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Assessment of genetic variability for yield and yield components in sesame (*Sesamum indicum* L.)

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Abstract

Sesame is an important oilseed crop of India. Assessment of genetic variability in sesame genotypes is a prerequisite for selecting desirable genotypes and traits for breeding efforts to improve yield potential. A set of 55 sesame genotypes were evaluated for 16 quantitative traits contributing for yield and components. Analysis of variance and genetic variability parameters including phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability (h^2) and genetic advance as per cent of mean (GAM) were estimated and analyzed. ANOVA showed that genotypic effects were significant for 12 out of 16 traits. High PCV and high GCV were observed for traits seed yield per plant, capsules per plant and number of secondary branches per plant. High heritability coupled with moderate to high genetic advance was observed for number of plant height, capsules per plant and seed yield per plant indicating that these traits would be valuable for improvement of seed yield and its components in sesame. The promising genotypes identified in this study could be used in sesame breeding programmes.

Keywords: Queen of oilseeds, *Sesamum indicum*, India, family pedaliaceae

Introduction

Sesame (*Sesamum indicum* L.) popularly known as “queen of oilseeds” is an important annual oilseed crop. It is commonly called as “benni seed”, “simsim”, “til”, “gingelly” *etc*. It is an essential source of edible oil; rich in various antioxidants such as sesamol, sesamin, sesamolin, and sesaminol. The sesame originated in Africa and spread to different parts of the world including India, Iran, Egypt, China *etc*. It is mostly cultivated in tropical and subtropical regions of Asia, Africa and Latin America. It is an often-cross pollinated crop with chromosome number 2n=26 and belongs to the family Pedaliaceae.

India imports about one lakh crores worth of edible oils annually to meet the domestic demand, which costs heavily on the exchequer. Therefore, achieving self-reliance in edible oilseed production is the major goal of R&D efforts in oilseeds. The sesame is an important crop in this endeavor. Globally, the sesame is grown in an area of 14 million ha with production of 6.8 million tonnes and productivity of 487 kg/ha (FAOSTAT, 2020) [6]. In India, it is grown in area of 1.52 million ha with the production of 0.66 million tonnes and productivity of 433 kg/ha (FAOSTAT, 2020) [6]. The estimates point out that the sesame acreage in India is low and needs to be increased through concerted efforts.

Major challenges in sesame cultivation in India are low and unstable yield, low adaptability, non-synchronous maturity, biotic and abiotic stresses (Sumathi and Muralidharan, 2010; Saxena and Bisen, 2017) [18, 15]. There is a need to tap the genetic potential available in the germplasm for improvement of productivity in sesame. Assessment of genetic variability in the sesame germplasm is a prerequisite to identify desirable genotypes and use them in breeding programmes for developing high yielding cultivars. In this study, main objective was to assess genetic variability and heritability parameters in a set of 55 sesame genotypes based on yield and yield components.

Materials and Methods

The experiment was conducted at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore, India, which is situated at about 11°N latitude and 77°E longitude at an altitude of 427 metres above MSL. The average annual rainfall is around 700 mm. The trial was conducted during summer 2022.

A set of 55 sesame genotypes (Table 1) were used for evaluation in Alpha Lattice design with two replications and 11 entries per block per replication. Each genotype was raised in a single row of three meters length with a spacing of 30 cm between rows and 30 cm between plants, following the recommended agronomic packages of practices during the experimental period.

Table 1: List of sesame genotypes used in the study

Code	Entries	Code	Entries
G1	NIC-16106	G29	SI-1769
G2	NIC-2939	G30	PAIYUR-1
G3	SI-2186	G31	KMR-87
G4	G-53	G32	SI-1771
G5	PSR-2000	G33	ES-71
G6	SI-9185	G34	TC-25
G7	NAE-79114/7	G35	SI-1236
G8	SI-801	G36	SI-1143-1
G9	NIC-8252	G37	SI-1214
G10	KMR-95	G38	RT-146
G11	IS-1516	G39	RT-106
G12	NIC-8283	G40	IS-249
G13	DS-1	G41	S-861
G14	NIC-8261	G42	SI-1967
G15	SI-769-2	G43	NIC-8317
G16	SI-395	G44	BS-27
G17	GUN-3-NL-1	G45	SI-2334
G18	DP1-15-25	G46	SI-533
G19	SI-9185-1	G47	SI-212
G20	SI-2289-2	G48	SI-328
G21	OTS-2	G49	SI-7613
G22	JTS-80	G50	SI-80-1
G23	SI-1760/1	G51	ANNAMALAI-NC-1
G24	SO-233	G52	SI-3171
G25	KMR-342	G53	SI-987/1
G26	SI-70	G54	KANDAPPAN KURICHY
G27	IC-2046-18	G55	CO-1
G28	SI-702		

