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Research Article

Genetic variability studies for yield and yield components in sesame (*Sesamum indicum L.*)

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Abstract
Sesame (*Sesamum indicum* L.) is one of the oldest oilseed crops and is widely cultivated in India and Worldwide. The present investigation was carried out to evaluate the sesame genotypes using 18 traits to elucidate the information on the amount of variability on yield and with yield attributing traits. Based on the variability parameters such as ANOVA (Analysis of variance), Phenotypic and Genotypic Coefficient of Variations (PCV, GCV) the selected yield contributing traits were number of capsules per plant, capsule length, number of seeds per capsule, 1000 seed weight, oil content and single plant yield. Heritability studies revealed that all the traits except capsule width and single plant yield showed high heritability, indicating heritability was mostly due to additive gene action. Genetic advance as per cent of mean was high for all the traits except plant height, capsule width and single plant yield. Based on the study, heritability was mostly due to additive gene action. Selection for highly hertitable and high genetic advance as per cent of mean traits may be effective for the improvement of sesame.

Key words
PCV, GCV, Heritability, Genetic advance, Sesame

Introduction

Sesame, considered to be one of the oldest crops and is widely cultivated in Asia and Africa (Kurdistani and Tohidinejad, 2011). Sesame is grown in many parts of the World; Asia is rich in diversity of cultivated sesame while Africa is prosperous in wild relatives (Sharma *et al.,* 2014). Sesame is the key source of edible oil and is widely used as one of the ingredients in food products especially in bakery foods and animal feed. Composition of sesame oil is quite unique as it contains both oil (57 to 63 per cent) and high amount of protein about 25.18 per cent (Alege and Mustapha, 2013). Amino acids like methionine and tryptophan are missing in many of vegetable protein and sesame is rich in these amino acids enhances the quality of the crop (Quasem *et al.,* 2009). Sesame oil is known to be resistant to natural oxidation, attributed to anti-oxidation activity of sesame lignans (Fukuda *et al.*, 1986).

India occupies second position in area and production of oilseed crops in the World next to Myanmar. Yield is the most important trait for any crop improvement. Since, yield is a complex trait controlled by many genes, yield can be enhanced by improving the yield contributing traits. The success of any crop improvement program depends upon the nature and magnitude of genetic variability present in the crop. High level of polymorphism in sesame has been reported earlier regarding its morphology (Sarkar and Saha, 2014). The characterization and evaluation are the important pre-requisites for effective utilization of germplasm and also to identify sources of useful genes. An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme because the presence of considerable genetic variability in the base material ensures better chances of evolving desirable plant type. Hence, the present investigation was undertaken to study the variability parameters among sesame genotypes to formulation of suitable selection indices for improvement in this crop.

Material and Methods

The experimental material consists of 53 genotypes from various geographical origins collected from

Regional Research Station, Vridhachalam and Department of Oil seeds, TNAU, Coimbatore and National Bureau of Plant Genetic Resources, Thrissur were listed in Table 1. Fifty three genotypes were raised in randomized block design (RBD) with two replications at specimen plot at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, Tamil Nadu during *Kharif*, 2014. Eighteen yield contributing traits were measured in five randomly selected plants from each replication in each genotype, to assess the magnitude of heritable variability among the sesame genotypes. The characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of primary branches, number of secondary branches, basal leaf area, basal petiole length, mid leaf area, mid petiole length, top leaf area, top petiole length, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, 1000 seed weight, oil content and single plant yield were recorded for this study. Leaf area is calculated by measuring mean length and width of five leaves from the main stem of randomly selected five plants; multiplied with a constant value of 0.3552 (Silva *et al*., 2002). Oil content was estimated using Soxhlet extractor installed at the Department of Food Science and Technology, Home Science College and Research institute, Madurai. The mean value of five random plants in each genotype in each replication was used for the analysis of variance as suggested by Panse and Sukhatme, 1961. Phenotypic and genotypic variances were estimated according to the formula given by Lush (1940). Phenotypic and genotypic coefficients of variation were computed according to the method suggested by Burton (1952) and traits were classified as having high (>20 per cent), moderate (10 to 20 per cent) or low (<10 per cent) range of variation as per the method suggested by Sivasubramanian and Menon (1973). Heritability in broad sense was calculated as per the formula given by Lush (1940). Range of heritability was categorized as high (>61 per cent), medium (31 to 60 per cent and low (<30 per cent) suggested by Jhonson *et al. (1955)*. Genetic advance was expressed as per cent of mean by using the formula suggested by Johnson *et al*. (1955).

