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DETERMINATION OF THE POTENTIALITY OF DIFFERENT SESAME (*Sesamum indicum* L.) GENOTYPES

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Abstract

A field experiment was carried out in Randomized Complete Block Design (RCBD) with three replications at the experimental field of Sher-e-Bangla Agricultural University (SAU), Dhaka during the *Kharif* season of 2022 to examine the genetic variability, correlation, and path analysis based on 12 characters of 43 sesame genotypes. Analysis of variance exhibited significant differences among the genotypes for most of the characters except the number of capsules per plant. The phenotypic variance and phenotype coefficient of variation were relatively higher than the respective genotypic variance and genotypic coefficient of variation for all the characters. High broad sense heritability together with high genetic advance in percent of mean was observed for number of secondary branches per plant (90.1%), 1000-seed weight (99.3%), and seed yield per plant (97.9%) while moderate heritability for days to 50% flowering (59.8%). The correlation coefficient analysis revealed that seed yield per plant had a significant positive correlation with plant height, days to 50% flowering, days to 80% maturity, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, height of the first capsule, and 1000-seed weight. It appears from path co-efficient analysis 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 a positive direct effect on the 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 a negative direct effect. Based on mean performance, heritability, and interrelationship, the genotypes G6, G12, and G36 for seed yield per plant, and the genotypes G26, G27, and G37 for early maturity could be selected for further varietal improvement of sesame.

Keywords: Correlation, Genetic variability, Heritability, Sesame genotype

Introduction

Sesame (*Sesamum indicum* L., 2n = 26) is an annual flowering plant of the Pedaliaceae family which is an ancient oilseed crops (Abdipour *et al.*, 2018). It is also known as "Till' in Bangladesh. Several wild relatives occur in Africa and a smaller number in India (Nayar and Mehra, 1970). It exhibits drought tolerance, grows well in

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most of the well-drained soils and various agro climatic regions, and is well adapted to different crop rotations (Tripathi *et al.*, 2013). The largest area of production is currently believed to be in India, but the crop is also grown in Myanmar, Sudan, Uganda, Ethiopia, Nigeria, Tanzania, Pakistan, Korea, Russia, Turkey, Mexico and South America (Kumar *et al.*, 2012). Sesame ranks sixth in the world in respect of edible oil seeds production 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. Sesame can be cultivated in both *Kharif* and *Robi* seasons in Bangladesh; nonetheless, more is produced (about two-third) in *Kharif* season (Chowdhury and Hassan, 2013). It loves high land with sandy loam soil. Sesame seeds containing 50% oil and 25% protein are used in baking, candy making, and some other food industries (Manikantan *et al.*, 2015). High quality edible and medicinal oil can be extracted from sesame seed, which can be stored for a long time. Sesame oilcake (byproduct) is used as feed for poultry, fish, cattle, goat and sheep (Khan *et al.*, 2009). Moreover, sesame oil contains about 47% oleic and 39% linoleic acid (Sultana *et al.*, 2019). It is used in cooking, salad and margarine as well as ingredients for pharmaceutical and cosmetic industries, and synergist for insecticides (Salunkhe and Desai, 1986). It also contains lignans and sesamol which are known to have anticancer activities (Kapadia *et al.*, 2002). Bangladesh has been suffering from serious deficit of edible oil since past several decades. To cope with this shortage, every year, huge amount of foreign currency is being spent for importing edible oil from abroad. The sesame production is still lower than other oilseed crops mainly due to the lack of high yielding varieties (HYV), biotic and abiotic stresses, and shattering problem. 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. Few sesame varieties have been released by this time from different research institutes but this is not enough to face the future challenges. Therefore, development of high yielding sesame variety having resistance/tolerance to biotic and biotic stresses is very much essential.

