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ASSESSMENT OF HERITABILITY AND GENETIC EFFICIENCY IN ADVANCED SESAME INBRED LINES

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ABSTRACT

The estimation of heritability is critical in selecting breeding strategies for various characteristics of agricultural plants. A randomized complete block design (RCBD) with four replications was used at Moghan Agricultural Research Station in Iran during the 2017-2018 crop years to evaluate heritability and genetic efficiency in 14 advanced sesame lines, and the Oltan cultivar was used as a control variety. The number of days to flowering (DF), growth period (GP), plant height (PH), number of capsules per plant (CN), capsule length (CL), 1000-seed weight (SW), seed (SY), and oil yield (OY) were all measured during the experiment. Selected sesame lines were utilized to estimate genetic parameters, heritability, and genetic advance using the REML/BLUP method. The results revealed moderate GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) values for CN (13.58, 17.24), SY (14.45, 17.74), and OY (15.08, 18.15), whereas the other traits had lower values. Moderately high heritability (broad sense) with high GAM (Genetic Advance as a Percentage of the Mean) was found in CN, SY, and OY, while low heritability and low GAM were found for phenological traits, DF, and GP. It may be stated that the selection strategy used in sesame breeding lines in terms of CN with moderately high heritability (broad sense) and high GAM, as well as a strong positive correlation of CN with SY and OY, could reach maximum efficiency, with which it provided the high-yielding genotypes that were needed for its breeding program.

Keywords: Correlation, Genetic advance, REML/BLUP, Selection, Yield

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INTRODUCTION

Studying the genetic diversity of traits and the association between yield and its attributes is one of the interests of breeders in implementing a successful breeding program. In crop breeding programs, evaluating genetic diversity is very important, and without diversity, there is no chance of success in selecting superior genotypes. Sesame (*Sesamum indicum* L.) may be humanity's oldest oilseed (Weiss, 2000). Minerals, including calcium, phosphorus, iron, copper, magnesium, zinc, and potassium, are found in sesame seeds as well as oils (45%–55%), proteins (18%–25%), vitamin E, A, and B complexes, and carbs (Ceccarelli *et al.*, 2009). The production of sesame from the approximately 12 million hectare world crop was 6.45 million tons, with an estimated average productivity of 535 kg/ha, according to the FAO. These figures are 42,000 hectares, 29,000 tons, and 690.5 kg/ha in Iran (FAOSTAT, 2021).

Success in any breeding program depends on the knowledge of effective key traits, genetic control systems, how these traits are inherited, and environmental factors affecting their occurrence (Chaghakaboodi *et al.*, 2012). The type and extent of genetic diversity are critical components of every crop development effort. To organize an effective breeding program to increase the yield potential of genotypes, it is crucial to obtain accurate information on the nature and extent of genetic variability. It is crucial for breeders to understand how various plant characteristics are linked to seed production to select the most productive genotypes (Teklu *et al.*, 2014). In plant breeding programs, the selection of cultivars is based on a large number of agronomic traits, and positive and negative correlations may exist among them, so to identify the effective number of traits in yield, multivariate analysis methods are valuable to researchers without losing useful information (Moradi *et al.*, 2017). In fact, it is important to predict and accurately estimate the genetic effects of individuals to select them for plant breeding programs (da Costa *et al.*, 2002), which will ultimately lead to maximum genetic advance (Furlani *et al.*, 2005).

On the other hand, the main purpose of data analysis for experimental plots is to estimate the performance of the tested lines in comparison with the control cultivars in the region. In the last few decades, the