Results and Discussion

Analysis of variance for 18 yield contributing characters was presented in Table 2 and revealed that the presence of significant differences among the genotypes for all the characters under studied, These significant differences could also be attributed to the composition of the population.

Studies on various variability parameters of 53 genotypes for 18 traits is presented in Table 3 and Fig. 1. Present investigation revealed that PCV ranged from 11.90 per cent to 94.18 per cent for days to maturity and number of secondary branches per plant respectively. The maximum GCV was observed to be 92.36 per cent for number of secondary branches whereas capsule width recorded minimum genotypic coefficient of variation of 10.55 per cent. Out of 18 traits, genotypic coefficient of variation was high in number of secondary branches (92.36 per cent), number of primary branches (64.39 per cent), base leaf area (56.43 per cent), top leaf area (48.16 per cent), mid leaf area (45.79 per cent), top petiole length (44.38 per cent), mid petiole length (34.60 per cent) and base petiole length (33.14 per cent) for the plant characters with respect to yield attributes. High GCV estimates for one or more of these traits were reported earlier by Khairnar and Monopara (2013), Bharathi *et al*. (2014). However, the genetic variability was found to be moderate in days to 50 per cent flowering (21.60 per cent), 1000 seed weight (18.95 per cent), number of capsules per plant (16.45 per cent), number of seeds per capsule (14.97 per cent), plant height (11.77 per cent), days to maturity (11.71 per cent), capsule length (11.68 per cent), single plant yield (11.33 per cent) and capsule width (10.55 per cent) indicating the accountable utility of these traits in selection programme. This is similar to the earlier findings of Bharathi *et al*. (2014) and Desawi Hdru Teklu *et al.* (2014).

The simple measures of variability like mean and coefficient of variation reveal the extent of variability but not the heritable portion of the total variation. To have the knowledge of heritable portion of variability, it is necessary to estimate the heritability of each character. The broad sense heritability gives an idea about the portion of observed variability attributable to genetic difference. The estimated values for heritability (broad sense) and genetic advance as per cent of mean for 53 sesame genotypes are tabulated in Table 3 & Fig. 2. All the characters studied in this research invariably showed high heritability (more than 60 per cent) except capsule width (48.32 per cent) and single plant yield (27.2 per cent). Oil content was observed to be the most heritable trait wit highest heritability (99.76 per cent) followed by base leaf area (98.32 per cent).

Heritability was least for single plant yield (27.2 per cent) among the 53 sesame genotypes studied, similar results of heritability for different traits were reported in sesame by Bharathi *et al.* (2014) and Desawi Hdru Teklu *et al.* (2014), whereas moderate heritability was observed by Jhansi Rani and Rama Kumar (2013) for single plant yield and low heritability by Sumathi and Muralidharan (2010) for capsule width. By considering variability and heritability estimates, the per cent genetic advance of mean is expected for the yield attributes, number of capsules per plant (28.87 per cent), capsule length (20.14 per cent), number of seeds per capsule (27.88 per cent), 1000 seed weight (34.71 per cent), oil content (35.56 per cent) and single plant yield (12.17 per cent). The traits plant height exhibited high heritability with moderate genetic advance as per cent of mean, capsule width moderate heritability and genetic advance as per cent of mean and single plant yield showed low heritability with moderate genetic advance as per cent of mean whereas all other traits recorded high heritability coupled with high genetic advance as per cent of mean indicating the scope for improvement and genetic gain through the selection for these traits, as earlier reported by Khairnar and Monopara (2013), Bharathi *et al.* (2014) and Desawi Hdru Teklu *et al.* (2014).

