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Genetic variability in sesame (*Sesamum indicum* L.) for yield and yield related traits

Verim ve verimle ilgili özellikler için susamda (Sesamum indicum L.) genetik değişkenlik

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ABSTRACT

Availability of genetic variability among a certain crop population and knowledge of the genetic parameters of yield and yield-related traits are the key preconditions to enhance seed yield. Therefore, sixty-four sesame genotypes consisting of fifty-nine accessions and five varieties were assessed in order to evaluate sesame genotypes for yield and yield-related traits and estimate the genetic parameters. An 8 x 8 simple lattice design was used to evaluate the experimental materials. Data were collected for the twenty traits. Analysis of variance revealed that sesame genotypes were significantly different ($P<0.05$) except for internode length and seed shattering-related traits. ASARC-ACC-SG-013 was the highest-yielding accession, while accession GK-012 (2) gave the highest oil content (60.09%), and the mean thousands seeds weight ranged from 2.00 g to 2.75 g, indicating the existence of elite sesame genotypes that can be considered to maximize yield, seed size, and oil content. The number of primary branches plant^{-1}, the number of capsules on the main stem plant^{-1}, and total capsules plant^{-1} all showed high coefficients of variation, demonstrating that the genotypes under study had sufficient variability for these traits. High heritability and genetic advance were obtained for traits such as plant height to the first branch (60.70%; 21.90%), capsule length (81.10%; 24.00%), primary branches plant^{-1} (63.10%; 36.30%), number of capsules on the main stem plant^{-1} (74.40%; 45.80%), and total capsules plant^{-1} (64.90%; 51.40%). Thus, the finding suggests a trustworthy estimate of the genetic advancement that may be anticipated through phenotypic selection for these traits.

Key Words: Genetic advance; Heritability; Oil content; Quantitative traits; Seed shattering

ÖZ

Belirli bir mahsul popülasyonu arasındaki genetik değişkenliğin mevcudiyeti ve verim ve verimle ilgili özelliklerin genetik parametrelerinin bilgisi, tohum verimini arttırmanın temel ön koşullarıdır. Bu nedenle, susam genotiplerini verim ve verime bağlı özellikler açısından değerlendirmek ve genetik parametreleri tahmin etmek için elli dokuz çeşit ve beş çeşitten oluşan altmış dört susam genotipi değerlendirilmiştir. Deney materyallerini değerlendirmek için 8 x 8 basit kafes tasarımı kullanıldı. Yirmi özellik için veri toplandı. Varyans analizi, susam genotiplerinin boğum arası uzunluk ve tohum parçalama ile ilgili özellikler dışında önemli ölçüde farklı olduğunu ($P<0.05$) ortaya çıkardı. ASARC-ACC-SG-013 en yüksek verimli çeşitken, GK-012 (2) çeşidi en yüksek yağ içeriğini (%60.09) vermiştir ve ortalama bin tohum ağırlığı 2.00 g ile 2.75 g arasında değişmektedir, bu da Verimi, tohum boyutunu ve yağ içeriğini maksimize ettiği düşünülebilecek elit susam genotipleri. Bitki-^{1} birincil dallarının sayısı, ana gövde bitki-^{1} üzerindeki kapsüllerin sayısı ve bitki^{-1} toplam kapsüllerinin tümü, yüksek varyasyon katsayıları gösterdi; bu, incelenen genotiplerin bu özellikler için yeterli değişkenliğe sahip olduğunu gösterdi. İlk dala kadar bitki boyu (%60.70; %21.90), kapsül uzunluğu (%81.10; %24.00), birincil dallar bitki^{-1} (%63.10; %36.30), kapsül sayısı gibi özelliklerde

özelliklerde yüksek kalıtım derecesi ve genetik ilerleme elde edilmiştir. ana gövde bitki^{-1} (%74.40; %45.80) ve toplam kapsül bitki^{-1} (%64.90; %51.40) üzerinde. Bu nedenle bulgu, bu özellikler için fenotipik seçilim yoluyla tahmin edilebilecek genetik ilerlemenin güvenilir bir tahminini önermektedir.

Anahtar Kelimeler: Genetik ilerleme; Kalıtım; Nicel özellikler; Yağ içeriği; Tohum parçalama

Introduction

Sesame is the oldest oilseed crop which has been grown from 3050 to 3500 B.C. (Bedigian and Harlan, 1986). *Sesamum indicum* is the most extensively grown one among the numerous species of the genus *Sesamum* (Ashri, 1998). Sesame is a self-pollinating crop with varying degrees of cross-pollination depending on the environment. Sesame thrives in tropical and subtropical ecological zones across the world. Although sesame is susceptible to rainy conditions, it requires a minimum of 300 to 400 mm of rainfall (Carlsson *et al*., 2008). Sesame has a great tolerance for drought and can produce seed yield well under fairly high temperatures (Ashri, 1998). In Ethiopia, suitable agro-ecologies of sesame are existing in Amhara, Tigray, Oromia, Benishangul Gumuz, and Somali regions (Terefe *et al*., 2012).

Currently, sesame has been extensively produced in Africa and Asia for its nutritious seeds (Dossa *et al*., 2017). Sesame is a valuable source of income for farmers and a major export commodity for Ethiopia (Abate *et al*., 2015). In spite of enormous nutritional and economic values, the productivity of sesame cultivars grown in Ethiopia is low due to the genetic and environmental factors. Low-yielding and poor adaptability of cultivars to harsh weather conditions, bacterial blight disease, and seed shattering are the major bottlenecks of sesame productivity in Ethiopia. There is an occasion of complete crop failure in North Western Ethiopia where the incidence and severity of bacterial blight (Xanthomonas campestris pv. sesami) disease exceeds 100% due to high humidity and extended rainfall (Terefe *et al*., 2012). Seed shattering in sesame is amongst the major worldwide constraint of sesame production (Islam *et al*., 2016). Determinate and indeterminate growth are the two types of growth habit in sesame (IPGRI and NBPGR, 2004), where the indeterminate growth habit favors subsequent capsule formation so long as the environment is suitable for growth (Najeeb *et al*., 2012; Gebremichael, 2017). Continuous capsule production leads to cracking of capsules at the base of the stem before the capsules at the tip attain physiological maturity, which results seed shattering. Thus, the primary objectives of Ethiopian sesame breeding are to develop high-yielding cultivars having bacterial blight resistance, better seed size and oil content, and tolerant to seed shattering (Gebremichael, 2017).