A total of 16 quantitative traits contributing for yield and yield components were recorded on five randomly selected plants of each genotype in each replication as per the standard procedures described for sesame (IPGRI and NBPGR, 2004). The traits measured were as follows: plant height (PHT) in cm, number of primary branches per plant (NPB), number of secondary branches per plant (NSB), basal leaf length (BLL) in cm, basal leaf width (BLW) in cm, top leaf length (TLL) in cm, top leaf width (TLW) in cm, days to first flower initiation (DTIF), days to 50 per cent flowering (DFF), days to maturity (DTM), capsule length (CL) in cm, capsule width (CW) in cm, number of capsules per plant (CPP), number of seeds per capsule (SPC), 1000 seed weight (TSW) in g and seed yield per plant (SYP) in g. The data were subjected to the following statistical analysis. Basic descriptive statistics *viz*., mean, range, standard deviation (SD) and coefficient of variation (CV) were obtained using the Excel software. Frequency distribution and Shapiro-Wilk normality test values (W-statistic) were obtained using R statistical software (v4.1.2; R Core Team 2021). Analysis of variance (ANOVA) was computed using the model 2 in R statistical software. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were computed as per Burton (1952) [3]. Broad sense heritability (h^2) was calculated based on the formula given by Lush (1940) [12], and genetic advance as per cent of mean (GAM) was computed as per the formula given by Johnson *et al.* (1955) [9].

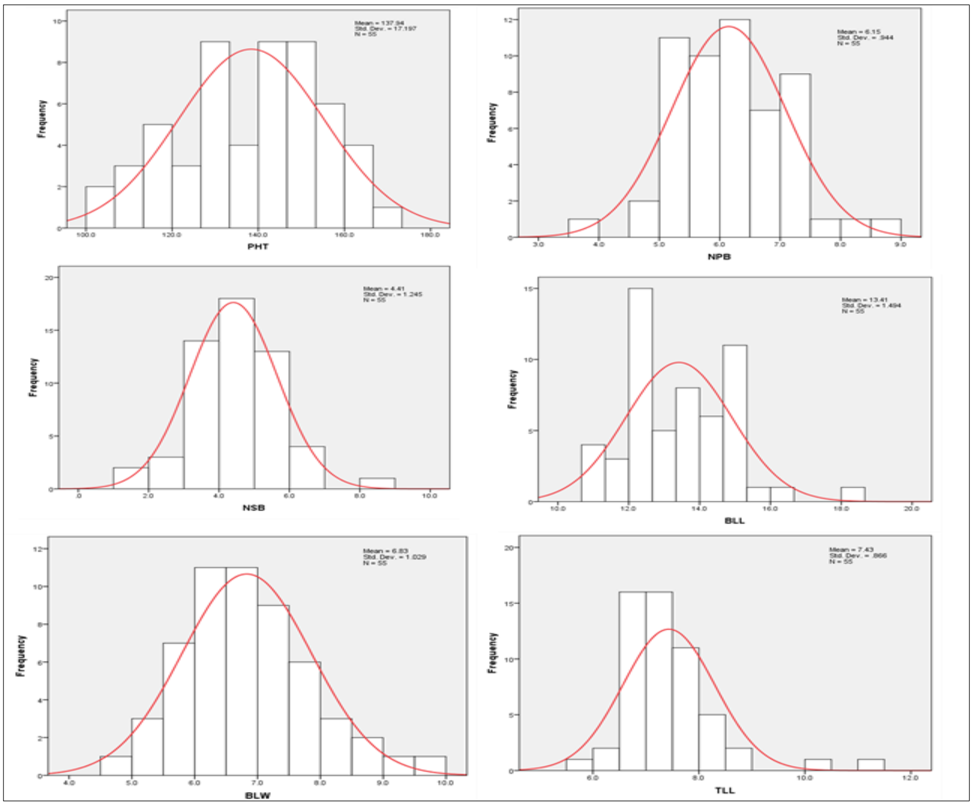

Fig 1a: Frequency distribution of yield and its components in a set of 55 sesame genotypes. PHT=Plant height in cm, NPB= Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL= Basal leaf length in cm, BLW= Basal leaf Width in cm, TLL= Top leaf length in cm