Up to now majority of the released sesame varieties in different countries are the product of selection and pedigree breeding. This is due to the lack of sufficient genetic variation within the existing germplasm collections, especially for traits such as resistance to various diseases and seed retention capacity etc. (Zanten, 2001). However, selection for high yield is made difficult due to its complex nature in sesame. The polygenic inheritance of yield components makes accurate selection more difficult. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, there is another option to hasten the genetic improvement which is known as indirect selection for yield. So, the phenotypic and genotypic variability studies play an important role to select the better sesame crop. Besides, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be useful for the breeding program. Therefore, the present research considered on genetic variability, heritability and genetic advance among different sesame germplasm to select potential genotypes for utilization in further varietal improvement of sesame.

Materials and Methods

The experiment was conducted at the experimental field of SAU, Dhaka during *Kharif* season 2022 with forty-three sesame genotypes with three replications following the randomized complete block design (RCBD). The sesame genotypes were from Plant Genetic Resources Centre (PGRC), Bangladesh Agricultural Research Institute (BARI) and different sesame growing regions of Bangladesh (Table 1). All the genotypes were randomly distributed to each plot with each block as per experimental design. The recommended dose of fertilizers and cow dung were applied and standard agronomic management was practiced. The total amount of TSP, MP, along with 50% of the urea were applied during final land preparation while rest amount of the urea was top-dressed at flower bud initiation stage. The data were collected on days 50% to flowering, days 80% to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length (cm), number of seeds per capsule, height of first capsule (cm), internode length (cm), thousand seed weight (g) and seed yield per plant (g). Analysis of variance (ANOVA), correlation coefficients were determined by R Studio package (https://www.rstudio.com). Phenotypic and genotypic variance was determined as per Johnson *et al.* (1955). Heritability and genetic advance were assessed following Singh and Chaudhury (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were estimated by the formula of Burton (1952).

Table 1. Different genotypes of sesame with their source of collection

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

Sl. No.	Genotype	Accession Number	Source of collection	Sl. No.	Genotype	Accession Number	Source of collection
17	G17	BD-11631	PGRC	39	G39	Si/GPB/22/00045	Kurigram
18	G18	BD-11632	PGRC	40	G40	Si/GPB/22/00046	Rangpur
19	G19	BD-11633	PGRC	41	G41	Si/GPB/22/00047	Moulovibazar
20	G20	BD-11634	PGRC	42	G42	Si/GPB/22/00048	Bagura
21	G21	BD-11635	PGRC	43	G43	Si/GPB/22/00049	Gazipur
22	G22	BD-11636	PGRC				

[1]PGRC: Plant Genetic Resources Centre, Bangladesh Agricultural Research Institute (BARI), Gazipur; [2]BADC: Bangladesh Agricultural Development Corporation

Results and Discussion

Genetic variability

The analysis of variance (ANOVA) showed highly significant variation among the sesame genotypes for all the traits (Table 3) suggesting a wide scope of selection for these characters which provides a good opportunity for improving traits of interest through breeding programs. The result showed that the genotypes G26 and G27 were early flowering that required only 50 days for 50% flowering, while the genotypes G40 (56.7 days) and G43 (56.7 days) were late in flowering (Table 2). Phenotypic and genotypic variance for 50 days to 50% flowering (DFF) was 2.99 and 1.79, respectively (Table 3). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for DFF were 2.46 and 3.18, respectively. The PCV was higher than GCV indicated environmental influence on the phenotypic expression of this trait. A moderate heritability (59.8%) with low genetic advance (2.13) and low genetic advance in percent of mean (3.91) was observed for this trait. Robinson *et al.* (1949) categorized the heritability as low (0-30%), moderate (30-60%) and high (60% and above) while the genetic advance as a percentage of the mean (GAPM) was classified by Johnson *et al.* (1955) as low (0-10%), moderate (10-20%) and high (20% and more). However, a high heritability with high genetic advance in percent of mean was reported by Pavani *et al.* (2020) for DFF which is dissimilar with the present results. The genotypic and phenotypic variances for days to 80% maturity (DEM) were 1.5 and 2.3, respectively (Table 3). The GCV (1.2) was lower than the PCV (1.5). The high heritability (65.95%) with low genetic advance (2.05) and genetic advance in percent of mean (2.07) were found for DEM indicating that the phenotypic selection would not be effective. Nonetheless, Thouseem *et al.* (2022) also reported low heritability for days to maturity in sesame. The maximum and minimum plant height (PH) were recorded in G12 (154.47 cm) and G33 (115.5 cm), respectively with the mean value of 132.9 cm (Table 2). The phenotypic variance (191.5) was higher than genotypic variance (40.5) (Table 3)