classical method of analysis of variance (ANOVA) has been widely used to analyze this type of data (Bhatia, 2011). However, in recent years, the use of mixed linear models has become more widely used in plant breeding (Akbarpour, 2017). Mixed linear models make it possible to consider all the effects in the model as a random effect, and there is no need to know the number of groups and their variance in advance. This model can also be used for experiments in which one or more experimental plots are missed during the growing season without calculating and replacing them; therefore, it is possible to analyze experiments with unbalanced data using mixed linear models (Bhatia, 2011). Accurate prediction of the genetic values of genotypes is of particular importance in plant breeding (da Costa *et al.*, 2002). Henderson (1975) introduced the best linear unbiased prediction (BLUP) methodology for the random prediction of genetic values. In parallel, (Patterson and Thompson, 1971) proposed the restricted maximum likelihood (REML) method as an optimal approach for estimating variance components and dissecting the total variation of a given trait, particularly in the case of unbalanced data. Despite these advancements, the widespread application of the REML/BLUP methodology in practical situations for providing more accurate and unbiased predictions of genetic parameters for evaluated genotypes without prior knowledge of variance components has not been extensive until recent years (Carvalho *et al.*, 2020). The REML approach is commonly employed as a computationally efficient option for handling large data sets and intricate linear mixed effects models. The REML/BLUP technique enables the partitioning of phenotypic variation into genetic, environmental, and genotype × environment components (Resende, 2007, Soler-Guilhen *et al.*, 2020).

The REML/BLUP method was first used to estimate genetic parameters in livestock breeding (Carvalho *et al.*, 2020). In the context of sesame breeding in Iran, the utilization of advanced estimators, such as the restricted maximum likelihood method, for estimating variance components, heritability, and genetic correlation has been infrequent. There is a notable scarcity of applications of these sophisticated techniques in the specific domain of sesame breeding within the country. In the realm of oilseed rape breeding in Iran, Zeinalzadeh-Tabrizi (2023) employed the REML/BLUP methodology to estimate variance components, heritability, and genetic advances. This approach was recently applied by Petsoulas *et al.* (2022) in utilizing spectral reflectance indices as a high-throughput selection tool within a sesame breeding scheme.

In this context, the objective of this study was to estimate genetic parameters, predict genotypic effects, estimate genotypic and phenotypic correlations among agronomic traits, and determine the relationships between yield and its components by using the REML/BLUP method in 14 advanced sesame lines and a check cultivar, Oltan, under Moghan ecological conditions.

MATERIALS AND METHODS

Location and soil type description: This study was carried out at the experimental field of Moghan Agricultural Research Station, Parsabad, Iran (N39°39' E 47°688' N, elevation=78 m) during the 2017-2018 crop years. According to IRIMO data (IRIMO, 2020), this location has a semihumid and mild-warm climate (251 mm of mean annual rainfall over the past 30 years, mainly in fall and early spring). The average maximum and minimum annual temperatures of the region are 35°C and 8°C, respectively. The minimum and maximum rainfall are 72.9 and 523 mm per year, respectively. The average annual relative humidity is approximately 71%. Table 1 presents meteorological data for the location during the experimental years. The soil texture of the experimental field was sandy-loam, and the soil type was cambisol, according to the World Reference Base for Soil Resources (WRB). The physicochemical properties of the soils in the experimental field are shown in Table 2.

Table 1. Meteorological data during the experimental years

	2017				2018			
Date	**Min (°C)**	**Max (°C)**	**Avr (°C)**	**Prc (mm)**	**Min (°C)**	**Max (°C)**	**Avr (°C)**	**Prc (mm)**
June	16.8	29.4	23.1	7.1	16.0	31.1	29.2	43.8
July	19.7	34.4	27.1	1.0	21.1	37.1	29.2	6.1
August	20.6	35.9	28.2	0.0	21.7	33.6	27.7	0.0
September	18.9	32.7	25.8	0.0	17.5	30.9	24.2	30.9
October	11.7	20.9	16.3	64.5	13.9	24.3	19.1	1.3

Min: Minimum monthly temperature; Max: Maximum monthly temperature; Avr: Average monthly temperature; Prc: Precipitation

Table 2. Physio-chemical properties of soils in the experimental field

Soil depth	Salinity (Ds m^{-1})	pH	Organic Carbon (%)	N (%)	Available P (ppm)	Available K (ppm)	Zn (ppm)	Fe (ppm)
0-30 cm	0.702	7.72	2.760	0.2	1.85	469	7.14	3.94
30-60 cm	0.736	7.75	0.781	0.7	1.09	267	10.46	4.27

