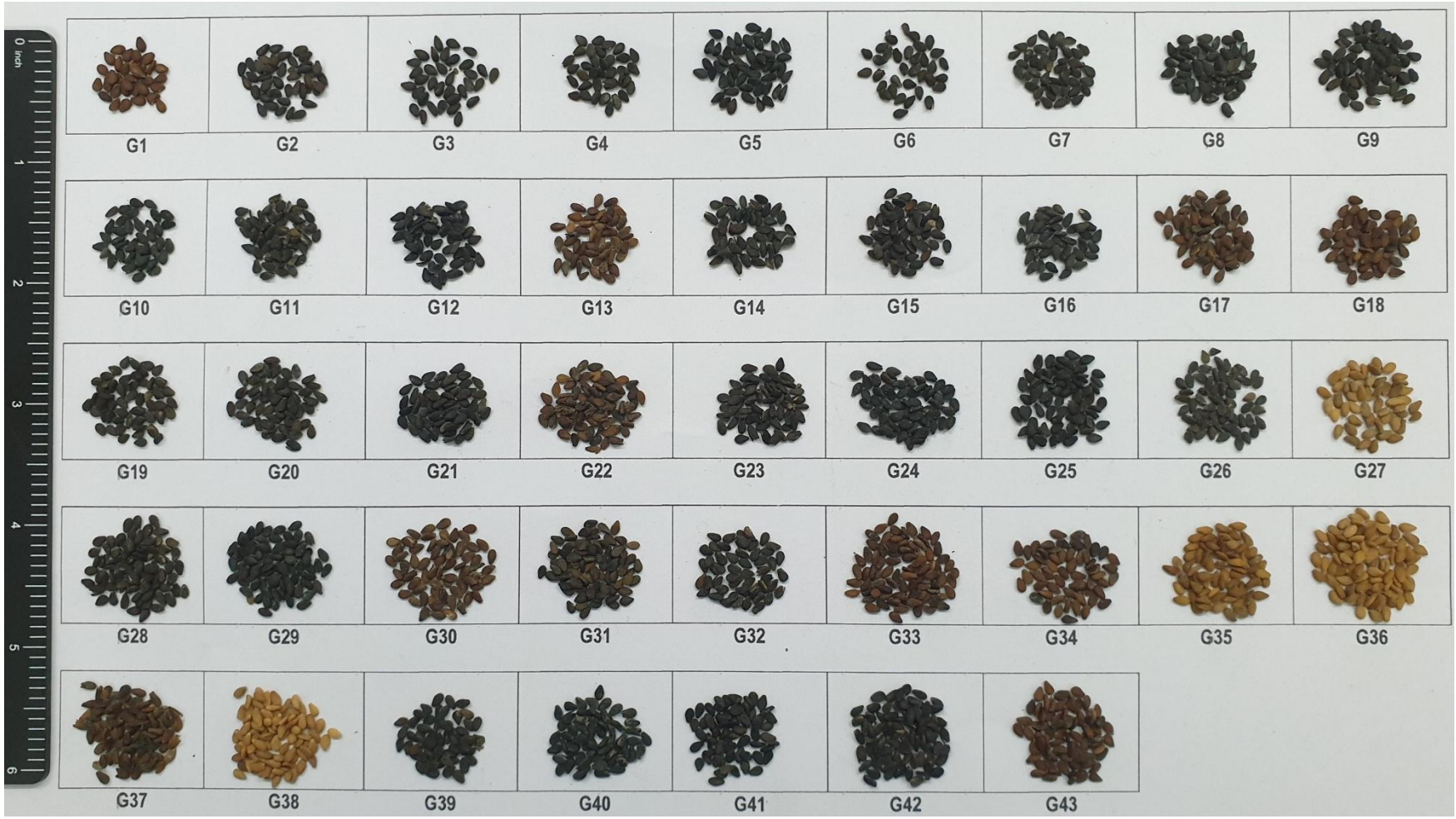

Plate 9. Photograph showing variations in seeds of various sesame genotypes

4.2 Correlation co-efficient

The correlation co-efficient is very helpful in plant breeding for selection of yield and its contributing traits. Moreover, it is possible to improve some other characters along with yield via correlation co-efficient. The genotypic and phenotypic correlation co-efficient of 12 character of 43 sesame genotypes are presented in Figure 2 and (Table 5).