suggested that there was influence of environment on the phenotypic expression of the genes controlling plant height. The PCV and GCV were 10.41and 4.79, respectively. Low heritability (21.16%) with low genetic advance (6.03) and low genetic advance in percent of mean (4.54) (Table 3) suggesting that PH was governed by non-additive gene. On the contrary, Durge *et al.* (2022) reported a high heritability coupled with moderate to high genetic advance for plant height. The lowest number of primary branches per plant (NPBP) was found in G19 (3.7) followed by G32 (4.1) whereas the highest was observed in G22 (7.5) with the mean value of 5.2 (Table 2 and Table 3). The phenotypic variance (1.4) was higher than genotypic variance (0.37) (Table 3) suggested that there was influence of environment on the phenotypic expression of this character. The PCV and GCV were 22.6 and 11.6, respectively. Low heritability (26.4%) with low genetic advance (0.65) and moderate genetic advance in percent of mean (12.3) (Table 3) indicated this character was governed by non-additive gene. But, high heritability for NPBP was reported by Kumar *et al.* (2022) in sesame. The lowest number of secondary branches per plant (NSBP) was observed in G38 (2.13) whereas the highest was observed in G20 (7.7) with the mean value of 4.2 (Table 2 and Table 3). The phenotypic variance (2.5) was slightly higher than genotypic variance (2.2) suggested that there was few influence of environment on the expression of the genes controlling this trait. The PCV and GCV were 32.1 and 30.5, respectively. High heritability estimated (90.06%) was recorded for NSBP with high genetic advance in percent of mean (59.6) (Table 3) 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 through phenotypic selection. Similar to our result Roy *et al.* (2022) also reported high heritability coupled with high genetic advance for number of branches 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 2). 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 (9.5) suggesting that the presence of adequate variation between the genotypes (Table 3). 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 NCP. The capsule length (CL) ranged from 1.31 cm (G22) to 4.08 cm (G28) (Table 2). 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 indicated that moderate variation exists among sesame genotypes for this trait (Table 3). The moderate heritability (39.69%) was observed for CL with moderate genetic advance in percent of mean is (19.16) suggesting that the additive genes controlling this trait. Therefore, phenotypic selection based for CL would be effective. Kumar *et al.* (2022) also reported a similar result as high heritability for capsule length. The maximum number of seeds per capsule (NSC) was recorded in G5 (69.4) while the minimum in G16 (44.3) (Table 2).