Baset on the present study, it may be conclude that the most important complex economic trait single plant yield exhibited low heritability, coupled with moderate genetic advance as per cent of mean, GCV values representing the availability of less variability for this trait. So the traits like number of capsules per plant, capsule length, number of seeds per capsule, seed weight and oil content that has high heritability coupled with high genetic advance as per cent mean and moderate GCV had to be selected simultaneously that will ultimately increase the single plant yield and this selection will be effective for this population.

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Table 1. List of genotypes used for study

Sl. No.	Genotypes	Species	Source
1.	**Mathvi**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
2.	**RT-125**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
3.	**Ponjas Til- 1**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
4.	**Swetha**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
5.	**VRI 2**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
6.	**CO 1**	*Sesamum indicum*	Department of oilseeds, TNAU, Coimbatore, India
7.	**Chandana**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
8.	**Varaha**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
9.	**TMV 3**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
10.	**SVPR 1**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
11.	**Shekar**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
12.	**VRI 1**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
13.	**TMV 7**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
14.	**TMV 4**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
15.	**TMV 6**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
16.	**Thilathara**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
17.	**Hima**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
18.	**TKG- 22**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
19.	**ORM- 17**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
20.	**KMR-77-1**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
21.	**RT- 103**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
22.	**N8**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
23.	**Usha**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
24.	**DS1**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
25.	**Kanak**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
26.	**JLT 7**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
27.	**Thilothama**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
28.	**Pragathi**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
29.	**RT 54**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
30.	**GT- 10**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
31.	**Nirmala**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
32.	**G Til- 1**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
33.	**Krishna**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
34.	**Rajeswari**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
35.	**Kaple**	*Sesamum indicum*	RRS, Vridhachalam, Tamil Nadu, India
36.	***Sesamum anamalyensis***	*Sesamum anamalyensis*	Department of oilseeds, TNAU, Coimbatore, India
37.	***Sesamum radiatum***	*Sesamum radiatum*	Department of oilseeds, TNAU, Coimbatore, India
38.	**TMV 5**	*Sesamum indicum*	Department of oilseeds, TNAU, Coimbatore, India
39.	**IC 199438**	*Sesamum indicum*	NBPGR, Thrissur, India
40.	**IC 205091**	*Sesamum indicum*	NBPGR, Thrissur, India
41.	**TCR 4731**	*Sesamum mulayanum*	NBPGR, Thrissur, India
42.	**IC 208657**	*Sesamum radiatum*	NBPGR, Thrissur, India
43.	**IC 208681**	*Sesamum radiatum*	NBPGR, Thrissur, India
44.	**IC 208680**	*Sesamum radiatum*	NBPGR, Thrissur, India
45.	**TCR 3148**	*Sesamum mulayanum*	NBPGR, Thrissur, India
46.	**TCR 480513**	*Sesamum mulayanum*	NBPGR, Thrissur, India
47.	**TCR 3341A**	*Sesamum malabaricum*	NBPGR, Thrissur, India
48.	**IC 208658**	*Sesamum radiatum*	NBPGR, Thrissur, India
49.	**TCR 4849**	*Sesamum malabaricum*	NBPGR, Thrissur, India
50.	**IC 127324**	*Sesamum indicum*	NBPGR, Thrissur, India
51.	**IC 199435**	*Sesamum indicum*	NBPGR, Thrissur, India
52.	**IC 208660**	*Sesamum indicum*	NBPGR, Thrissur, India
53.	**IC 127325**	*Sesamum indicum*	NBPGR, Thrissur, India