Plant material and experimental design: The plant materials utilized in this research were sourced from the sesame breeding program in Iran, which has successfully cultivated 14 advanced inbred lines labeled No. 1-14. These inbred lines underwent preliminary evaluation trials in 2016, representing a noteworthy achievement in the program's continual pursuit of elevating sesame varieties. The outcomes of these trials provide valuable insights that contribute to the ongoing refinement and enhancement of sesame crops in the region. Table 3 provides a detailed description of the experiment's sesame genotypes, offering a comprehensive overview of the characteristics and attributes of each genotype under investigation. This study was performed in a randomized complete block design (RCBD) with four replications during two crop years, 2017-2018.

Table 3. Overview of the sesame genotypes used in the experiment

No.	Genotype pedigree	Type
1	(Sis) × M-19× Haj(1)	Advanced Inbred line
2	(Sis) × M-19× Haj(2)	Advanced Inbred line
3	(Sis) × M-19× Haj(3)	Advanced Inbred line
4	(Sis) × M-19× 2822(1)	Advanced Inbred line
5	(Sis) × M-19× 2822(2)	Advanced Inbred line
6	M-19 × Henj × J-142	Advanced Inbred line
7	(TN-238) × PM× Haj	Advanced Inbred line
8	(TN-238) × M-19× Haj	Advanced Inbred line
9	Isf × Ch	Advanced Inbred line
10	Isf × India	Advanced Inbred line
11	Isf × 2822(1)	Advanced Inbred line
12	Isf × 2822(2)	Advanced Inbred line
13	Isf × 2822(3)	Advanced Inbred line
14	Non-Dehiscent	Advanced Inbred line
15	Oltan	Commercial Check Cultivar

Experimental technique: The experimental field was under wheat cultivation the previous year. The field was prepared in mid-spring. During planting, 150 kg ha^{-1} of phosphorus in the form of triple superphosphate was administered. Furthermore, 200 kg ha^{-1} of nitrogen, supplied as ammonium nitrate, was applied, with half of the nitrogen distributed at the time of planting and the remaining half during the stem elongation stage. Additionally, 3 kilograms per hectare of 20-20-20 NPK fertilizer was applied as a foliar spray before the flowering stage. No indications of disease were noted throughout the growth phase. The irrigation was carried out four times using furrow irrigation in accordance with area practices. Weed control was carried out manually.

Each experimental plot was made up of 6 m lines separated by 30 cm. The field was treated with preplant trifluralin herbicide at a rate of 2 liters per hectare. Every crop year, planting took place on June 25. The final harvest was performed by removing two lateral lines as margins. The crop harvest was carried out individually for each experimental plot, determined by the physiological maturity date.

Data collection: During the experiment, traits: days to flowering (DF), growth period (GP), plant height (PH), number of capsules per plant (CN), capsule length (CL), 1000-seed weight (SW), seed (SY), and oil yield (OY) were recorded.

Statistical analysis: The data were checked for outliers using the Grubbs test and for normality using the Shapiro–Wilk test before the variance analysis was performed. After that, the Levene test was used to check for the assumption of homogeneity of variance.

The statistical model used for the analysis of variances is as follows:

$Y_{ijk} = \mu + Env_i + Rep_j(Env_i) + Gen_k + Env_i \times Gen_k + \varepsilon_{ijk}$

where Y_{ijk} is the trait of interest, μ is the mean effect, $Rep_j(Env_i)$ is the effect of the jth replicate within the ith

environment, Gen*k* is the effect of the *k*th genotype, Ɛijk is the error associated with the *i*th environment, the *j*th replicate within the *i*th environment, and the *k*th genotype, and the assumption is made that it follows a normal distribution with a zero mean and a homoscedastic variance. To determine BLUPs and broad-sense heritability, all factors are treated as random.