The phenotypic variance (43.6) was much higher than the genotypic variance (24.2) indicated a great influence of environment on the phenotypic expression of this trait. The PCV (11.5) was also higher than the GCV (8.6) for NSC suggesting a moderate variation among the sesame genotypes (Table 4). This character also showed a moderate heritability (55.4%) with moderate genetic advance in percent of mean (13.1). The result revealed that the additive genetic effect plays an important role for the phenotypic expression. Thus, phenotypic selection for this character would be so rewarding. Srikanth and Ghodke (2022) also reported high heritability coupled with high genetic advance as percentage of mean for number of seeds per capsule in sesame. The maximum values for height of first capsule (HFC) was found in G38 (73.9 cm) whereas the minimum was in G26 (31.2 cm) with the mean vale of 53.2 cm (Table 2). The phenotypic and genotypic variances for HFC were 68.96 and 78.46, respectively (Table 3). The PCV and GCV were 22.8 and 15.61, respectively (Table 4). The moderate heritability (46.78%) was found for HFC with moderate 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. The highest internode length (IL) was recorded in G9 (13.46 cm) whereas the lowest was in G32 (5.4 cm) with the mean vale of 8.6 cm (Table 2). The phenotypic and genotypic variances were 3.83 and 1.47, respectively (Table 3). The PCV and GCV were 22.8 and 14.11, respectively. The moderate heritability (38.45%) was found for IL with moderate 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. The highest thousand seed weight (TSW) was found in G14 (4.3) and G23 (4.3) whereas the lowest in G29 (0.72) with the 2.7 g mean value (Table 2). There was a few difference between genotypic (0.66) and phenotypic (0.69) variances suggested 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 few difference between PCV and GCV, indicating less environmental influence on this trait. A very high heritability (99.31%) with high genetic advance in percent of mean (63.25). It is suggested 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. The highest 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 2). The phenotypic variances and genotypic variances for this trait were 12.95 and 12.67, respectively. The PCV and GCV were 32.01 and 31.7, respectively. The less differences between genotypic and phenotypic variances as well as PCV and GCV indicated that there is less influence of environmental factors on this trait. The SYP showed a very high heritability (97.89%) with high genetic advance in percent of mean (64.54) (Table 3). 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.