The availability of genetic variation and knowledge of the genetic parameters for quantitative traits are the prerequisites for crop improvement. In order to enhance sesame productivity, assessing the extent of genetic variability among sesame germplasm collected from various agro-ecologies and understanding the genetic parameters of quantitative traits are the core activities of sesame breeding. An available genetic resource can be used through a selection of elite genotypes for direct variety development or to combine desirable traits (Najeeb *et al*., 2012). Earlier studies showed genetic variation within the Ethiopian sesame germplasm (Abate *et al*., 2015; Teklu *et al*., 2017), which has been exploited for decades in improving sesame productivity through selection and hybridization. In addition, information on the genetic parameters such as heritability and genetic advance is a foundation of choosing an appropriate crop improvement strategy. In sesame, high heritability recorded in flowering period, physiological maturity, plant height, seed yield, number of branches, and number capsules per plant (Saxena and Bisen, 2017; Divya *et al*., 2018). Further, high heritability and genetic advance were observed in the 1000 seed weight,

oil content, and number of seeds per capsule (Saxena and Bisen, 2017). Heritability shows the magnitude of relationship between the genotype and observed phenotype while the genetic gain reflects the anticipated response as a result of selection (Shukla *et al*., 2004). The best conditions for selection are those with high genetic advance and high heritability (Larik *et al*., 2000). Thus, an experiment was carried out in order to evaluate sesame genotypes for yield and yield-related traits; identify promising sesame genotypes for better yield, seed size, and oil content; and estimate the genetic parameters for quantitative traits.

Materials and Methods

Experimental area, materials used and design

The study was conducted in 2019 at research station of Pawe Agricultural Research Center, which is situated in the Metekel zone of Ethiopia's Benishangul Gumuz region. The Pawe Agricultural Research Center is located about 562 kilometers to the northwest of Addis Ababa, at latitude of 11°18' North and longitude of 36°24' East. The location is 1120 meters above sea level with a mean annual rainfall of 1586 mm. The mean annual minimum and maximum temperature are 16.50°c and 32.60°c, respectively. A total of 64 genotypes, which consisted of 59 accessions and five varieties (abasena, gondar-1, setit-1, setit-2, and humera-1), were used for an experiment (Table 1). The fifty-nine accessions were obtained from the Ethiopian Biodiversity Institute (EBI), Werer agricultural research center (WARC), and Assosa agricultural research center (AsARC), whereas the three varieties (setit-1, setit-2, and humera-1) were obtained from the Humera agricultural research center (HuARC), one variety (abasena) from WARC, and one variety (Gondar-1) from the Gondar agricultural research center (GARC). The experimental design used was an 8 x 8 simple lattice design. Each experimental material was planted on a plot with two rows that were each 4 meters long. The intra-row and inter-row spacing was 10 cm and 40 cm, respectively.

Table 1. Sesame genotypes used in the study and their locality

		Locality	
S.No.	**Genotype**	**Region**	**Administrative zone**
1	EBI17697	Oromia	Eastern Wellega
2	EBI17702	Oromia	Eastern Wellega
3	EBI17703	Oromia	Eastern Wellega
4	EBI17704	Oromia	Western Wellega
5	EBI17708	Oromia	Western Wellega
6	EBI23548	Benishangul-Gumuz	Metekel
7	EBI23565	Benishangul-Gumuz	Metekel
8	EBI28301	Amhara	North Gondar
9	EBI28302	Amhara	North Gondar
10	EBI28303	Amhara	North Gondar
11	EBI28304	Amhara	North Gondar
12	EBI28306	Amhara	North Gondar
13	EBI28308	Amhara	North Gondar
14	EBI28309	Amhara	North Gondar
15	EBI28316	Amhara	North Gondar
16	EBI28318	Amhara	North Gondar
17	EBI28320	Amhara	North Gondar
18	EBI202514	Benishangul-Gumuz	Assosa
19	EBI207957	Gambella	Zone 1
20	Abasena		
21	ASARC-ACC-S-001	Benishangul-Gumuz	Kamashi
22	ASARC-ACC-S-003	Benishangul-Gumuz	Kamashi
23	ASARC-ACC-S-004	Benishangul-Gumuz	Kamashi
24	ASARC-ACC-S-006	Benishangul-Gumuz	Kamashi
25	ASARC-ACC-S-010	Benishangul-Gumuz	Kamashi
26	ASARC-ACC-S-022	Benishangul-Gumuz	Kamashi

S.No.	Genotype	Locality	
		Region	Administrative zone
27	ASARC-ACC-SA-002	Benishangul-Gumuz	Kamashi
28	ASARC-ACC-SA-007	Benishangul-Gumuz	Kamashi
29	ASARC-ACC-SA-008	Benishangul-Gumuz	Kamashi
30	ASARC-ACC-SA-009	Benishangul-Gumuz	Kamashi
31	ASARC-ACC-SA-011	Benishangul-Gumuz	Kamashi
32	ASARC-ACC-SA-016	Benishangul-Gumuz	Kamashi
33	ASARC-ACC-SA-017	Benishangul-Gumuz	Kamashi
34	ASARC-ACC-SA-019	Benishangul-Gumuz	Kamashi
35	ASARC-ACC-SA-020	Benishangul-Gumuz	Kamashi
36	ASARC-ACC-SA-022	Benishangul-Gumuz	Kamashi
37	ASARC-ACC-SG-005	Benishangul-Gumuz	Kamashi
38	ASARC-ACC-SG-013	Benishangul-Gumuz	Kamashi
39	ASARC-ACC-SG-018	Benishangul-Gumuz	Kamashi
40	GK-012 (1)	Benishangul-Gumuz	Not available
41	GK-012 (2)	Benishangul-Gumuz	Not available
42	GM-012 (1)	Benishangul-Gumuz	Not available
43	GM-012 (2)	Benishangul-Gumuz	Not available
44	Gondar-1		
45	HM-012 (1)	Amhara	Wollo
46	HM-012 (2)	Amhara	Wollo
47	Humera-1		
48	KG-012 (1)	Oromia	Ilubabor
49	KG-012 (2)	Oromia	Ilubabor
50	MG-012 (1)	Benishangul-Gumuz	Not available
51	MG-012 (2)	Benishangul-Gumuz	Not available
52	MT-023 (1)	Benishangul-Gumuz	Not available
53	MT-075 (1)	Amhara	Wollo
54	Setit-1		
55	Setit-2		
56	TM-023 (2)	Benishangul-Gumuz	Not available
57	TZ-013 (1)	Amhara	Gojam
58	TZ-013 (2)	Amhara	Wollo
59	TZ-054 (1)	Amhara	Wollo
60	TZ-054 (2)	Amhara	Wollo
61	ZT-013 (1)	Amhara	Gojam
62	ZT-013 (2)	Amhara	Shewa
63	ZT-054 (1)	Amhara	Wello
64	ZT-054 (2)	Amhara	Shewa