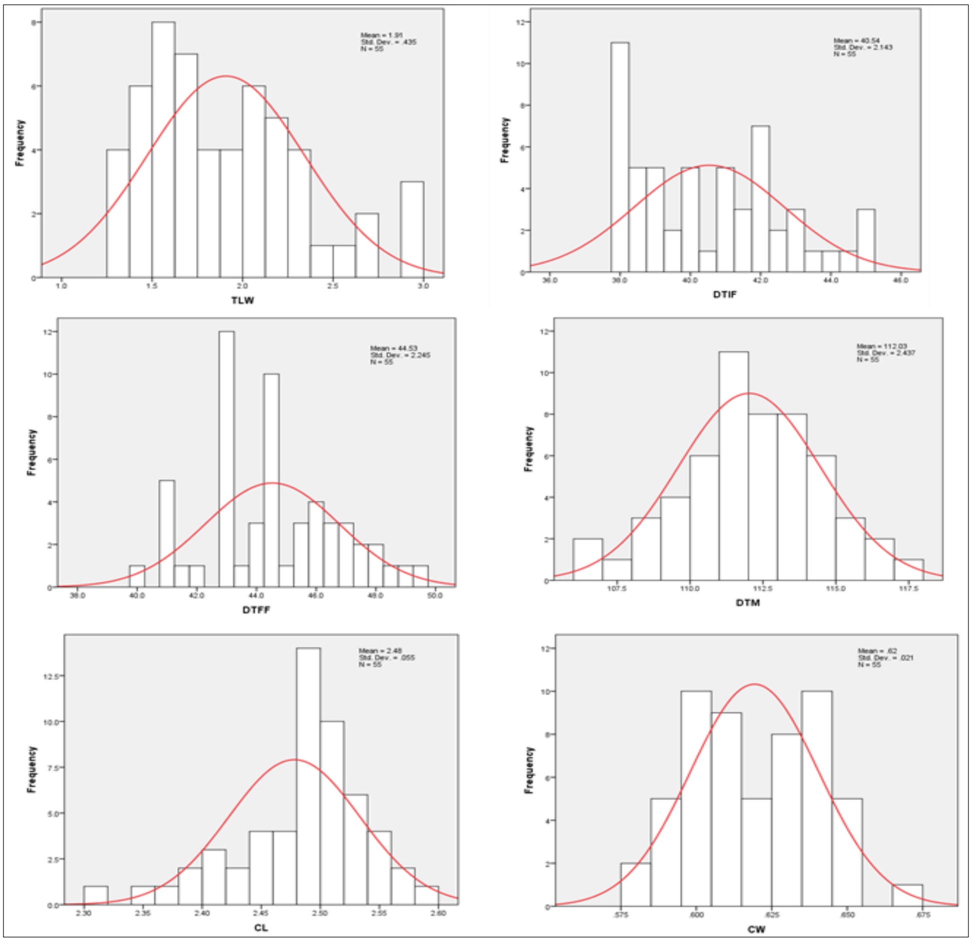

Fig 1b: Frequency distribution of yield and its components in a set of 55 sesame genotypes. TLW=top leaf width in cm, DTIF= Days to first flower intiation, DFF= Days to 50 per cent flowering, DTM= Days to maturity, CL= Capsule length in cm, CW= Capsule width in cm