4.2.1 Plant height (cm)

Plant height (PH) had a significant positive correlation with days to 50% flowering (DFF) (r_g=0.754**; r_p=0.208*), days to 80% maturity (DEM) (r_g=0.797**; r_p=0.176*) capsule length (CL) (r_g=0.567**; r_p=0.245*), height of first capsule (HFC) (r_g=0.491**; r_p=0.558**), internode length (IL) (r_g=0.846**; r_p=0.384**) and yield per plant (YPP) (r_g=0. 546**; r_p=0.246*) at both the genotypic and phenotypic level (Table 5). It had also a non-significant positive correlation with number of seeds per capsule (NSC) (r_g=0.198; r_p=0.045) and thousand seed weight (TSW) (r_g=0.140; r_p=0.060) at both the genotypic and phenotypic level. Moreover, it had highly significant positive correlation with number of primary branches per plant (NPBP) (r_g=0.500**) at the genotypic level while non-significant negative correlation with (r_p=-0.074) at phenotypic level. In addition, PH showed a non-significant negative correlation with number of secondary branches per plant (NSBP) (r_g=-0.004; r_p = -0.024) at both the genotypic and phenotypic level. The results suggested that the increase of PH will also increase the SYP, and the phenotypic selection for PH would meaningful for sesame improvement. Goudappagoudra *et al.* (2011), Sumathi and Muralidharan (2010), Sultana *et al.* (2019) and Saravanan *et al.* (2020) were also reported a significantly positive correlation of PH with YPP in sesame.

4.2.2 Days to 50% flowering (days)

Days to 50% flowering showed significant positive correlation with DEM (r_g=0.999**; r_p =0.4589**), NPBP ((r_g=-0.595**; r_p=0.276**), HFC (r_g=0.847**; r_p=0.440**) IL (r_g=0.521**; r_p=0.215*) and SYP (r_g=0.587**; r_p=0.448**) at both the genotypic and phenotypic level (Table 5). It had also significant positive correlation with TSW (r_p=0.226*) at phenotypic level but non-significant correlation (r_g=0.291) at genotypic level. Besides, DFF showed non-significant positive correlation with number of capsules per plant (NCP) (r_g=0.265; r_p=0.085), CL (r_g=0.186; r_p=0.070), NSC (r_g=0.175; r_p=0.105) both the genotypic and phenotypic level (Table 5). Moreover, it had a non-significant negative correlation with NSBP (r_g=-0.026; r_p=-0.010) at both the genotypic and phenotypic level. Aye and Htwe (2019) also reported that DFF had a significant positive correlation with SYP.

4.2.3 Days to 80% maturity (days)

Days to 80% maturity exhibited a significant and positive correlation with HFC (r_g=0.707**; r_p=0.211**), TSW (r_g=0.336*; r_p=0.180*) and SYP (r_g=0.615**; r_p=0.321**) at both the genotypic and phenotypic level (Table 5). It had highly significant positive correlation with NPBP (r_g=0.647**), NCP (r_g=0.403**) and IL (r_g=0.337**) at genotypic level while non-significant positive correlation at phenotypic level. Sumathi and Muralidharan (2011), and Lalpantluangi, and Shah (2018) were also found a significantly positive correlation of DEM with YPP in sesame.

4.2.4 Number of primary branches per plant

Number of primary branches per plant had significant positive correlation with NSBP (r_g=0.389**; r_p=0.220*), NCP (r_g=0.675**; r_p=0.368**), HFC (r_g=0.769**; r_p=0.261**) and SYP (r_g=0.650**; r_p=0.344**) at both the genotypic and phenotypic level (Table 5). This character also showed a non-significant negative correlation with CL (r_g=-0.216; r_p=-0.097) at both the genotypic and phenotypic level. Besides, NPBP had a significant positive correlation with NSBP (r_g=0.389**; r_p = 0.220*) at both the genotypic and phenotypic level. Our results are in agreement with the findings of Meenakumari and Ganesamurthy (2015) for number of primary branches per plant in sesame.

4.2.5. Number of secondary branches per plant

Number secondary branches per plant had a highly significant positive correlation only with NCP (r_g=0.748**; r_p=0.371**) at both the genotypic and phenotypic level (Table 5). NSBP also showed a non-significant positive correlation with NSC (r_g=0.196; r_p=0.145), IL (r_g=0.167; r_p=0.060) and SYP (r_g=0.135; r_p=0.123) at both the genotypic and phenotypic level. Moreover, NSBP had a non-significant negative correlation with CL (r_g=-0.141; r_p = -0.070) and TSW (r_g=-0.102; r_p=-0.020) at both the genotypic and phenotypic level. Sumathi and Muralidharan (2010) observed that SYP had significantly positive correlation with number of branches per plant.