Data collected

Data were collected for each replication on a plot, plant, and capsule basis. On a plot-by-plot basis, data on days to 50% flowering (DF), days to first capsule-opening (DFCO), and days to 90% maturity (DM) were gathered. The number of days passed between DFCO and DM was used for data analysis to examine the extent of uniformity in capsule ripening.

On five random plants, plant-based data were assessed on the severity of the bacterial blight disease (BBDS), plant height (PH), plant height to first branching (PHFB), the internode length (IL), the length of the capsule-bearing zone (LCBZ), the number of capsule-bearing primary branches plant^{-1} (PBPP), capsules on the main stem plant^{-1} (NCMS), capsules plant^{-1} (CPP), and opened capsules plant^{-1} (OCPP). The percent of opened-capsules plant^{-1} (OCPP) was computed according to the following formula:

$$OCPP = \frac{Number\ of\ opened\ capsules\ per\ plant}{Total\ number\ of\ \ capsules\ per\ plant} x100$$

The disease susceptibility recorded in 1 to 9 scale was converted to the percentage severity index (PSI) as applied by Wheeler (1969).

$$PSI\ (\%) = \frac{Sum\ of\ all\ disease\ scores}{number\ of\ ratings \times maximum\ disease\ grade} x\ 100$$

Five unopened capsules were assessed for the number of seeds per capsule (SPC), capsule length (CL) in mm, and capsule width (CW) in mm.

Seed shattering related data were recorded on opened capsules of plants which were not included in the sample used for recording yield and yield related traits.

Five opened capsules were investigated for seed shattering related traits such as the length of opened capsules (LOC) in mm, the length of cracking on opened capsules (LCOC) in mm, the number of seeds dropped-down per opened-capsule (SDPOC), seeds dropped-down per opened-capsule while the capsule inverted downward (SDPOCI), and seeds retained per opened-capsule (SPOC). The average length of cracking on opened-capsules (LCOC) was converted into a percentage as follows:

$$LCOC = \frac{Average\ length\ of\ cracking\ on\ opened\ capsules}{Average\ length\ of\ opened\ capsules} x\ 100$$

Seed shattering in percentage was calculated and used for data analysis as follows:

$$Seed\ shattering = \frac{SDPOC + SDPOCI}{SDPOC + SDPOCI + SPOC} x100$$

Seed yield per plant (SYPP) in grams was the average seed yield of five random plants. Data in relation to the weight of 1000 seeds (TSW) in grams and the percent of oil content (OC) were examined from seeds taken from the harvest of five random plants after measuring seed yield.

Data analysis

Analysis of variance (ANOVA) was conducted using R software (R Core Team, 2021). ANOVA was implemented using the *PBIB.test* function in the agricolae package (de Mendiburu, 2021). A model applied in the ANOVA was:

$$y_{ijk} = \mu + rep_i + block_j\ (rep_i) + gen_k + e_{ijk}$$

where y_{ijk} denotes an observed effect, μ denotes the mean, rep_i denotes the i^{th} replicate, and $block_j$ (rep_i) denotes the j^{th} incomplete block within the i^{th} replicate, gen_k is the kth genotypic effect, and e_{ijk} is the experimental error. Fisher's Least significance difference test (LSD) at 5% probability was conducted by using *LSD.test* function in the *agricolae* package. According to Syukur *et al*. (2010), the mean squares were used to estimate the variances and coefficients of variation. Based on Deshmukh *et al*. (1986) classification, coefficients of variation below 10% considered as low, 10-20% as moderate, and above 20% as high. For the traits under consideration, heritability in a broad sense (H^2) was calculated as suggested by Allard (1960), and heritability estimates below 20% were considered as low, 10-20% as moderate, and above 50% as high (Syukur *et al*., 2010). Computation of genetic advance and classification of genetic advance as a percentage of the mean (GAM) were done by adopting Johnson *et al*. (1955).

Results and Discussion

Analysis of variance

The existence of variability in a certain population is fundamental for proposing crop improvement strategy. In the present study, analysis of variance showed highly significant differences ($p<0.01$) among the sesame genotypes for 50% flowering, 90% physiological-maturity, plant height, height to the first branch, the length of the capsule-bearing zone, the length of capsule, the number of capsule-bearing primary branches plant^{-1}, capsules on the main stem plant^{-1}, total capsules plant^{-1}, seeds capsule^{-1}, and oil content (%) (Table 2). In addition, the ANOVA indicated a significant difference ($p<0.05$) among the 64 sesame genotypes for the bacterial blight disease severity index (%), the number of days in between first capsule-opening and physiological-maturity, the length of capsule, capsule width, 1000 seeds weight, and yield plant^{-1}. Similarly, previous studies conducted in sesame indicate the existence of variability for capsules plant^{-1}, seeds capsule^{-1}, 1000 seeds weight, and yield (Bandila *et al*., 2011; Teklu *et al*., 2017). In