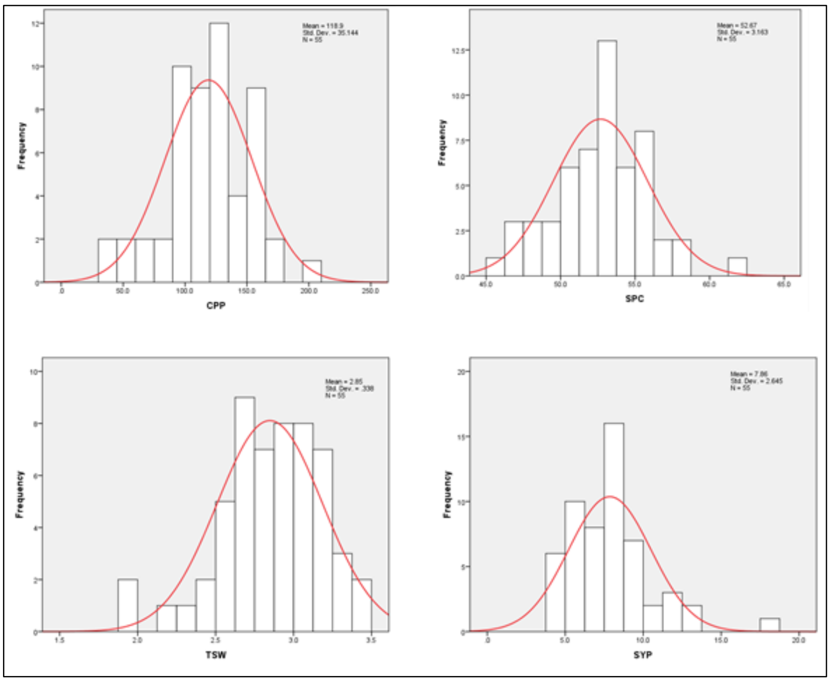

Fig 1c: Frequency distribution of yield and its component in a set of 55 sesame genotypes. CPP= Number of capsules per plant, SPC= Number of seeds per capsule, TSW= 1000 seed weight in g and SYP= Seed yield per plant in g.

Results and Discussion

The basic descriptive statistics recorded for the quantitative traits in sesame are presented in Table 2. Plant height ranged from 100.67 to 171.62 cm. The mean NPB and NSB recorded were 6.15 and 4.41, respectively. The genotype KMR-95 recorded the lowest number of NPB and NSB, while NIC-8317 recorded the maximum. The mean of BLL and BLW were 13.41 cm and 6.83 cm, respectively. The TLL ranged from 5.90 cm (SI-80-1) to 11.2 cm (NIC-16106). The TLW ranged from 1.31 cm (SI-80-1) to 2.96 cm (SI-7613). The mean values for DTIF, DFF and DTM were 40.5, 44 and 112 days, respectively. Seven genotypes recorded DTIF in 38 days after sowing. The mean values for CL and CW were 2.78 cm and 0.62 cm. The CPP ranged from 31.7 (G-53) to 206 (SI-702). The average SPC and TSW were 52.67 and 2.85 g, respectively. The SYP ranged from 3.99 g (G-53) to 17.80 g (KMR-342) with a mean of 7.85 g.

Table 2: Basic statistics of traits studied in sesame genotypes

Trait	Mean	SE	Minimum*	Maximum*	SD	CV (%)
PHT	137.94	8.5153	100.67 (SI-1214)	171.62 (KMR-95)	17.20	8.6
NPB	6.15	0.8759	3.50 (KMR-95)	8.60 (NIC-8317)	0.94	18.3
NSB	4.41	0.7587	1.70 (KMR-95)	8.60 (NIC-8317)	1.25	23.5
BLL	13.41	1.3292	10.76 (SI-7613)	18.34 (SI-1771)	1.45	10.3
BLW	6.83	0.8654	4.80 (SI-1236)	9.85 (DP1-15-25)	1.03	13
TLL	7.43	0.721	5.90 (SI-80-1)	11.12 (NIC-16106)	0.87	9.2
TLW	1.91	0.2767	1.31 (SI-80-1)	2.96 (SI-7613)	0.44	16
DTIF	40.54	1.6733	38.00 (NIC-16106)	45.00 (SI-1760/1)	2.14	5.1
DFF	44.53	1.8606	40.00 (SI-1236)	49.50 (SI-801)	2.25	4.6
DTM	112.03	2.1966	106.10 (NIC-16106)	117.00 (NAE-79114/7)	2.44	2.4
CL	2.48	0.0516	2.31 (ES-71)	2.58 (KMR-87)	0.06	2.8
CW	0.62	0.0201	0.58 (NIC-8283)	0.67 (PSR-2000)	0.02	4.7
CPP	118.90	16.268	31.70 (G-53)	206.00 (SI-702)	35.14	19.8
SPC	52.67	3.9914	45.20 (SI-1236)	62.00 (SI-987/1)	3.16	10.9
TSW	2.85	0.2743	1.91 (SI-9185)	3.49 (NIC-8283)	0.34	12.3
SYP	7.85	0.9156	3.99 (G-53)	17.80 (KMR-342)	2.65	16.3

*Names in the parenthesis indicate genotypes possessing the trait value

PHT=Plant height in cm, NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL=Basal leaf length in cm, BLW=Basal leaf width in cm, TLL=Top leaf length in cm, TLW=Top leaf width in cm, DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CL=Capsule length in cm, CW=Capsule width in cm, CPP=Number of capsules per plant, SPC=Number of seeds per capsule, TSW=1000 seed weight in g and SYP=Seed yield per plant in g.