Table 2. Mean performances of 43 sesame genotypes in respect of 12 traits

Genotypes	DFF	DEM	PH	NPBP	NSBP	NCP	CL	NSC	HFC	IL	TSW	SYP
G1	54.67c-f	99.00b-g	134.44b-f	6.33a-d	7.47ab	150.93b-h	2.52b	54.40i-m	59.20b-g	8.94b-j	2.09no	14.89cd
G2	55.33a-d	102.33a	140.37a-d	5.33c-j	5.73d-g	181.47a-c	2.50b	58.60c-k	46.40g-o	9.17b-j	1.81qr	9.17lm
G3	55.33a-d	100.67a-d	147.57a-d	5.67c-i	6.47cd	124.13c-h	2.18b-e	54.87h-m	69.53a-c	10.03b-f	2.48j	2.74s
G4	53.00f-h	97.67f-i	126.33f-h	4.27h-j	7.33ab	131.67c-h	2.23b-e	65.20abc	42.07k-p	7.40g-l	2.57ij	10.24ijk
G5	55.67a-d	99.33b-f	140.78a-d	4.87d-j	4.53j-n	139.33c-h	2.23b-e	69.40a	47.27g-o	7.86f-l	2.20mn	10.99i
G6	55.00a-e	100.67a-d	130.84b-h	5.40c-i	7.53ab	208.33ab	2.10b-e	65.80ab	44.07i-p	8.14e-k	4.12b	18.07a
G7	54.00d-f	101.33ab	140.18a-f	4.40g-j	2.47st	130.53c-h	2.18b-e	57.53e-l	49.67f-n	8.74b-j	2.60i	10.77i
G8	55.00a-e	99.33b-f	117.23gh	4.87d-j	5.67d-g	126.40c-h	1.87b-f	62.67a-g	55.13d-l	7.46g-l	3.47e	7.42pq
G9	55.67a-d	98.33d-i	134.97a-h	4.80d-j	6.87bc	137.40c-h	2.17b-e	64.07a-e	57.47b-i	13.46a	1.30t	12.17gh
G10	54.67b-f	100.33a-e	128.78c-h	4.87d-j	7.53ab	141.47c-h	2.15b-e	57.07e-l	50.60e-n	8.24c-k	2.31kl	12.05h
G11	54.00d-f	100.00a-f	131.02b-h	5.00c-j	5.33f-j	172.53a-f	2.16b-e	54.53i-m	47.13g-o	6.90j-l	4.20b	14.12de
G12	56.00a-c	99.67b-f	154.47a	6.27a-e	5.53f-h	186.53a-c	2.29bc	64.80a-d	63.93a-f	10.60b-e	4.20b	17.39ab
G13	54.00d-f	98.67c-h	140.38a-f	4.87d-j	4.67i-n	138.27c-h	2.08b-e	61.07b-j	46.00g-o	8.19d-k	2.36k	9.81kl
G14	54.33cd-f	100.00a-f	136.67a-g	5.27c-j	3.27q-s	117.60d-h	2.39bc	62.47a-g	57.87b-i	10.12b-f	4.32a	12.51gh
G15	54.00d-f	98.67c-h	123.03e-h	4.60f-j	5.00g-l	146.13b-h	2.22b-e	54.73h-m	40.67m-p	7.05i-l	1.54s	7.69op
G16	53.33e-g	99.00b-g	117.57gh	4.73d-j	5.13f-k	101.20h	2.27b-d	44.27o	46.47g-o	8.43b-j	1.98op	8.09op
G17	54.67b-f	98.33d-i	133.65b-h	5.40c-i	7.47ab	174.47a-e	2.30bc	61.20b-i	51.80e-n	8.18d-k	3.02f	15.34c
G18	54.33c-f	98.67c-h	142.32a-e	6.07a-f	5.93d-f	149.33b-h	2.31bc	52.67k-n	63.53a-f	9.42b-i	1.98op	10.70ij
G19	54.67b-f	99.00b-g	123.51e-h	3.73j	3.53o-r	107.60gh	2.26b-e	51.73k-n	51.67e-n	8.32c-k	2.53ij	8.28no
G20	54.00d-f	99.33b-f	132.87b-h	5.53c-i	7.73a	159.33a-h	2.19b-e	46.60no	44.73h-p	8.78b-j	1.54s	8.31no
G21	54.67b-f	100.00a-f	150.38ab	5.20c-j	3.27q-s	137.80c-h	2.13b-e	57.07e-l	64.93a-e	8.53b-j	2.31klm	16.65b
G22	55.00a-e	100.00a-f	126.57d-h	7.53a	6.40c-e	219.40a	1.31f	57.00e-l	56.73c-j	6.81jkl	3.96c	13.82e