Table 2. Analysis of variance for 18 traits in Sesame

S. No.	Characters	Genotypes Mss	Error Mss	SE	CD	CV%
1.	**Days to 50 per cent flowering**	175.47**	7.90	1.99	5.65	6.64
2.	**Days to maturity**	239.17**	3.92	1.40	3.97	2.14
3.	**Plant height (cm)**	497.46**	117.46	7.66	21.74	9.25
4.	**Number of primary branches**	16.18**	0.50	0.50	1.42	16.27
5.	**Number of secondary branches**	40.92**	0.80	0.63	1.79	18.46
6.	**Basal leaf area(cm^2)**	345.05**	2.93	1.21	3.43	7.39
7.	**Basal petiole length (cm)**	9.87**	0.56	0.53	1.50	11.44
8.	**Mid leaf area (cm^2)**	126.29**	4.36	1.48	4.20	12.25
9.	**Mid petiole length (cm)**	7.82**	0.28	0.37	1.05	9.38
10.	**Top leaf area (cm^2)**	26.94**	1.14	0.75	2.13	14.29
11.	**Top petiole length(cm)**	2.03**	0.26	0.36	1.02	24.12
12.	**Number of capsules per plant**	814.95**	129.47	5.74	16.29	10.11
13.	**Capsule Length (mm)**	20.55**	3.61	0.99	2.81	10.80
14.	**Capsule width (mm)**	1.31**	0.45	0.47	1.33	10.86
15.	**Number of seeds per capsule**	155.95**	15.70	1.94	5.51	7.09
16.	**1000 seed weight(g)**	0.73**	0.09	0.21	0.60	9.74
17.	**Oil Content (%)**	114.91**	0.14	0.26	0.74	0.85
18.	**Single plant yield (g)**	5.82*	3.33	0.63	1.79	18.53

** Significant @ 1% level of significance

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Table 3. Estimation of variability and genetic parameters for 18 traits in *Sesamum indicum L.*

S.No.	Characters	Mean	Range		PCV%	GCV%	ECV%	Heritability	Genetic Advance	GA as % of mean
			Min.	Max.						
1.	**Days to 50 per cent flowering**	42.37	31.50	73.00	22.60	21.60	6.63	91.38	18.02	42.54
2.	**Days to maturity**	92.61	69.50	120.00	11.90	11.71	2.14	96.77	21.98	23.73
3.	**Plant height**	117.14	60.1	148.10	14.97	11.77	9.25	61.80	22.32	19.06
4.	**Number of primary branches**	4.35	2.00	12.50	66.41	64.39	16.27	94.00	5.59	128.60
5.	**Number of secondary branches**	4.85	0.00	20.00	94.18	92.36	18.46	96.16	9.05	186.57
6.	**Basal leaf area**	23.18	8.60	72.60	56.91	56.43	7.39	98.32	26.71	115.27
7.	**Basal petiole length**	6.51	2.40	13.30	35.06	33.14	11.44	89.35	4.20	64.53
8.	**Mid leaf area**	17.05	3.10	40.10	47.40	45.79	12.25	93.32	15.54	91.12
9.	**Mid petiole length**	5.61	1.80	12.00	35.85	34.60	9.39	93.14	3.86	68.78
10.	**Top leaf area**	7.46	1.30	20.70	50.23	48.16	14.29	91.91	7.09	95.11
11.	**Top petiole length**	2.12	0.50	5.40	50.51	44.38	24.12	77.20	1.70	80.33
12.	**Number of capsules per plant**	112.53	69.50	151.50	19.31	16.45	10.11	72.58	32.49	28.87
13.	**Capsule Length**	24.92	17.50	33.00	13.95	11.68	7.63	70.09	5.02	20.14
14.	**Capsule width**	6.18	5.00	8.30	15.18	10.55	10.91	48.32	0.93	15.11
15.	**Number of seeds per capsule**	55.92	38.50	75.50	16.57	14.97	7.09	81.71	15.59	27.88
16.	**1000 seed weight**	3.00	1.920	4.16	21.31	18.95	9.74	79.09	1.04	34.71
17.	**Oil Content**	43.83	25.66	54.25	17.30	17.28	0.85	99.76	15.59	35.56
18.	**Single plant yield**	9.85	7.13	15.19	21.72	11.33	18.53	27.20	1.20	12.17