4.2.6. Number of capsules per plant

Number of capsules per plant (NCP) showed significant positive correlation with NSC (r_g= 0.307*; r_p= 0.195*) and SYP ($r_{g=}$ 0.775**; $r_{p=}$ 0.275**) at both the genotypic and phenotypic level (Table 5). NCP also showed a significant positive correlation with TSW (r_g= 0.433**) whereas highly positive with HFC (r_g= 0.433**) at the genotypic level. Moreover, NCP had a non-significant negative correlation with IL (r_g=-0.107; $r_{p\,=}$ -0.089) at both the genotypic and phenotypic level. The result suggested that the increase of NCP will also increase the SYP and phenotypic selection for this trait would be effective. Meenakumari and Ganesamurthy (2015), Aye and Htwe (2019), Sultana *et al.* (2019) also reported the significant positive correlation of NCP with SYP in sesame.

4.2.7. Capsule length (cm)

Capsule length (CL) had a highly significant positive correlation only with IL (r_g=0.480**) at genotypic level (Table 5). It showed non-significant positive correlation with SYP at both the genotypic (r_g=0.068) and phenotypic (r_p=0.033) level. It had negative correlation with NSC (r_g=-0.287; r_p=-0.160) and TSW (r_g=-0.190; r_p=-0.112).

4.2.8. Number seeds per capsule

Number of seeds per capsule (NSC) showed significant positive correlation with SYP (r_g=0.320*; r_p=0.240**) at both the genotypic and phenotypic level (Table 5). It had significant positive correlation with TSW (r_p=0.214*) at phenotypic level only.

Table 5. Genotypic and phenotypic correlation coefficients among various yield and its contributing characters of sesame genotype

Characters		PH	DFF	DEM	NPBP	NSBP	NCP	CL	NSC	HFC	IL	TSW
PH	r_g											
	r_p											
DFF	r_g	0.754**										
	r_p	0.208*										
DEM	r_g	0.797**	0.999**									
	r_p	0.176*	0.458**									
NPBP	r_g	0.500**	0.595**	0.647**								
	r_p	-0.074	0.276**	0.120								
NSBP	r_g	-0.004	-0.026	-0.122	0.389**							
	r_p	-0.024	-0.010	-0.044	0.220*							
NCP	r_g	0.309*	0.265	0.403**	0.675**	0.748**						
	r_p	0.081	0.085	0.138	0.368**	0.371**						
CL	r_g	0.567**	0.186	-0.034	-0.216	-0.141	-0.015					
	r_p	0.245**	0.070	-0.012	-0.097	-0.070	0.035					
NSC	r_g	0.198	0.175	0.177	0.196	0.047	0.307*	-0.287				
	r_p	0.045	0.105	0.091	0.145	0.005	0.195*	-0.160				
HFC	r_g	0.491**	0.847**	0.707**	0.769**	-0.107	-0.426**	-0.018	0.042			
	r_p	0.558**	0.440**	0.211*	0.261**	0.113	-0.150	0.073	-0.027			
IL	r_g	0.846**	0.521**	0.337*	0.267	0.167	-0.107	0.480**	0.049	0.707**		
	r_p	0.384**	0.215*	0.030	0.076	0.060	-0. 089	0.165	-0.031	0.434**		
TSW	r_g	0.140	0.291	0.336*	0.274	-0.102	0.433**	-0.190	0.298	0.274	-0.178	
	r_p	0.060	0.226*	0.180*	0.130	-0.020	0.134	-0.112	0.214 *	0.182*	-0.108	
SYP	r_g	0.546**	0.587**	0.615**	0.650**	0.135	0.775**	0.068	0.320 *	0.376*	0.228	0.377*
	r_p	0.246**	0.448**	0.321**	0.344**	0.123	0.275**	0.033	0.240 **	0.254**	0.141	0.373**

* ,** = Significant at 5% and 1% level of significance, respectively

Here, PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Days of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = Capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm), TSW = Thousand seed weight (g) and SYP = Seed yield per plant (g)