addition, Teklu *et al*. (2017) also reported genetic variability within the population in terms of flowering and maturity period, plant height, and primary branches plant^{-1}. Further, genetic variability that has been observed in sesame genotypes for oil content was in agreement with the result of Pathak *et al*. (2014). Genetic variability among sesame genotypes for seed yield, seed yield-related traits, oil content, and weight of 1000 seeds revealed the existence of genetic potential to enhance seed yield, seed size and oil content through selection of promising genotypes. On other hand, in the present study, the ANOVA indicated a non-significant difference ($p<0.05$) among the genotypes for the internode length, the length of scratch on an opened-capsule (%), the number of opened-capsules plant^{-1} (%), and seed shattering (%). The maximum mean seed shattering recorded was 77.78% with mean seed shattering of 51.22%. Thus, the result of the experiment pointed out low scope of improvement for seed shattering resistance through the evaluation of Ethiopian sesame germplasm. All cultivars grown in Ethiopia are shattering types (Terefe *et al*., 2012). However, the study indicated a significant difference among the genotypes for days in between the first capsule-opening to maturity, noticing the presence of genotypes that might be described by uniform capsule ripening. As a result of synchronous capsule ripening, sesame may avoid seed shattering from bottom capsules while farmers wait for capsules on branches and tips of the plant to become mature. Further, synchronous capsule ripening might enhance the uniformity of seeds in terms of size and color.

Table 2. Analysis of variance for the 20 quantitative traits of sesame

	Mean Squares			
	Replication (Degree of freedom=1)	Block (Replication) (Degree of freedom=14)	Genotype (Degree of freedom=63)	Error (Degree of freedom=49)
Days of 50% flowering	9.57	2.7	11.84**	2.06
Bacterial-blight susceptibility index (%)	7.56	239.13	201.64*	121.44
Days of 90% physiological-maturity	34.03	11.63	61.99**	6.8
Days from first capsule-opening up to 90% maturity	25.38	3.45	6.35*	3.55
Plant-height (cm)	309.76	344.08	257.30**	131.63
Plant-height to the first branch (cm)	339.5	46.02	74.09**	29.07
The length of capsule-bearing zone (cm)	523.95	89.15	123.85**	57.38
Internode length in mm	204.02	86.9	78.38ns	61.56
Capsule length in mm	10.45	8.96	25.30**	4.76
Length of scratch on opened-capsule (%)	66.77	232.33	151.15ns	192.33
Capsule width in mm	3.7	0.58	0.82*	0.52
Number of capsule-bearing primary branches plant^{-1}	2.65	1.36	1.39**	0.51
Number of capsules on the main stem plant^{-1}	46.95	37.15	75.50**	19.28
Number of total capsules plant^{-1}	885.05	381.46	553.35**	194.16
Number of opened capsules plant^{-1} (%)	28.35	79.72	252.54ns	181.76
Number of seeds capsule^{-1}	6.6	43.55	122.87**	24.34
Seed shattering (%)	259.86	421.51	235.55ns	240
1000 seeds weight (g)	0.78	0.04	0.09*	0.05
Seed yield plant^{-1} (g)	13.02	5.02	4.85*	2.74
Oil content (%)	0.74	0.76	16.22**	0.52

*** = highly significant at p<0.01, * = significant at p<0.05, ns = non-significant at p<0.05*

Performance of sesame genotypes for yield and yield-related traits

Mean performance of sesame genotypes for 10 quantitative traits presented in Table 3. Among the 64 genotypes, the three varieties (setit-1, setit-2, and humera-1) were early maturing genotypes with 93 days (setit-1 and setit-2) and 95 days (humera-1) of maturity

period, whereas EBI28306 was a late maturing sesame genotype. The lowest and the highest percentage of disease severity index (%) were recorded on EBI28316 and ZT-054 (1), respectively. ASARC-ACC-SG-013 produced the highest number of capsules plant^{-1}, while KG-012 (2) was the lowest capsule producing genotype. Genotype EBI202514, ASARC-ACC-SA-016, and ASARC-ACC-SG-005 produced the highest number of seeds capsule^{-1}. The highest seed yield (9.65 g plant^{-1}) was recorded from ASARC-ACC-SG-013 followed by EBI17697 (9.51 g plant^{-1}) and ASARC-ACC-SA-011 (8.86 g plant^{-1}). ASARC-ACC-SG-013 and EBI17697 had 35.75% and 34.80% yield advantage, respectively, over the mean seed yield of all genotypes. In regard to seed quality-related traits, the lowest oil content recorded was 44.15% while the highest (60.09%) was recorded from GK-012 (2). Genotypes such as EBI28302, EBI28306, and EBI23565 were large-seeded with 1000 seeds weight of 2.75 g. Gebremichael (2017) reported a wide range of variation among Ethiopian sesame germplasm for oil content ranging from 34.10% to 55.50% and the weight of 1000 seeds ranging from 1.30 g to 4.10 g. Generally, the present study revealed the presence of elite sesame genotypes which can be proposed for better seed yield, seed size, and oil content.

Estimates of genetic parameters

The estimates of genetic parameters for the twenty quantitative traits are presented in Table 4. Both genotypic and phenotypic coefficients of variation (GCV and PCV) were higher for days from the first capsule-opening to physiological-maturity, number of primary branches plant^{-1}, capsules on the main stem plant^{-1}, total capsule plant^{-1}, and opened-capsules plant^{-1}. Similarly, primary branches plant^{-1} and capsules plant^{-1} had high GCV and PCV values (Abate *et al*., 2015). High GCV estimates were shown for days to flowering (Gidey *et al*., 2012) and capsules plant^{-1} (Teklu *et al*., 2017; Abhijatha *et al*., 2017]. The highest PCV and GCV for days to the first capsule-opening to physiological-maturity, primary branches plant^{-1}, the number of capsules on the main stem plant^{-1}, and total capsules plant^{-1} showed the existence of variability among the genotypes with a significant contribution of genotypic variance to an observed variation. High PCV values coupled with high GCV values ensure the existence of sufficient variation within the study genotypes in regard to these traits. On other hand, the resistance of sesame genotypes against bacterial blight, plant height to the first branch, the length of capsule-bearing zone, capsule length, and seeds capsule^{-1} all had moderate (10 – 20%) GCV and PCV estimates. Moreover, moderate GCV and high PCV were seen in seed yield plant^{-1}. In contrast, Bandila *et al*. (2011) reported high GCV for seed yield plant^{-1}. Moderate GCV and high PCV on yield plant^{-1} indicated that the phenotypic variation was attributed to genetic and environmental effects. Further, both GCV and PCV values were moderate for diseases susceptibility index (%), plant height to first branch, the length of capsule-bearing zone, capsule length, and seeds capsule^{-1}. However, low (0 - 10%) GCV and PCV estimates were exhibited on days to flowering, days to 90% physiological-maturity, oil content, 1000 seeds weight, and the width of the capsule. Low PCV and GCV estimates obtained for flowering period, physiological-maturity, capsule width, 1000 seeds weight, and oil content revealed that sesame genotypes had little variation and a low response to selection regarding these traits.