G23	55.00a-e	99.33b-f	124.09e-h	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
G24	54.33c-f	100.00a-f	122.85e-h	5.73b-i	3.27q-s	127.40c-h	1.61d-f	61.87b-h	50.93e-n	7.12i-l	2.55ij	12.95fg
G25	54.67b-f	101.00a-c	142.67a-e	5.00c-j	4.40k-n	128.67c-h	2.47b	62.87a-f	58.67b-h	9.75b-g	1.75r	14.13de
G26	50.00i	96.33hi	117.12gh	4.67e-j	4.33k-o	129.13c-h	1.61ef	58.00d-k	31.20p	5.87kl	1.90pq	7.42pq
G27	50.00i	96.67g-i	121.44f-h	4.73d-j	5.47f-i	149.13b-h	1.80c-f	62.47a-g	34.13op	6.95i-l	1.87q	5.10r
G28	54.00d-f	98.00e-i	141.12a-f	4.47f-j	3.53o-r	169.47a-g	4.08a	54.47i-m	41.87l-p	8.31c-k	3.12f	10.23ijk
G29	52.00gh	96.00i	127.33d-h	4.40g-j	4.20l-p	143.73c-h	2.43bc	52.53k-n	39.87n-p	8.38b-j	1.72r	6.77q
G30	54.67b-f	99.67b-f	141.25a-f	5.73b-i	5.93d-f	137.87c-h	2.36bc	54.73h-m	58.80b-h	9.63b-h	3.75d	13.74ef
G31	55.67a-d	100.00a-f	133.59b-h	5.07c-j	3.47p-r	105.20h	2.38bc	53.67k-n	64.87a-e	9.30b-j	2.35k	12.67gh
G32	54.33c-f	99.67b-f	126.74d-h	4.13ij	2.80r-t	143.93c-h	2.47b	54.00j-m	42.60j-p	5.43l	2.26k-m	9.10lmn
G33	54.33c-f	98.67c-h	115.47h	6.60a-c	3.27q-s	124.20c-h	2.37bc	58.60c-k	59.87a-g	7.24h-l	2.81gh	8.10op
G34	56.00a-c	99.33b-f	135a-h	5.87b-h	4.20lm-p	108.60gh	2.43bc	55.53g-m	67.60a-d	8.34b-k	3.08f	14.03e
G35	56.00a-c	101.00a-c	132.74b-h	5.73b-i	3.53o-r	138.60c-h	1.92b-f	66.47ab	56.53c-j	7.15h-l	3.91c	14.27de
G36	56.33ab	101.00a-c	124.87d-h	7.33ab	4.58j-n	179.27a-d	2.39bc	62.87a-f	55.53c-l	10.65b-d	2.21lm	17.24ab
G37	51.33hi	96.00i	128.87c-h	4.67e-j	4.73h-m	109.53f-h	2.32bc	52.73k-n	54.73d-m	10.82b	2.59ij	5.90r
G38	55.67a-d	100.00a-f	144.58a-d	4.60f-j	2.13t	125.07c-h	2.25bcde	60.87b-j	73.93a	10.73bc	2.89g	7.67op
G39	56.00a-c	100.00a-f	131.76b-h	6.00a-g	5.60e-g	150.73b-h	2.20b-e	48.53m-o	59.27b-g	8.75b-j	2.51ij	12.60gh
G40	56.67a	100.00a-f	137.53a-f	4.80d-j	3.87n-q	141.60c-h	2.34bc	52.80k-n	49.60f-n	9.23b-j	2.86gh	12.54gh
G41	54.67b-f	99.33b-f	123.81e-h	4.53f-j	3.93m-q	146.20b-h	2.34bc	53.60k-n	46.93g-o	8.52b-j	2.53ij	8.46m-o
G42	54.00d-f	100.00a-f	144.35a-d	4.27h-j	4.00m-q	129.47c-h	2.45bc	50.47l-o	56.40c-k	9.75b-g	2.75h	13.90e
G43	56.67a	100.00a-f	142.65a-e	6.53a-c	5.13f-k	125.40c-h	2.43bc	56.53f-l	71.33ab	10.19b-f	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 3. 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											
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
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
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.