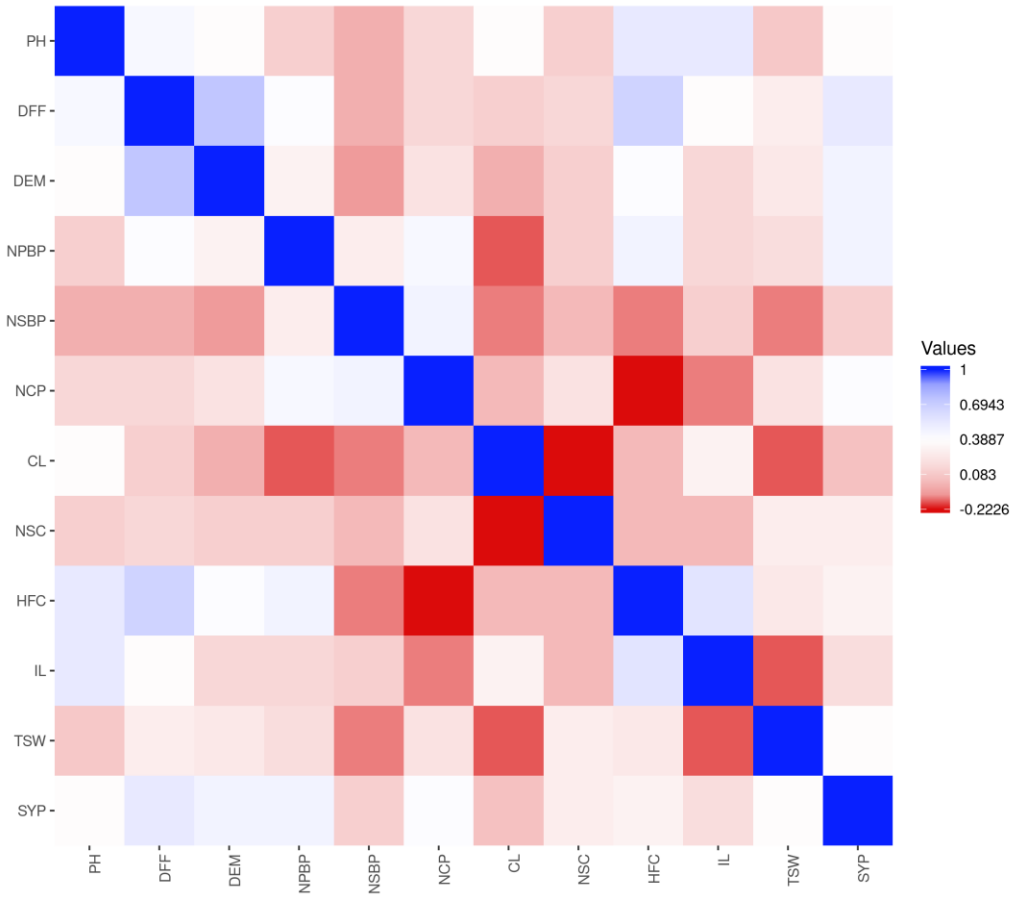

Figure 2. Correlation matrix showing correlation between different traits of sesame (using Spearman's rank correlation). The red and blue colors in the legend indicates highest and lowest values, respectively. Here, PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Days of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = Capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm), TSW = Thousand seed weight (g) and SYP = Seed yield per plant (g). (This correlation matrix was generated by http://www.heatmapper.ca)

The result suggested that SYP increase with the increase of NSC. Goudappagoudra *et al.* (2011), Meenakumari and Ganesamurthy (2015), Sultana *et al.* (2019) also reported the significant positive correlation of NSC with SYP in sesame.

4.2.9. Height of first capsule (cm)

Height of first capsule (HFC) showed highly significant positive correlation with IL at both genotypic (r_g=0.707**) and phenotypic (r_p=0.434**) level (Table 5). It also showed significant positive correlation with SYP at genotypic (r_g=0.376*) and phenotypic (r_p=0.254**) level. Moreover, it had also a significant positive correlation with TSW (r_p=0.182*) at phenotypic level (Table 5),

4.2.10. Internode length (cm)

Internode length (IL) had non-significant positive correlation with SYP (r_g=0.228; r_p=0.141) at both genotypic and phenotypic (Table 5). It also had non-significant negative correlation with TSW (r_g=-0.178; r_p=-0.108) at both the genotypic and phenotypic level.

4.2.11. Thousand seed weight (g)

Thousand seed weight (TSW) had significant positive correlation with SYP (r_g=0.377*; r_p=0.373**) at both genotypic and phenotypic level (Table 5). Sumathi and Muralidharan (2011) and Kehie *et al.* (2020) also reported similar result for TSW and SYP in sesame.