Among traits, the largest CV was observed for NSB (23.5%) followed by CPP (19.8%), NPB (18.3%) and SYP (16.3%). The CV was the least for flowering related traits namely DTIF, DFF and DTM (<5.1%) followed by capsule traits such as CL and CW (<4.7%).

The frequency distribution for the quantitative traits is presented in Fig 1. Although the traits showed continuous variation, PHT, NPB, NSB, BLL, BLW, DTFF, DTM, CPP, SPC, TSW followed normal distribution based on the significance of W statistic (Table 3). TLL, TLW, DTIF, CL, CW and SYP followed non-normal distribution. It is important that the quantitative traits are normally distributed. The non-normal distribution of data may suggest that the traits are highly influenced by the environment and needs to be handled cautiously in breeding experiments.

Table 3: Shapiro-Wilk normality test values of quantitative traits measured in sesame genotypes

Trait	W statistic	p-value	Distribution
PHT	0.97198	0.2256	Normal
NPB	0.98719	0.8224	Normal
NSB	0.97782	0.4005	Normal
BLL	0.95871	0.05648	Normal
BLW	0.97457	0.2928	Normal
TLL	0.83299	2.304e-06	Non-normal
TLW	0.93304	0.004375	Non-normal
DTIF	0.9152	0.0008792	Non-normal
DFF	0.97221	0.231	Normal
DTM	0.99043	0.9395	Normal
CL	0.94532	0.01437	Non-normal
CW	0.95322	0.03198	Non-normal
CPP	0.97549	0.3204	Normal
SPC	0.98464	0.7038	Normal
TSW	0.96952	0.1751	Normal
SYP	0.92366	0.001849	Non-normal

PHT=Plant height in cm, NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL=Basal leaf length in cm, BLW=Basal leaf width in cm, TLL=Top leaf length in cm, TLW=Top leaf width in cm, DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CL=Capsule length in cm, CW=Capsule width in cm, CPP=Number of capsules per plant, SPC=Number of seeds per capsule, TSW=1000 seed weight in g and SYP=Seed yield per plant in g.

The ANOVA showed significant differences among the genotypes for all the traits studied except for NPB, CL, CW and SPC suggesting that wide genetic variation is present in the experimental material (Table 4). The genetic variability parameters were worked out only for the traits that showed significant differences among the genotypes and are presented in Table 5. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits, indicating that additive nature of gene action controlling these quantitative characters and the influence of environment on the expression of these traits.

Table 4: Testing for the significance of genotypic effect (ANOVA) of quantitative traits in sesame

Trait	Sum Square	Mean Square	F value	Pr(>F)
PHT	31939	591.5	4.1816	1.080e-06 ***
NPB	96.29	1.783	1.4080	0.11821
NSB	167.361	3.099	2.8857	0.0001718 ***
BLL	240.874	4.4606	2.3416	0.001857 **
BLW	114.432	2.1191	2.6948	0.0003901 ***
TLL	80.949	1.499	3.2034	4.572e-05 ***
TLW	20.3667	0.3772	4.0647	1.648e-06 ***
DTIF	495.85	9.1825	2.1368	0.004677 **
DFF	544.42	10.0818	2.4312	0.001244 **
DTM	641.5	11.8796	1.6113	0.04977 *
CL	0.33624	0.00623	1.3156	0.17127
CW	0.04705	0.00087	1.0263	0.4667
CPP	133389	2470.2	4.4779	3.817e-07 ***
SPC	1080.18	20.003	0.6047	0.962
TSW	12.359	0.22887	1.8728	0.01548 *
SYP	755.42	13.9893	8.5248	6.041e-12 ***

PHT=Plant height in cm, NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL=Basal leaf length in cm, BLW=Basal leaf width in cm, TLL=Top leaf length in cm, TLW=Top leaf width in cm, DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CL=Capsule length in cm, CW=Capsule width in cm, CPP=Number of capsules per plant, SPC=Number of seeds per capsule, TSW=1000 seed weight in g and SYP=Seed yield per plant in g.