Correlation studies

The genotypic and phenotypic correlation coefficients among thirteen characters were presented in Table 4. Days to 50% flowering (DFF) showed significant positive correlation with DEM (rg=0.999; rp =0.458), NPBP (rg-0.595; rp=0.276), HFC (rg=0.847; rp=0.440), IL (rg=0.521; rp=0.215) and SYP (rg=0.587; rp=0.448) at both the genotypic and phenotypic level (Table 4). It had also significant positive correlation with TSW (rp=0.226) at phenotypic level but non-significant correlation (rg=0.291) at genotypic level. Besides, DFF showed non-significant positive correlation with number of capsules per plant (NCP) (rg=0.265; rp=0.085), CL (rg=0.186; rp=0.070), NSC (rg=0.175; rp=0.105) both the genotypic and phenotypic level. Moreover, it had a non-significant negative correlation with NSBP (rg=-0.026; rp=-0.010) at both the genotypic and phenotypic level. Aye and Htwe (2019) also reported that DFF had a significant positive correlation with SYP. Days to 80% maturity (DEM) exhibited a significant and positive correlation with HFC (rg=0.707; rp=0.211), TSW (rg=0.336; rp=0.180*) and SYP (rg=0.615; rp=0.321) at both the genotypic and phenotypic level (Table 5). It had significant positive correlation with NPBP (rg=0.647), NCP (rg=0.403) and IL (rg=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. Plant height (PH) had a significant positive correlation with days to 50% flowering (DFF) (rg=0.754; rp=0.208), days to 80% maturity (DEM) (rg=0.797; rp=0.176) capsule length (CL) (rg=0.567; rp=0.245), height of first capsule (rg=0.491; rp=0.558), internode length (IL) (rg=0.846; rp=0.384) and yield per plant (YPP) (rg=0. 546; rp=0.246) at both the genotypic and phenotypic level. It had also a non-significant positive correlation with number of seeds per capsule (NSC) (rg=0.198; rp=0.045) and thousand seed weight (TSW) (rg=0.140; rp=0.060) at both the genotypic and phenotypic level. Moreover, it had highly significant positive correlation with number of primary branches per plant (NPBP) (rg=0.500) at the genotypic level while non-significant negative correlation with (rp=-0.074) at phenotypic level. In addition, PH showed a non-significant negative correlation with number of secondary branches per plant (NSBP) (rg=-0.004; rp = -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 (2011), Sultana *et al.* (2019) were also reported a significantly positive correlation of PH with YPP in sesame. Similar result was also reported by Sumathi and Muralidharan (2010). Number of primary branches per plant (NPBP) had significant positive correlation with NSBP (rg = 0.389; rp = 0.220), NCP (rg=0.675; rp = 0.368), HFC (rg=0.769; rp = 0.261) and SYP (rg=0.650; rp = 0.344) at both the genotypic and phenotypic level. This character also showed a non-significant negative correlation with CL (rg = -0.216; rp = -0.097) at both the genotypic and phenotypic level. Besides, NPBP had a significant posative correlation with NSBP (rg=0.389; rp = 0.220) at both the genotypic and phenotypic level. Our results are in agreement with the findings of Meenakumari and Ganesamurthy (2015) for NPBP in sesame. Number secondary branches per plant (NSBP) had a highly significant positive correlation only with NCP (rg = 0.748; rp=0.371) at both the genotypic and phenotypic level. NSBP also showed a non-significant positive correlation with NSC (rg = 0.196; rp=0.145), IL (rg = 0.167; rp = 0.060) and SYP (rg = 0.135; rp=0.123) at both the genotypic and phenotypic level. Moreover, NSBP had a non-significant negative correlation with CL (rg = -0.141; rp = -0.070) and TSW (rg = -0.102; rp = -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. Number of capsules per plant (NCP) showed significant positive correlation with NSC (rg= 0.307; rp= 0.195) and SYP (rg= 0.775; rp= 0.275) at both the genotypic and phenotypic level (Table 5). NCP also showed a significant positive correlation with TSW (rg= 0.433) whereas highly positive with HFC (rg= 0.433) at the genotypic level. Moreover, NCP had a non-significant negative correlation with IL (rg=-0.107; rp = -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. Capsule length (CL) had a highly significant positive correlation only with IL (rg = 0.480) at genotypic level. It

showed non-significant positive correlation with SYP at both the genotypic (rg = 0.068) and phenotypic (rp = 0.033) level. It had negative correlation with NSC (rg = -0.287; rp = -0.160) and TSW (rg = -0.190; rp = -0.112). Number of seeds per capsule (NSC) showed significant positive correlation with SYP (rg = 0.320; rp = 0.240) at both the genotypic and phenotypic level. It had significant positive correlation with TSW (rp = 0.214) at phenotypic level only. 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. Height of first capsule (HFC) showed highly significant positive correlation with IL at both genotypic (rg = 0.707) and phenotypic (rp = 0.434) level. It also showed significant positive correlation with SYP at genotypic (rg = 0.376) and phenotypic (rp = 0.254) level. Moreover, it had also a significant positive correlation with TSW (rp = 0.182) at phenotypic level. Internode length (IL) had non-significant positive correlation with SYP (rg = 0.228; rp = 0.141) at both genotypic and phenotypic. It also had non-significant negative correlation with TSW (rg = -0.178; rp = -0.108) at both the genotypic and phenotypic level. Thousand seed weight (TSW) had significant positive correlation with SYP (rg = 0.377; rp = 0.373) at both genotypic and phenotypic level. Sumathi and Muralidharan (2011) and Kehie *et al*. (2020) also reported similar result for TSW and SYP in sesame.