Calculating genotypic and phenotypic coefficients of variation:

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

where:

σ_p^2=Phenotypic variance

σ_g^2=Genotypic variance

$\bar{x}$=Grand mean of a character

Estimation of heritability in broad sense:

According to Allard (1999), on a genotype-mean basis, broad sense heritability (H^2) was calculated as the proportion of the ratio of genotypic variation (g) to phenotypic variance (p) (p).

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2/nEnvs + \sigma_e^2/(nEnvs \times nreps)}$$

where $nEnvs$ is the number of environments in the study, $nreps$ is the number of replicates, and σ_{ge}^2 is the genotype by environment interaction variance component. For well-known characteristics and environments, the estimated broad-sense heritability (repeatability) provides useful information about the quality of a breeding program.

The phenotypic correlations among characteristics are straightforward Pearson correlations between distinct pairs of attributes.

Using the following formula, the genetic correlation between attributes is calculated:

$$\rho_g = \frac{\overline{\sigma_{g(ij)}}}{\overline{\sigma_{g(i)}\sigma_{g(j)}}}$$

where $\overline{\sigma_{g(ij)}}$represents the arithmetic mean of all pairwise genotypic covariances between characteristics *j* and *j'* and $\overline{\sigma_{g(i)}\sigma_{g(j)}}$ represents the arithmetic mean of all pairwise geometric means among the genotypic variance components of the traits.

The formula for determining the coefficient of variation is:

$$CV = 100 \times \frac{ASED}{grand\ mean}$$

ASED = Average Standard Error of Differences in Means.

Estimation of genetic advance: Using the techniques described by Johnson *et al.* (1955) and assuming selection of the top 5% of genotypes, genetic advance (GA) and percentage of the mean (GAM) were calculated as follows:

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

where:

GA=Expected genetic advance

k is the standard deviation of the selection ratio with a selection intensity of 5% (K = 2.063).

$$GAM(\%) = \frac{GA}{\bar{x}} \times 100$$

Selected sesame lines were utilized to estimate genetic parameters, heritability, and genetic advance using the restricted maximum likelihood (REML)/best unbiased linear prediction (BLUP) method.

In this study, the META-R software (Alvarado *et al.*, 2020) calculates BLUPs for all traits when random effects from genotypes are taken into account. The grand mean is added to the estimated random effect that arises from each genotype to arrive at the BLUP for each genotype.

RESULTS AND DISCUSSION

For every characteristic examined in this study, a highly significant difference between sesame genotypes was found (Table 4). These results showed that the investigated sesame genotypes exhibit substantial diversity. Similarly, Parameshwarappa *et al.* (2009) found statistically significant differences between 151 sesame accessions in terms of days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capsules per plant, length of capsules, number of seeds per capsule, oil content, and seed yield per plant. Furthermore, Gidey *et al.* (2012) found highly significant variations among 81 sesame accessions with regard to days to 50% flowering, days to maturity, capsule filling period, plant height, number of capsules per plant, number of primary branches per plant, capsule length, number of seeds per capsule, 1000 seed weight, oil content, and seed yield per hectare. Similar outcomes, as reported by Kumari and Kumhar (2023), revealed significant genotype-based differences for all eleven traits in the analysis of variance, highlighting considerable genetic variability in their sesame experimental material.

Estimation of variance components and coefficients of variation: Table 5 shows estimates of phenotypic, genotypic, genotype by environment, and environmental variances, as well as phenotypic coefficients of variation

(PCV) and genotypic coefficients of variation. The GCV ranged from 0.60 for GP to 15.08 for OY. PCV ranged from 1.74 for GP to 18.15 for OY. The results of this study showed that the PCV values were greater than the GCV values, suggesting that environmental factors were more influential in the expression of these traits. The findings above are consistent with those of Umamaheswari *et al.* (2019), Pavani *et al.* (2020) and Kumari and Kumhar (2023) regarding sesame genetic variability in India.