High PCV but low GCV estimates which have been recorded on the length of scratch on the opened capsule and seed shattering indicated an observed phenotypic variation was mainly attributed to environmental effect. GCV and PCV values were very close to each other for period of flowering and physiological-maturity, capsule length, seed capsule^{-1}, and oil content. Little difference between PCV and GCV estimates indicated that an observed phenotype in regard to these traits was majorly attributed to genetic effects. On other hand, high PCV and GCV difference was exhibited for days from the first capsule opening up to maturity, internode length, and the number of opened capsules per plant (%).

The highest differences between GCV and PCV values indicate the greater contribution of environmental effect on observed phenotype (Bandila *et al*., 2011). On other hand, high PCV but zero GCV estimates were recorded for the length of scratch on the opened capsule (%) and seed shattering (%). In the current study, high heritability values validated the larger importance of the genetic factor on the phenotype of various characters. High heritability (H2 >50%) was realized on flowering period, physiological-maturity, plant height to first branch, length of capsule-bearing zone, capsule length, primary branches plant^{-1}, capsules on the main stem plant-1, total capsules plant^{-1}, seeds capsule^{-1}, and oil content. Similar findings were noticed for branches plant^{-1} and capsules plant^{-1} (Abhijatha *et al*., 2017).

Further, the result was in agreement with Abate *et al*. (2015) for seeds capsule^{-1} and oil content. Heritability values were found moderate (20% - 50%) for bacterial blight disease severity index, days from first capsule-opening to physiological-maturity, plant height, internode length, capsule width, the number of opened-capsules plant^{-1}, 1000 seeds weight, and seed yield plant^{-1}. Moderate heritability observed on yield plant^{-1} was in agreement with Abate *et al*. (2015) but inconsistent with the result of Khairnar and Monpara (2013) who found out high heritability estimate. However, heritability estimates were completely zero for traits such as length of scratch on the opened-capsule and seed shattering. The highest genetic advance as a percentage of the mean (GAM) was recorded on number of days in between first capsule-opening to physiological-maturity, plant height to first branching, capsule length, primary branches plant^{-1}, capsules on the main stem plant^{-1}, total capsules plant^{-1}, opened-capsules plant^{-1}, and yield plant^{-1}. Moreover, moderate GAM values were obtained for the length of capsule-bearing zone, seeds capsule^{-1}, and oil content.