4.3 Path Co-efficient analysis:

Path co-efficient analysis partitioned the correlation coefficient as direct and indirect effect of yield on different yield contributing traits. Yield is treated as dependent trait and plant height, days to 50% flowering, days to 80% maturity, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, height of first capsule, internode length and 1000-seed weight a were considered as independent traits (causes). The direct and indirect effects of path co-efficient analysis for sesame are presented in Table 6.

4.3.1. Pant height (cm)

Plant height (PH) had maximum direct positive effect (0.856) followed by number of primary branches per plant on seed yield per plant. It had indirect positive effect on SYP via days to 80 % maturity (0.181), NPBP (0.234), capsule length (CL) (0.147), number of seed per capsule (NSC) (0.042), height of first capsule (HFC) (0.005), and thousand seed weight (TSW) (0.021). Furthermore, it had indirect negative effect on SYP via days to 50% flowering (DFF) (-0.150), NSB (-0.001), NCP (-0.114) and IL (-0. 675). Finally, it made positive significant effect with SYP (0.546**) (Table 6). The result indicated that if PH increases then SYP also increases through the positive indirect effect of PH with other traits. The phenotypic selection based on PH would be effective.

4.3.2 Days to 50% flowering (days)

Days to 50% flowering (DFF) had the direct negative direct effect (-0.198) on SYP (Table 6). DFF had positive indirect effect on SYP via PH (0.645), DEM (0.246), NPBP

(0.278), CL (0.048), NSC (0.037), HFC (0.009) and TSW (.045). Moreover, it had indirect negative effect on SYP via NSBP (-0.011), NCP (-0.097) and IL (-0.416). Ultimately, it made positive significant correlation with SYP (0.587**) (Table 6). It revealed that relationship between these traits and selection for this trait will be rewarding for yield improvement.

4.3.3 Days to 80 % maturity (days)

Days to 80 % maturity had direct positive effect (0.227) on SYP (Table 6). It had indirect positive effect on SYP through PH (0.682), NPBP (0.302), NSC (0.037), HFC (0.007) and TSW (0.052). It had indirect negative effect on SYP via DFF (-0.214), NSBP (-0.053), NCP (-0.149), CL (-0.008) and IL (-0.269). Eventually, it made positive significant correlation with SYP (0.615**) (Table 6).

4.3.4 Number of primary branches per plant

Number of primary branches per plant had second highest direct positive effect (0.467) on SYP (Table 6). This trait also showed indirect positive effect on yield via PH 0.428), DFF (0.118), DEM (0.147), NSBP (0.171), NSC (0.020), HFC (0.008) and TSW (0.042). NPBP had indirect negative effect on SYP via NCP (-0.249), CL (-0.055) and IL (-0.213). Finally, it made positive significant effect with seed YPP (0.650**) (Table 6). Thus indicated that if NPBP increases then SYP also increases through the positive indirect effect of other traits.

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant (NSBP) had positive direct effect (0.441) on SYP (Table 6). It had indirect positive effect on yield via DFF (0.005), NPBP (0.182), NSC (0.001) and HFC (0.001). NSBP had indirect negative effect on SYP via PH (-0.003), DEM (-0.027), NCP (-0.276), CL (-0.036), IL (-0.133) and TSW (-0.016). Lastly, it made NON-significant but positive effect with seed YPP (0.135) (Table 6).

4.3.6 Number of capsules per plant

Number of capsules per plant (NCP) had the direct negative effect (-0.370) on SYP followed by indirect positive effect via PH (0.264), DEM (0.091), NPBP (0.315), NSBP (0.330), NSC (0.065), HFC (0.004), IL (0.070) and TSW (0.067) (Table 6). NCP had indirect negative effect on yield via DFF (-0.052) and CL (-0.003) (Table 6). Finally, it had highly significant positive genotypic correlation with SYP (0.775**). The results indicated that correlation was mainly due to the direct effect of the trait and it was realized via indirect effects. Similar to our result for NCP was reported by Sumathi and Muralidharan (2010).

4.3.7 Capsule length (cm)

Capsule length (CL) had direct positive effect (0258) on SYP (Table 6). It also exhibited indirect negative effect via all the traits except via PH (0.485) and NCP (0.005). CL finally exhibited a non-significant positive correlation SYP (0.068).