Table 4. Combined analysis of variance for agro-morphological traits in sesame genotypes

Source	df	DF	GP	CN	CL	PH	SW	SY	OY
Y	1	3413.33**	2244.68**	913.01*	504.30**	3785.63**	29.61**	59.15**	15.64**
R (Y)	6	2.3778	0.2083	316.29	13.28	271.35	0.04	3.72	1.02
G	14	17.1012**	13.6226**	510.47*	20.53**	417.38**	0.16**	3.49**	0.96**
G×Y	14	13.244**	11.0321**	193.54	9.53*	217.42*	0.03	1.60	0.41
E	84	1.3837	0.0655	183.76	5.08	116.75	0.05	1.26	0.34

Y: year; R: replication; G: genotype; E: error; DF: Days to Flowering; GP: Growth Period; PH: Plant Height; CN: Number of Capsules per Plant; CL: Capsule Length; SW: 1000-Seed Weight; SY: Seed Yield; OY: Oil Yield

Table 5. Estimates of genetic parameters for traits of sesame genotypes using the REML/BLUP method

Statistic	DF	GP	CN	CL	PH	SW	SY	OY
H^2	0.23	0.12	0.62	0.54	0.48	0.71	0.66	0.69
GA	0.68	0.46	10.22	1.77	7.13	0.23	277.07	152.50
GAM	1.30	0.43	22.05	6.68	5.85	7.15	24.24	25.80
GCV	1.33	0.60	13.58	4.43	4.10	4.08	14.45	15.08
PCV	2.80	1.74	17.24	6.05	5.93	4.80	17.74	18.15
Min	43.00	92.00	13.33	20.30	84.00	2.14	330.00	169.52
Max	61.00	116.00	93.00	36.00	158.33	4.37	2395.80	1264.02
σ^2_g	0.48	0.41	39.62	1.38	25.00	0.01	27304.61	7941.76
σ^2_{ge}	2.97	5.27	2.45	1.11	25.17	0.00	2016.14	250.73
σ^2_e	56.65	22.34	9.78	8.11	56.89	0.49	113398.58	30076.54
Residual Variance	1.38	3.32	183.76	5.08	116.75	0.05	102862.22	27523.65
Grand Mean	52.17	106.68	46.34	26.45	121.87	3.17	1143.22	591.04

DF: Days to Flowering; GP: Growth Period; PH: Plant Height; CN: Number of Capsules per Plant; CL: Capsule Length; SW: 1000-Seed Weight; SY: Seed Yield; OY: Oil Yield; H^2: Broad-sense Heritability; GA: Genetic Advance; GAM: Genetic Advance as a Percentage of the Mean; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; Min: Minimum; Max: Maximum; σ^2_g: Genotype Variance; σ^2_{ge}: Genotype × Environment Variance; σ^2_e: Environmental Variance

The environment generally has a significant impact on quantitative traits. Deshmukh *et al.* (1986) found that PCV and GCV levels above 20% are deemed high, whereas values below 10% are regarded as low, and those between 10% and 20% are regarded as medium. Accordingly, CN, SY and OY had medium PCV and GCV, whereas the other traits had lower values for them (Table 5). Selecting for characteristics with high PCV and GCV is likely to provide desirable results, and the presence of these qualities in the phenotype is indicative of strong genetic potential (Teklu *et al.*, 2014). Greater than average GCV and PVC values indicate substantial variation for these characteristics (Terfa and Gurmu, 2020), whereas moderate GCV and PCV were recorded for CN (17.24 and 13.58), SY (17.74 and 14.45) and OY (18.15 and 15.08), respectively. Similar results were found for the lowest PCV and GCV values for the growth period in the Ahmed and Ahmed (2013) and Kumari and Kumhar (2023) studies and for days to flowering in the Umamaheswari *et al.* (2019) study. Some traits in this study had moderate to low variation, which showed that the base population needs to be improved (Terfa and Gurmu, 2020).