Table 3. Mean performance of sesame genotypes for yield and yield-related traits

Genotype	DF	BBDS	DM	PBPP	NCMS	CPP	SPC	TSW	OC	SYPP
EBI17697	55.34*j-q*	41.83*mn*	113.16*d-k*	3.50*b-l*	25.63*b-j*	63.46*a-g*	70.29*g-u*	2.25*bc*	57.71*bc*	9.51*ab*
EBI17702	56.45e-o	44.87*j-n*	112.77*d-k*	3.95*a-i*	24.10*b-n*	59.51*a-j*	70.17*g-u*	2.25*bc*	54.51*g-m*	7.53*a-l*
EBI17703	56.17*h-q*	44.86*k-n*	114.18*b-j*	3.45*b-m*	24.13*b-m*	61.20*a-i*	66.21*l-x*	2.50*ab*	52.96*n-s*	7.66*a-j*
EBI17704	54.14*n-r*	43.61*lmn*	111.39*f-l*	3.57*b-k*	25.31*b-k*	54.39*a-l*	73.24*d-q*	2.25*bc*	53.73*k-q*	8.08*a-h*
EBI17708	56.60*d-n*	41.80*mn*	113.63*c-k*	4.60*ab*	21.99*d-r*	63.40*a-h*	75.00*d-o*	2.00*c*	54.87*g-k*	7.48*a-l*
EBI23548	54.02*n-r*	44.71*k-n*	110.74*h-m*	3.78*b-j*	23.48*c-p*	69.48*abc*	75.51*d-n*	2.00*c*	52.67*p-u*	7.76*a-i*
EBI23565	56.79*d-n*	50.29*g-n*	113.21*d-k*	3.47*b-l*	24.34*b-l*	49.58*b-n*	69.89*h-u*	2.75*a*	57.97*b*	6.78*a-p*
EBI28301	57.36*c-l*	60.70*a-n*	100.00*qr*	3.03*c-p*	20.41*e-u*	43.48*c-q*	68.25*j-v*	2.00*c*	47.19*ef*	6.71*a-p*
EBI28302	53.67*o-r*	60.14*a-n*	104.50*opq*	2.50*j-r*	15.01*o-z*	31.93*k-t*	77.76*b-j*	2.75*a*	50.85*wxyzAB*	5.41*d-q*
EBI28303	57.79*c-k*	70.15*a-h*	108.55*k-o*	2.17*k-t*	11.56*u-z*	28.65*k-t*	75.94*c-l*	2.25*bc*	50.00*yzABC*	4.89*g-q*
EBI28304	57.81*c-k*	57.09*b-n*	112.47*e-k*	2.03*m-t*	16.79*k-y*	29.04*k-t*	79.84*b-g*	2.00*c*	52.34*q-v*	4.09*m-q*
EBI28306	57.40*c-l*	48.47*h-n*	123.17*a*	2.97*c-p*	31.50*abc*	61.03*a-i*	82.23*b-f*	2.75*a*	55.33*d-j*	8.47*a-d*
EBI28308	57.48*c-l*	52.09*g-n*	111.13*g-l*	2.84*d-q*	21.95*d-r*	42.35*c-r*	79.83*b-h*	2.00*c*	50.23*xyzABC*	5.58*c-q*
EBI28309	53.40*p-r*	59.86*b-n*	102.66*pq*	2.52*j-r*	14.96*p-z*	32.41*j-t*	68.52*i-v*	2.00*c*	49.46*BCD*	5.32*d-q*
EBI28316	55.09*k-q*	40.41*n*	101.23*pq*	2.88*c-p*	19.92*e-v*	51.85*b-n*	63.25*r-y*	2.25*bc*	53.15*m-r*	7.24*a-m*
EBI28318	57.41*c-l*	46.38*i-n*	111.93*e-l*	2.49*j-r*	27.24*a-h*	49.79*b-n*	83.17*bcd*	2.50*ab*	49.61*A-D*	8.18*a-g*
EBI28320	53.21*q-r*	51.11*g-n*	114.84*b-h*	2.65*g-q*	27.17*a-h*	48.99*b-o*	71.13*g-t*	2.50*ab*	50.36*xyzABC*	7.37*a-m*
EBI202514	56.26*h-q*	42.63*lmn*	112.42*e-k*	2.89*c-p*	21.33*e-r*	38.60*f-t*	95.20*a*	2.25*bc*	53.91*j-p*	6.95*a-o*
EBI207957	53.95*n-r*	55.28*d-n*	111.34*g-l*	2.96*c-p*	17.23*j-x*	37.94*f-t*	65.86*m-x*	2.50*ab*	51.98*r-w*	5.75*c-q*
Abasena	55.67*j-q*	76.52*a-d*	109.13*i-o*	1.42*q-t*	18.41*h-x*	24.56*n-t*	61.96*t-y*	2.50*ab*	51.37*u-z*	4.21*l-q*
ASARC-ACC-S-001	59.29*a-e*	57.78*b-n*	112.19*e-k*	4.01*a-g*	23.20*c-q*	54.74*a-l*	73.34*d-q*	2.25*bc*	54.98*e-k*	7.39*a-m*
ASARC-ACC-S-003	58.09*b-j*	52.77*g-n*	118.87*a-c*	3.30*b-n*	23.43*c-p*	48.80*b-p*	62.96*r-y*	2.00*c*	50.93*vwxyzA*	8.24*a-f*
ASARC-ACC-S-004	59.14*a-g*	63.60*a-m*	116.79*b-f*	2.50*j-r*	17.98*j-x*	33.84*i-t*	62.72*r-y*	2.00*c*	55.16*e-k*	6.15*c-q*
ASARC-ACC-S-006	57.90*c-k*	60.00*a-n*	115.32*b-h*	2.42*j-s*	23.59*c-o*	42.73*c-q*	54.87*y*	2.25*bc*	56.33*c-f*	4.70*i-q*
ASARC-ACC-S-010	59.45*a-d*	64.19*a-l*	110.95*h-l*	2.20*k-t*	18.47*h-x*	25.24*m-t*	70.28*g-u*	2.00*c*	53.40*l-r*	4.28*k-q*
ASARC-ACC-S-022	55.78*i-q*	55.14*d-n*	111.26*g-l*	2.67*g-q*	30.39*a-d*	56.04*a-k*	61.26*u-y*	2.25*bc*	55.83*d-g*	6.15*c-q*
ASARC-ACC-SA-002	56.28*g-q*	55.83*c-n*	112.79*d-k*	3.71*b-j*	27.08*a-h*	56.65*a-k*	63.96*q-y*	2.25*bc*	54.27*h-o*	7.14*a-m*
ASARC-ACC-SA-007	58.03*c-j*	44.98*j-n*	112.66*e-k*	4.12*a-e*	21.98*d-r*	52.47*a-m*	75.31*d-o*	2.50*ab*	52.96*n-s*	6.90*a-o*
ASARC-ACC-SA-008	58.98*a-h*	49.98*g-n*	118.08*a-d*	3.99*a-h*	28.15*a-f*	69.06*a-d*	78.05*b-i*	2.25*bc*	53.79*k-q*	8.66*a-d*
ASARC-ACC-SA-009	54.67*l-q*	46.12*j-n*	116.97*b-e*	4.11*a-f*	21.02*e-s*	53.21*a-m*	65.67*n-x*	2.25*bc*	54.40*h-n*	6.14*c-q*
ASARC-ACC-SA-011	56.24*h-q*	53.47*e-n*	113.50*c-k*	2.97*c-p*	31.00*abc*	66.61*a-e*	82.46*b-e*	2.25*bc*	54.94*f-k*	8.86*abc*
ASARC-ACC-SA-016	57.40*c-l*	49.74*g-n*	112.40*e-k*	2.61*h-q*	28.73*a-e*	41.30*d-r*	87.34*ab*	2.50*ab*	52.41*q-u*	6.65*a-p*
ASARC-ACC-SA-017	57.12*d-m*	52.36*g-n*	114.53*b-i*	3.03*c-p*	26.74*a-i*	61.28*a-i*	61.97*s-y*	2.00*c*	56.42*cde*	7.04*a-n*
ASARC-ACC-SA-019	56.20*h-p*	54.31*d-n*	112.34*e-k*	3.58*b-k*	27.07*a-h*	66.59*a-e*	76.23*c-k*	2.25*bc*	52.83*o-t*	8.56*a-d*
ASARC-ACC-SA-020	55.05*k-q*	51.68*g-n*	111.05*h-l*	2.96*c-p*	35.27*a*	61.59*a-i*	59.66*v-y*	2.25*bc*	44.79*G*	6.26*b-q*
ASARC-ACC-SA-022	57.74*c-k*	55.56*c-n*	114.10*b-j*	3.07*c-o*	19.04*g-w*	37.65*f-t*	69.15*i-v*	2.25*bc*	52.45*q-u*	6.04*c-q*
ASARC-ACC-SG-005	58.67*a-i*	50.55*g-n*	117.08*b-e*	3.99*a-i*	24.35*b-l*	44.00*c-q*	85.75*abc*	2.25*bc*	56.62*bcd*	6.58*a-p*
ASARC-ACC-SG-013	57.09*d-m*	50.84*g-n*	111.70*e-l*	5.24*a*	30.43*a-d*	79.73*a*	77.15*c-j*	2.50*ab*	54.87*g-k*	9.65*a*