Table 6. Partitioning of genotypic correlations into direct (bold) and indirect effects of 12 important traits by path analysis of sesame genotypes

Characters	PH	DFF	DEM	NPBP	NSBP	NCP	CL	NSC	HFC	IL	TSW	SYP (r_g)
PH	**0.856**	-0.150	0.181	0.234	-0.001	-0.114	0.147	0.042	0.005	-0.675	0.021	0.546**
DFF	0.645	**-0.198**	0.246	0.278	-0.011	-0.097	0.048	0.037	0.009	-0.416	0.045	0.587**
DEM	0.682	-0.214	**0.227**	0.302	-0.053	-0.149	-0.008	0.037	0.007	-0.269	0.052	0.615 **
NPBP	0.428	0.118	0.147	**0.467**	0.171	-0.249	-0.055	0.020	0.008	-0.213	0.042	0.650**
NSBP	-0.003	0.005	-0.027	0.182	**0.441**	-0.276	-0.036	0.001	0.001	-0.133	-0.016	0.135
NCP	0.264	-0.052	0.091	0.315	0.330	**-0.370**	-0.003	0.065	0.004	0.070	0.067	0.775**
CL	0.485	-0.036	-0.007	-0.101	-0.062	0.005	**0.258**	-0.061	-0.001	-0.383	-0.029	0.068
NSC	0.169	-0.034	0.040	0.045	0.002	-0.113	0.074	**0.213**	0.001	0.024	0.046	0.320*
HFC	0.419	-0.167	0.160	0.359	-0.047	0.157	-0.004	0.009	**0.011**	-0.565	0.042	0.376*
IL	0.723	-0.103	0.076	0.125	0.073	0.032	0.124	-0.006	0.007	**-0.799**	-0.027	0.228
TSW	0.119	-0.057	0.076	0.128	-0.045	-0.160	0.049	0.063	0.003	0.142	**0.156**	0.377*

Residual effect (R) = 0.147

* ,** = Significant at 5% and 1% level of significance, respectively

PH = Plant height (cm), DFF = Days to 50% flowering, DEM = Days of 80% maturity, NPBP = Number of primary branches per plant, NSBP = Number of secondary branches per plant, NCP = Number of capsules per plant, CL = Capsule length (cm), NSC = Number of seeds per capsule, HFC = Height of first capsule (cm), IL = Internode length (cm), TSW = Thousand seed weight (g) and SYP = Seed yield per plant (g)

4.3.8 Number of seeds per capsule

Number of seeds per capsule (NSC) had direct positive effect (0.213) on SYP (Table 6). It had also exhibited indirect positive effect via all the traits except via DFF (-0.034) and NCP (-0.113). This trait finally exhibited significant positive correlation with seed yield per plant (0.320**).

4.3.9 Height of first capsule (cm)

Height of first capsule (HFC) had direct positive effect (0.011) on SYP (Table 6). It had indirect positive effect via PH (0.419), DEM (0.160), NPBP (0.359), NCP (0.157), NSC (0.009) and TSW (0.042) whereas indirect negative effect via DFF (-0.167), NSBP (-0.047), CL (-0.004) and IL (-0.565). This trait also highly correlated with SYP (0.376**).

4.3.10 Internode length (cm)

Internode length (IL) had direct negative effect (-0.799) on SYP (Table 6). It also showed indirect positive effect via PH (0.723), DEM (0.076), NPBP (0.125), NSBP (0.073), NCP (0.032), CL (0.124) and HFC (0.007) while indirect negative effect via DFF (-0.103), NSC (-0.006) and TSW (-0.027). IL had non-significant but positive genotypic correlation with SYP (0.228).

4.3.11 Thousand seed weight (g)

Thousand seed weight (TSW) had a direct positive effect (0.156) on SYP (Table 6). It also showed indirect positive effect via PH (0.119), DEM (0.076), NPBP (0.128), CL (0.049), NSC (0.063), HFC (0.003) and IL (0.142) whereas indirect negative effect via

DFF (-0.057), NSBP (-0.045) and NCP (-0.160). Finally, TSW had highly significant positive genotypic correlation with SYP (0.377**). Onginjo and Ayiecho (2009) showed that TSW had positive direct effect on seed yield in sesame. The residual effect (R) was 0.147 which indicated that the contribution of component characters was 85.3 percent. The rest 14.70 percent was the contribution of other factors.