Genetic advance and heritability estimation: Estimation of heritability, genetic advance, and genetic advance as a percentage of the mean (GAM) for all traits are shown in Table 5. Heritability ranged from 0.12 for GP to 0.71 for SW. A very high heritability rate is defined as 80 percent or more; a moderately high rate is 60 to 79 percent; a medium rate is 40 to 59 percent; and a low rate is less than 40 percent (Singh, 2001). Accordingly, the heritability estimate was moderately high for CN, SW SY and OY; medium for CL and PH; and low for DF and GP (Table 5). Siva *et al.* (2013) reported high heritability values for days to 50% flowering, which was in conflict with the findings of this experiment. Heritability is a good way to predict how traits from parents will be passed on to their progenies.

Estimates of heritability can be used to foretell how far a population is likely to go as a result of selective pressures. As a result, high heritability facilitates accurate character selection.

Rather than relying only on heritability, the selection impacts of a population may be predicted with more accuracy by including genetic advance, as reported by Johnson *et al.* (1955). Genetic advance (GA) under selection refers to improvements in genotypic value for the new population compared to the base population throughout one cycle of selection at a certain selection intensity (Singh, 2001). Heritability and genetic advance represent interconnected concepts, wherein heritability values serve as predictive indicators for genetic advance through selection, enabling an assessment of the efficacy and significance of the selection process (Kumari and Kumhar, 2023). Higher values for heritability and genetic advance in SY and OY were observed in this research (Table 5). Similar results in sesame have previously been reported by Rao *et al.* (2013), Teklu *et al.* (2014) and Kumar *et al.* (2022) for SY in sesame, which validates our findings. The outcomes for these traits suggest that heritability primarily stems from additive gene effects, suggesting the potential effectiveness of selection in sesame. Characteristics of this nature could be enhanced through mass selection and other breeding approaches grounded in progeny testing (Kalaiyarasi *et al.*, 2019, Kumar *et al.*, 2022).

According to the genetic advance as a percentage of the mean (GAM) scale established by Johnson *et al.* (1955), genetic progress is deemed to be high when it is 20% or more, moderate when it is 10%-20%, and low when it is 0%-10%. The range for GAM was from 0.43% for GP to 25.80% for OY (Table 5). High GAM values were observed for CN (22.05%), SY (24.24%) and OY (25.80%), and low values were observed for DF (1.30%), GP (0.43%), CL (6.68%), PH (5.85%) and SW (7.15%). Similar results for high GAM values were observed in Rao *et al.* (2013), Umamaheswari *et al.* (2019), whereas low GAM values were reported by Pavani *et al.* (2020) for SY. Moderately high heritability in broad sense with high GAM was found in CN, SY and OY (Table 5). CN was found to have fairly high heritability and GAM by Siva *et al.* (2013) and Kumari and Kumhar (2023), suggesting that the number of capsules per plant is regulated by additive gene action and that phenotypic selection for this attribute will be successful. Similarly, Mahajan *et al.* (2007) and Kalaiyarasi *et al.* (2019) found a high heritability and high GAM for the yield characteristic, which was in agreement with the findings of this experiment.

In this experiment, phenological traits (DF and GP) had low heritability and GAM (Table 5). These characteristics may have a nonadditive (dominant or epistatic) gene effect. This finding was inconsistent with those of Hika *et al.* (2015), Kiruthika *et al.* (2018), Umamaheswari *et al.* (2019) and Pavani *et al.* (2020) with high heritability and high genetic advance estimates for phenological traits and in conflict with the findings of Gangadhara *et al.* (2012) and Kumari and Kumhar (2023), who reported high heritability coupled with moderate genetic advance for days to 50 percent flowering and days to maturity. In contrast, for DF, low heritability and genetic advance are seen, implying that selection would provide no advantage, which was similar to the Kalaiyarasi *et al.* (2019) study.

Genotypic and phenotypic correlations: Genotypic and phenotypic correlation coefficients of sesame traits are shown in Table 6. The results revealed a significant positive genetic correlation between DF and GP (1.000^{**}), SY and OY (0.995^{**}), CN and SY, OY (0.713^{**}, 0.750^{**}), and DF and PH (0.743^{**}) at the 0.01 percent probability level (Table 6). A highly positive and significant genetic correlation between DF and GP was also reported in the Gidey *et al.* (2012) study. Abate and Mekbib (2015) reported a negative and significant genotypic correlation between days to flowering and growth period, which was contrary to the results of this research. They also reported a positive and significant genotypic correlation between CN and SY, which was in accordance with the results of this research.