Path co-efficient analysis

Path co-efficient analysis partitioned the correlation coefficient as direct and indirect effect of yield of different yield contributing traits. The direct and indirect effects of path co-efficient analysis for sesame are presented in Table 5. Days to 50% flowering (DFF) had the direct negative direct effect (-0.198) on SYP. 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**). It revealed that relationship between these traits and selection for this trait will be rewarding for yield improvement. Days to 80 % maturity had direct positive effect (0.227) on SYP. 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**). 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**). 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. Number of primary branches per plant had second highest direct positive effect (0.467) on SYP. 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**). Thus indicated that if NPBP increases then SYP also increases through the positive indirect effect of other traits. Number of secondary branches per plant (NSBP) had positive direct effect (0.441) on SYP. 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). 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). 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). Capsule length (CL) had direct positive effect (0258) on SYP. 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). Number of seeds per capsule (NSC) had direct positive effect (0.213) on SYP. 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). Height of first capsule (HFC) had direct positive effect (0.011) on SYP. 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**). Internode length (IL) had direct negative effect (-0.799) on SYP. 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). Thousand seed weight (TSW) had a direct positive effect (0.156) on SYP. 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). The lower residual effect (R) of 0.147 indicated that the contribution of component characters was 85.3 percent. The rest 14.70 percent was the contribution came from other factors.

Table 4. 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).

Selection of sesame genotypes through cluster analysis

Cluster analysis was carried out using 43 sesame genotypes for 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 1 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 1, Table 2 and Table 6). Moreover, the genotype of cluster II, G26 and G27 showed minimum mean values for days 50% flowering and days to 80% maturity suggesting early maturing genotypes belongs to this cluster. Sultana *et al.* (2019) reported similar results in sesame.

Table 5. 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)

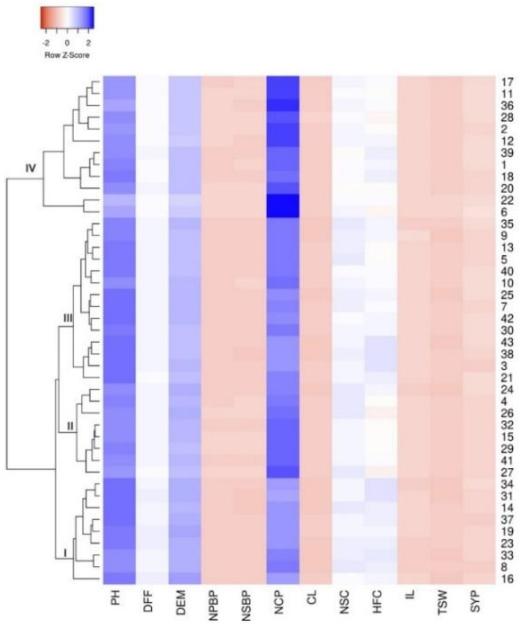

Fig. 1. Heatmap representation of 43 sesame genotypes into four clusters in respect of 12 traits.

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

Conclusion

The genetic variability, correlation and path analysis of yield and yield contributing traits of 43 sesame genotypes were evaluated. The result revealed significant differences for most of the characters except number of capsules per plan. High broad sense heritability together with high genetic advance in percent of mean was observed for number of secondary branches per plat, thousand seed weight and seed yield per plant while the lowest heritability was found for number of capsule per plant. The significant positive correlation with seed yield per plant was found for plant height, days to 50% flowering, days to 80% maturity, number of primary branches, number of capsules per plant, number of seeds per capsule, height of first capsule and 1000-seed weight. Plant height, days to 80% maturity, number of primary branches per plant, number of secondary branches per plant, capsule length and number of seeds per capsule had the positive direct effect on yield per plant whereas, internode length followed by number of capsules per plant and days to 50% flowering 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 utilization in future varietal improvement of sesame.

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Conflicts of Interest

The authors declare no conflicts of interest regarding publication of this manuscript.

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