5. Selection of elite sesame genotypes

Cluster analysis was carried out using 43 sesame genotypes for 12 yield and its contributing traits by an online clustering tool (http://www2.heatmapper.ca). The results revealed that 43 sesame genotypes were grouped into four clusters (Figure 3 and Table 6). The maximum genotypes were included in cluster III (14) followed by cluster IV (12) and cluster II (9) while minimum genotypes in cluster I (8) (Table 6). The sesame genotype G6, G12 and G36 which were grouped in cluster IV exhibited better performance for yield per plant (Figure 2, Table 3 and Table 6). Moreover, the genotype of cluster II, G26 and G27 showed minimum mean values for days to 50% flowering and days to 80% maturity suggesting early maturing genotypes belongs to this cluster. Sultana *et al.* (2019) reported similar results in sesame the clustering of genotypes.

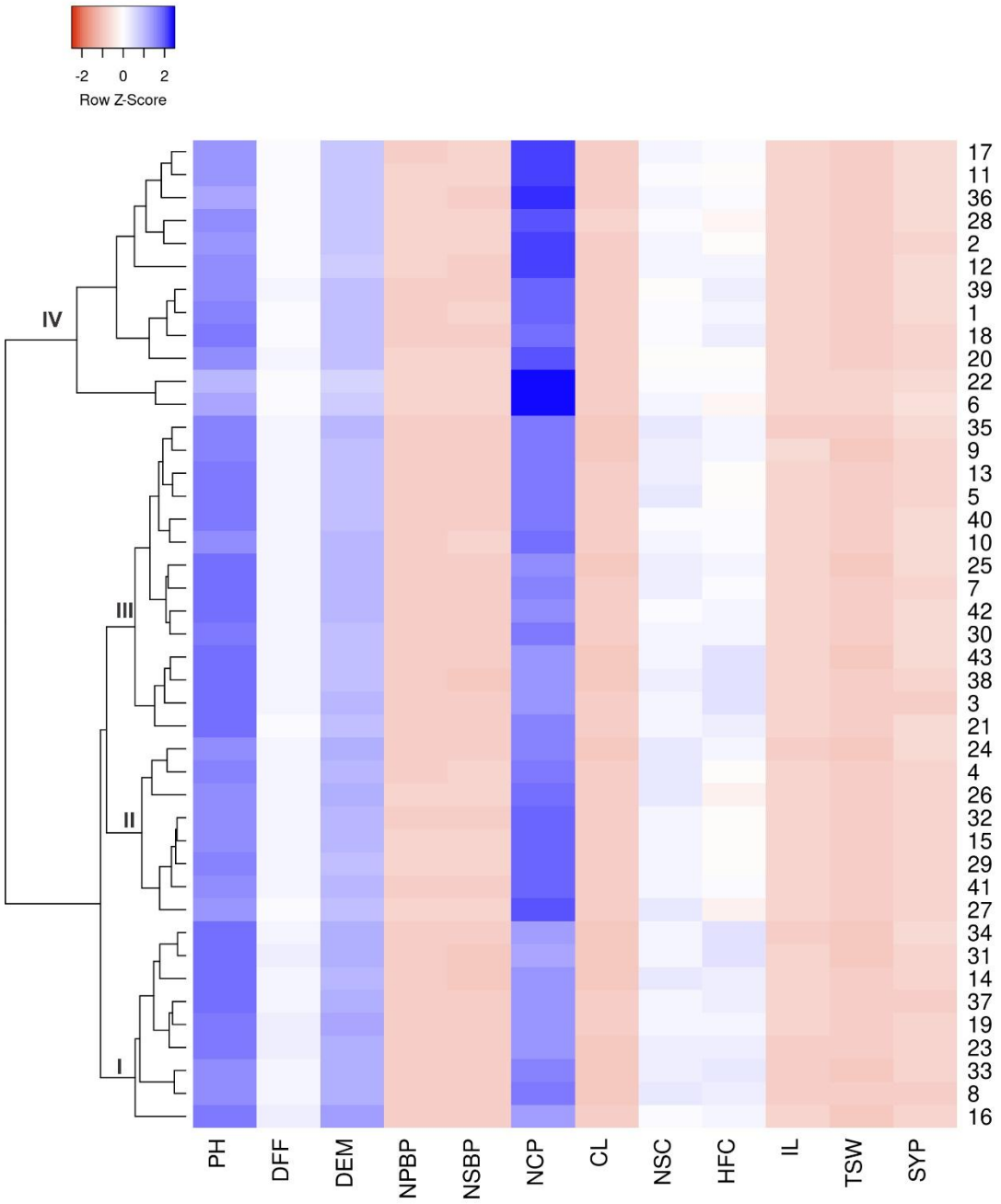

Figure 3. Heatmap representation of 43 sesame genotypes into four clusters in respect of 12 traits