Table 6. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients of sesame traits

Traits	DF	GP	CN	CL	PH	SW	SY	OY
DF	1	0.746^{**}	0.004	-0.356	0.152	0.097	-0.034	-0.028
GP	1.000^{**}	1	-0.205	-0.692^{**}	-0.390	-0.031	-0.070	-0.071
CN	0.108	0.167	1	0.400	0.469	0.323	0.410	0.461
CL	-0.589^{*}	-1.000^{**}	0.543^{*}	1	0.550^{*}	0.289	0.403	0.412
PH	0.743^{**}	0.553^{*}	0.503^{*}	0.679^{**}	1	0.023	0.165	0.210
SW	0.475	-0.056	0.306	0.404	-0.161	1	0.313	0.299
SY	0.090	0.123	0.713^{**}	0.672^{**}	0.586^{*}	0.393	1	0.996^{**}
OY	0.079	0.169	0.750^{**}	0.672^{**}	0.636^{*}	0.348	0.995^{**}	1

DF: Days to Flowering; GP: Growth Period; CN: Capsule Number; CL: Capsule Length: PH: Plant height; SW: 1000-Seed Weight; SY: Seed Yield; OY: Oil Yield

Correlation analysis in the present investigation showed that SY exhibited a positive, nonsignificant correlation with PH (Rao *et al.*, 2013, Umamaheswari *et al.*, 2019), CN (Gidey *et al.*, 2012) and SW (Ismaila and Usman, 2012) at the phenotypic level. Additionally, the results showed a significant positive phenotypic correlation between SY and OY (0.996**), PH and CL (0.550*), and DF and GP (0.746**). The results also revealed that there was a strong negative phenotypic correlation between GP and CL (-0.692**) (Table 6). Umamaheswari *et al.* (2019) also reported negative but nonsignificant genotypic and phenotypic correlations between days to 50% flowering and capsule length. A significant positive phenotypic correlation between CN and SY was reported by Akbar *et al.* (2011) and Uzun *et al.* (2013), which was in accordance with the results of this research. Significant positive genotypic and phenotypic correlations between PH and CL were observed in this research, which were similar to those of Umamaheswari *et al.* (2019). Positive but nonsignificant genotypic and phenotypic correlations were observed between CL and SW (0.404, 0.289), which were similar to those of Umamaheswari *et al.* (2019). In general, the positive and strong correlation between phenotypic and genotypic pairs of traits substantiated the likelihood of a correlated response to selection (Teklu *et al.*, 2014).

Conclusion: Genetic diversity and heritability play pivotal roles in successful crop breeding endeavors. Analyzing genetic variation assists breeders in selecting the most effective methods for enhancing desired traits. Achieving high-yielding sesame varieties requires accurate selection indices, focusing on features with substantial heritability and genetic advance. The current research revealed varying levels of variability, heritability, and genetic advance as a percentage of the mean (GAM) among genotypes. Traits such as CN, SY, and OY demonstrated medium PCV and GCV values, indicating significant variability, while others showed lower values. Heritability estimates were moderately high for CN, SW, SY, and OY; medium for CL and PH; and low for DF and GP. CN, SY, and OY exhibited moderately high heritability and high GAM, suggesting additive gene action. On the other hand, phenological traits such as DF and GP showed low heritability and GAM, indicating nonadditive gene action and making direct selection challenging due to environmental influences. Correlation analysis indicated positive and significant correlations between SY, OY, CN, CL, and PH at the genotypic level, with positive but nonsignificant correlations at the phenotypic level. The breeding strategy targeting CN, with moderately high heritability and high GAM, along with its strong positive correlation with SY and OY, proved effective in obtaining high-yielding genotypes for the sesame breeding program.

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