Table 5: Estimates of genetic variability parameters in sesame

Trait	Mean	SE	CV (%)	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
PHT	137.93	8.51	8.73	13.91	10.83	60.62	17.37
NSB	4.40	0.75	24.34	33.08	22.39	45.83	31.23
BLL	13.41	1.32	14.01	14.9	5.07	11.59	3.56
BLW	6.82	0.86	17.92	19.70	8.16	17.18	6.97
TLL	7.42	0.72	13.72	15.16	6.45	18.10	5.65
TLW	1.91	0.27	20.53	27.02	17.56	42.24	23.51
DTIF	40.54	1.31	4.59	6.20	4.16	45.14	5.77
DFF	44.53	1.31	4.18	5.84	4.08	48.82	5.87
DTM	112.1	1.45	1.83	2.43	1.59	42.91	2.15
CPP	118.90	16.26	19.34	32.57	26.20	64.71	43.41
TSW	2.84	0.27	13.63	15.30	6.95	20.65	6.51
SYP	7.85	0.91	16.49	35.64	31.59	78.60	57.70

PHT=Plant height in cm, NSB=Number of secondary branches per plant, BLL=Basal leaf length in cm, BLW=Basal leaf width in cm, TLL=Top leaf length in cm, TLW=Top leaf width in cm, DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CPP=Number of capsules per plant, TSW=1000 seed weight in g and SYP=Seed yield per plant in g.

Higher PCV and GCV values were recorded for the traits *viz.*, SYP, CPP and NSB. These results are in agreement with the findings of Sumathi and Muralidharan (2010), Chandramohan (2011), Ismaila and Usman (2014), Bharathi *et al.* (2014), Saxena and Bisen (2017), Divya *et al.* (2018), Singh *et al.* (2018), Kadvani *et al.* (2020), Mohanty *et al.* (2020), Kant *et al.* (2021) and Aboel Kassem *et al.* (2021) [18, 15, 8, 5, 17, 10, 11, 1]. High values of PCV and low values of GCV were observed for TSW, BLL, BLW and TLL.

Moderate values of PCV were observed for PHT as reported by Singh *et al*. (2018) and Mohanty *et al*. (2020) [17]. Lower values of PCV and GCV were observed for DFF and DTM as reported by Sumathi and Muralidharan (2010), Saxena and Bisen (2017), Singh *et al*. (2018), Kadvani *et al*. (2020), Mohanty *et al*. (2020), Kant *et al*. (2021) and Aboelkassem *et al*. (2021) [18, 17, 10, 11, 1].

Heritability in the broad sense is the ratio of genotypic variance to the total phenotypic variance and is used as an index for the transmission of characters from parents to their progenies. In this study, PHT, CPP and SYP exhibited high heritability. The remaining traits exhibited low heritability. However, heritability itself does not provide any indication towards the amount of genetic progress that would result in selecting the best individual; rather it depends upon the amount of genetic advance. In the present study low heritability coupled with low genetic advance was recorded for BLL, BLW, TLL, TLW and TSW. Low heritability combined with low genetic advance was noted for TSW by Singh *et al*. (2018) and Shekhawat *et al*. (2013) [17]. Moderate heritability estimates were observed for DTIF, DFF and DTM. High heritability coupled with high genetic advance was observed for CPP and SYP, while PHT had high heritability coupled with moderate genetic advance indicating the role of both additive and non-additive gene action. High heritability and high genetic advance for seed yield and capsules per plant has also been reported by Sumathi and Muralidharan (2010), Chandramohan (2011), Ismaila and Usman (2014), Bharathi *et al.* (2014), Saxena and Bisen (2017), Divya *et al.* (2018), Singh *et al.* (2018), Kadvani *et al.* (2020), Mohanty *et al.* (2020), Kant *et al.* (2021) and Aboel Kassem *et al.* (2021) [18, 15, 8, 5, 17, 10, 11, 1]. Traits exhibiting high heritability coupled with high genetic advance are amenable for improvement through simple phenotypic selection. In conclusion, the results of the present study suggested that plant height (PHT), number of capsules per plant (CPP) and seed yield per plant (SYP) were the most important traits to be considered for seed yield improvement in sesame.

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