Table 6. Distribution of 43 sesame genotypes into four clusters

Cluster	No. of Genotypes	Genotypes
I	8	G8, G18, G19, G23, G31, G33, G34 and G37
II	9	G4, G15, G24, G26, G27, G28, G29, G32 and G41
III	14	G3, G5, G7, G9, G10, G13, G21, G25, G30, G35, G38, G40, G42 and G43
IV	12	G1, G2, G6, G11, G12, G17, G18, G20, G22, G28, G36 and G39

CHAPTER V

SUMMARY AND CONCLUSION

This present study was carried out in Randomized Complete Block Design with 3 replications at the experimental farm of Sher-e-Bangla Agricultural University to understand the genetic variability, correlation and path analysis based on 12 characters of 43 sesame genotypes. Analysis of variance exhibited significant differences for most of the characters except number of capsules per plant. The maximum plant height was observed in G12 (154.47 cm) and lowest in G33 (115.47 cm). The early flowering genotypes were G26 (50.00 days), G27 (50.00 days) and G37 (51.33 days) while G43 (56.67 days) was the late flowering. The maximum number of primary branches per plant was found in G22 (7.53) and minimum in G19 (3.37). The highest number of secondary branches per plant was found in G20 (7.73) and lowest number in G38 (2.13). The highest number of capsules per plant was found in G22 (219.40) and the lowest was found in G16 (101.20). The highest capsule length was found in G28 (4.08) and the lowest in G22 (1.31). The maximum number of seeds per capsule was found in G5 (69.40) and the minimum in G16 (44.27). The lowest height of first capsule was observed in G26 (31.20) and the minimum in G38 (73.93 cm). The height internode length was found in G9 (13.46 cm) while the lowest in G32 (5.43). The maximum 1000-seeds weight was found in G-22 and the lowest in G-30. The hundred seed weight was found highest in G23 (4.32) and the lowest in G29 (1.72). The highest seed yield per plant was found in G6 (18.07) followed by G12 (17.39) and G36 (17.24) while the lowest observed in G27 (5.10). The phenotypic variance and phenotype co-efficient of variation were more than the respective genotypic variance and genotypic co-efficient of variation for all

the characters. Phenotypic variance and PCV were also very close to genotypic variance and GCV for NSBP, TSW and SYP. High broad base heritability together with high genetic advance in percent of mean was observed for NSBP (90.06%), TSW (99.31%) and SYP (97.89%) while moderate heritability for PH (59.81%). In the contrary, the lowest heritability was found for NCP (10.79%) followed by PH (21.16%). Furthermore, the correlation co-efficients and the path analysis for 12 characters among the sesame genotypes were determined to understand the association between yield and yield contributing characters. Most of the studied characters exhibited the higher genotypic correlation co-efficient than the phenotypic correlation co-efficient indicating that there were a statble association between the characters and suppressive effect of the environment altered the phenotypic expression of these characters by decreasing the phenotypic correlation coefficients. The significant positive correlation with seed yield per plant was found for plant height (r_g = 0.546**, r_p= 0.246**), days to 50% flowering (r_g = 0.587**, r_p= 0.448**), days to 80% maturity (r_g = 0.615**, r_p= 0.321**), number of primary branches (r_g = 0.650**, r_p= 0.344**), number of capsules per plant (r_g = 0.775**, r_p= 0.275**), number of seeds per capsule (r_g = 0.320*, r_p= 0.240**), height of first capsule (r_g = 0.376*, r_p= 0.254**) and 1000-seed weight (r_g = 0.377**, r_p= 0.373**). Path co-efficient analysis revealed that plant height (0.856), days to 80% maturity (0.227), number of primary branches per plant (0.467), number of secondary branches per plant (0.441), capsule length (0.258) and number of seeds per capsule (0.213) had the positive direct effect on yield per plant whereas, internode length (-0.799) followed by number of capsules per plant (-0.370) and days to 50% flowering (-0.198) had the negative direct effect. Based on mean performance, heritability and interrelationship, genotype G6, G12

and G36 for seed yield per plant, and G26, G27 and G37 for early maturity could be selected for further improvement.

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Appendix I. Location of the experimental site

The experimental site under study