Genotype	DF	BBDS	DM	PBPP	NCMS	CPP	SPC	TSW	OC	SYPP
ASARC-ACC-SG-018	56.34*f-o*	50.01*g-n*	112.73*d-k*	4.60*ab*	32.86*ab*	73.68*ab*	57.68*wxy*	2.50*ab*	55.35*d-j*	8.28*a-e*
GK-012(1)	57.17*d-m*	45.42*j-n*	113.05*d-k*	2.77*e-q*	19.56*f-w*	35.98*g-t*	66.96*k-w*	2.50*ab*	55.67*d-h*	6.29*b-q*
GK-012(2)	54.45*m-q*	53.34*f-n*	114.61*b-h*	4.30*abc*	20.48*e-t*	63.21*a-h*	69.72*i-u*	2.25*bc*	60.09*a*	6.65*a-p*
GM-012(1)	56.38*f-o*	64.60*a-l*	110.02*h-n*	1.99*n-t*	18.08*i-x*	35.59*h-t*	64.95*p-x*	2.50*ab*	53.11*m-s*	5.87*c-q*
GM-012(2)	56.14*h-p*	55.40*d-n*	108.81*j-o*	1.59*p-t*	12.67*s-z*	20.26*q-t*	70.21*g-u*	2.00*c*	50.43*xyzABC*	3.78*n-q*
Gondar-1	58.02*i-j*	44.85*k-n*	110.90*h-l*	4.28*a-d*	27.36*a-g*	69.01*a-d*	74.27*d-p*	2.50*ab*	50.16*yzABC*	8.50*a-d*
HM-012(1)	56.07*i-q*	71.23*a-g*	108.42*k-o*	2.72*f-q*	15.28*m-z*	32.31*j-t*	63.85*q-y*	2.50*ab*	51.67*s-x*	5.64*c-q*
HM-012(2)	60.12*abc*	70.69*a-h*	114.89*b-h*	2.97*c-p*	12.35*s-z*	26.57*m-t*	69.81*i-u*	2.25*bc*	53.02*n-s*	4.35*j-q*
Humera-1	59.24*a-f*	62.50*a-n*	94.66*rs*	2.07*l-t*	19.58*f-w*	32.24*j-t*	60.75*u-y*	2.50*ab*	52.66*p-u*	5.19*e-q*
KG-012(1)	58.05*b-j*	77.92*ab*	105.40*m-q*	0.81*t*	14.35*q-z*	13.39*st*	60.62*u-y*	2.25*bc*	48.51*DE*	3.73*n-q*
KG-012(2)	60.12*abc*	75.27*a-f*	116.55*b-g*	1.67*o-t*	7.53*z*	11.10*t*	79.77*b-h*	2.00*c*	53.14*m-r*	3.18*q*
MG-012(1)	53.62*o-r*	67.77*a-i*	111.37*g-l*	3.13*c-n*	17.56*j-x*	40.95*d-s*	76.02*c-l*	2.50*ab*	54.01*i-p*	6.06*c-q*
MG-012(2)	59.29*a-e*	49.59*g-n*	106.61*l-p*	3.80*a-j*	24.37*b-l*	65.52*a-f*	75.75*d-m*	2.50*ab*	54.80*g-l*	7.62*a-k*
MT-023(1)	58.14*b-j*	59.87*b-n*	104.81*n-q*	4.06*a-j*	18.88*g-w*	51.57*b-n*	68.75*i-v*	2.00*c*	52.38*q-u*	6.61*a-p*
MT-075(1)	55.76*j-q*	77.65*abc*	104.39*opq*	2.78*e-q*	13.53*r-z*	27.83*l-t*	56.47*xy*	2.50*ab*	48.99*CD*	5.00*f-q*
Setit-1	46.71*t*	54.02*e-n*	93.36*s*	2.29*k-s*	18.66*g-w*	30.21*k-t*	66.12*l-x*	2.50*ab*	53.14*m-r*	5.66*c-q*
Setit-2	49.83*s*	61.25*a-n*	93.47*s*	1.19*rst*	16.92*j-y*	21.16*p-t*	57.11*wxy*	2.25*bc*	50.51*xyzAB*	4.76*h-q*
TM-023(2)	59.36*a-d*	53.61*e-n*	115.34*b-h*	2.58*i-r*	19.79*f-w*	35.09*i-t*	66.21*l-x*	2.25*bc*	52.70*p-u*	5.03*e-q*
TZ-013(1)	51.48*rs*	69.45*a-h*	102.48*pq*	2.99*c-p*	11.33*v-z*	24.05*n-t*	59.38*v-y*	2.50*ab*	51.41*t-y*	4.31*k-q*
TZ-013(2)	56.57*d-n*	60.83*a-n*	119.34*ab*	2.91*c-p*	13.45*r-z*	26.79*m-t*	71.86*g-s*	2.25*bc*	51.45*t-y*	4.80*h-q*
TZ-054(1)	58.95*a-h*	65.97*a-k*	113.19*d-k*	2.81*e-q*	14.72*p-z*	27.04*m-t*	68.81*i-v*	2.25*bc*	49.95*zABC*	4.32*j-q*
TZ-054(2)	60.91*ab*	75.68*a-e*	104.08*opq*	3.04*c-o*	8.06*yz*	15.39*rst*	62.22*s-y*	2.25*bc*	46.62*F*	3.59*pq*
ZT-013(1)	56.60*d-n*	63.60*a-m*	113.21*d-k*	3.50*b-l*	15.49*l-z*	38.62*e-t*	72.62*e-r*	2.00*c*	44.15*G*	4.68*i-q*
ZT-013(2)	57.55*c-l*	66.81*a-j*	109.05*j-o*	2.44*j-r*	11.28*w-z*	21.24*o-t*	63.44*q-y*	2.50*ab*	55.38*d-i*	4.74*i-q*
ZT-054(1)	54.09*n-r*	81.52a	112.21*e-k*	2.43*j-r*	11.81*t-z*	20.26*q-t*	72.30*f-r*	2.50*ab*	57.69*bc*	4.25*l-q*
ZT-054(2)	61.40*a*	66.11*a-k*	113.01*d-k*	0.97*st*	9.59*xyz*	14.48*rst*	65.47*o-x*	2.50*ab*	52.98*n-s*	3.65*opq*
Mean	56.58	56.98	110.79	2.98	20.56	43.23	70.04	2.30	52.77	6.20
Pr(>F)	$5.538e^{-10}$	0.01	$1.47e^{-13}$	$3.225e^{-05}$	1.78^{e-07}	$2.25e^{-05}$	$2.741e^{-09}$	0.02	$2.2e^{-16}$	0.0074
Sig.	***	*	***	***	***	***	***	*	***	**

DF=days to flowering; BBDS=disease susceptibility index (%); DM=days to physiological-maturity; PBPP=capsule-bearing primary branches plant^{-1}; NCMS=capsules on the main stem plant^{-1}; CPP=total capsules plant^{-1}; SPC=seeds capsule^{-1}; TSW=1000 seeds weight in g; OC=oil content (%); SYPP=seed yield (g plant^{-1}).

Means indicated with different letters are significantly different (p<0.05), and – sign between letters indicate the range of a group (compact letter display).

Further, lower GAM (0 - 10%) estimates were observed on flowering and maturity period, the internode length, capsule length, 1000 seeds weight, length of scratch on the opened-capsule, and seed shattering. High heritability along with high GAM for branches plant^{-1}, capsules on the main stem plant^{-1}, total capsules plant^{-1}, and the length of the capsule revealed a greater contribution of genotypic variance and availability of enriched variability which suggests that phenotypic selection would bring a progressive genetic gain. Whenever yield-related characters governed by additive genes as evidenced by high heritability coupled with high GAM, yield can be enhanced through indirect selection for yield-related characters (Rajput *et al*., 2017). Estimation of heritability provides details on the level of genetic influence over the manifestation of a certain trait as well as the accuracy of phenotypic prediction of breeding value. Breeding programs usually consider heritability as a measure of how well desirable genes are passed on from parents to offspring (Falconer, 1996). Moderate heritability with high GAM obtained for yield plant^{-1}, which suggests selection of elite genotypes for higher yield should undergone in later generations until the fixation of desirable alleles of yield contributing traits. High heritability and low GAM for flowering and maturity period showed the manifestation of high genetic influence despite inadequate variability among sesame genotypes in regard to these traits. Furthermore, high heritability along with moderate GAM for seeds capsule^{-1} and oil content indicated a high contribution of genetic effects on an observed variability. On other hand, zero heritability and zero GAM for the length of scratch on the opened-capsule and seed shattering revealed that the phenotype of these characters was completely attributed to the environmental effects, and limited scope of improvement to mitigate yield loss due to seed shattering.

Table 4. Genetic parameters for the twenty yield and yield-related characters

	mean±sd	Genotypic variance(σ2g)	Phenotypic variance(σ2p)	Environmental variance(σ2e)	GCV(%)	PCV(%)	Heritability(H^2)	Genetic advance	GAM(%)
V1	56.6±2.8	4.9	5.9	2.1	3.9	4.3	82.6	4.1	7.3
V2	57.0±13.3	40.1	100.8	121.4	11.1	17.6	39.8	8.2	14.4
V3	110.8±6.1	27.6	31.0	6.8	4.7	5.0	89.0	10.2	9.2
V4	3.4±2.3	1.4	3.2	3.6	34.5	52.0	44.1	1.6	47.2
V5	98.7±14.8	62.8	128.7	131.6	8.0	11.5	48.8	11.4	11.6
V6	34.7±7.7	22.5	37.1	29.1	13.7	17.6	60.8	7.6	22.0
V7	44.7±10.0	33.2	61.9	57.4	12.9	17.6	53.7	8.7	19.5
V8	41.2±8.7	8.4	39.2	61.6	7.1	15.2	21.5	2.8	6.7
V9	24.7±3.9	10.3	12.7	4.8	13.0	14.4	81.2	6.0	24.1
V10	30.3±13.1	0.0	96.2	192.3	0.0	32.3	0.0	0.0	0.0
V11	7.6±0.8	0.2	0.4	0.5	5.1	8.4	36.9	0.5	6.4
V12	3.0±1.0	0.4	0.7	0.5	22.2	28.0	63.1	1.1	36.4
V13	20.6±7.2	28.1	37.8	19.3	25.8	29.9	74.5	9.4	45.8
V14	43.2±20.1	179.6	276.7	194.2	31.0	38.5	64.9	22.2	51.5
V15	18.6±14.3	35.4	126.3	181.8	32.0	60.4	28.0	6.5	34.9
V16	70.0±8.8	49.3	61.4	24.3	10.0	11.2	80.2	13.0	18.5
V17	51.2±15.8	0.0	120.0	240.0	0.0	21.4	0.0	0.0	0.0
V18	2.3±0.3	0.0	0.1	0.1	6.4	9.4	46.7	0.2	9.0
V19	6.2±2.0	1.1	2.4	2.7	16.6	25.1	43.5	1.4	22.5
V20	52.8±3.0	7.9	8.1	0.5	5.3	5.4	96.8	5.7	10.8

V1=days-to-flowering; V2=disease-severity index (%); V3=physiological-maturity; V4=days from first capsule-opening to physiological-maturity; V5=plant-height (cm); V6=plant-height to first-branching (cm); V7=length of capsule-bearing-zone (cm); V8= the internode-length (mm); V9=capsule-length (mm); V10= the length of cracking on opened capsule (%); V11=capsule width (mm); V12=capsule-bearing primary branches plant^{-1}; V13= capsules on the main stem plant^{-1}; V14=total capsules plant^{-1}; V15=opened capsules plant^{-1} (%); V16=seeds capsule^{-1}; V17=seed shattering (%); V18=1000 seeds weight (g); V19=seed yield (g plant^{-1}); and V20=oil content (%)

Conclusion

The experiment indicated the presence of polymorphism for yield and yield-related characters, oil content, and seed size which indicated availability of genetic potential that can be used to enhance yield, oil content, and seed size. On other the hand, ANOVA revealed non-significant difference within the studied genotypes regarding seed-shattering-related

traits, implying that mitigation of yield loss which caused by seed-shattering requires an introduction and evaluation of indehiscent sesame lines and transfer of desirable genes into local cultivars. Further, high heritability with the highest genetic advance on yield-related traits revealed that breeders can expect a reliable response from selection underlying these traits.

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