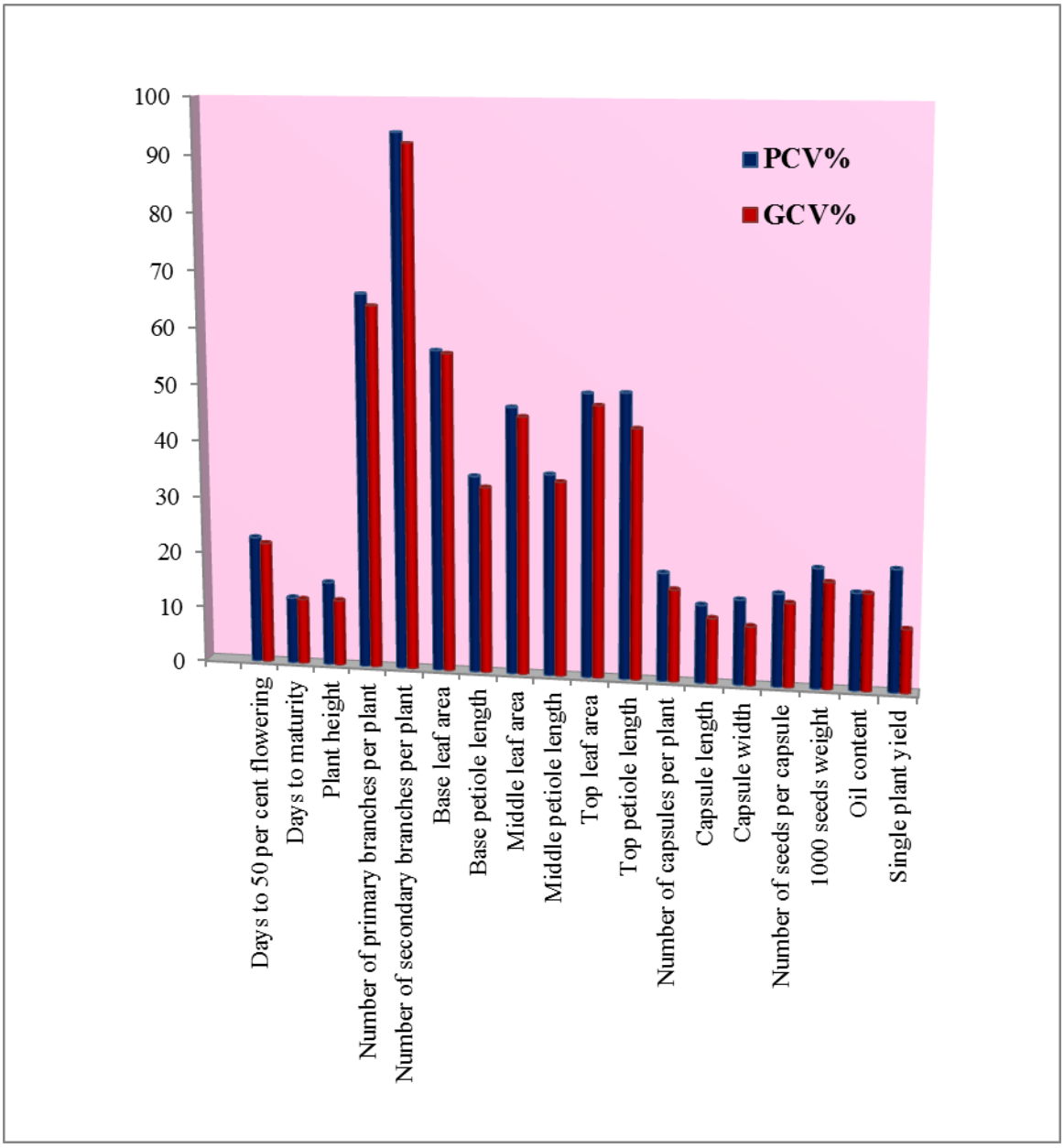

Fig. 1. Estimation of variability and genetic parameters for eighteen quantitative traits in Sesame (*Sesamum indicum L*)

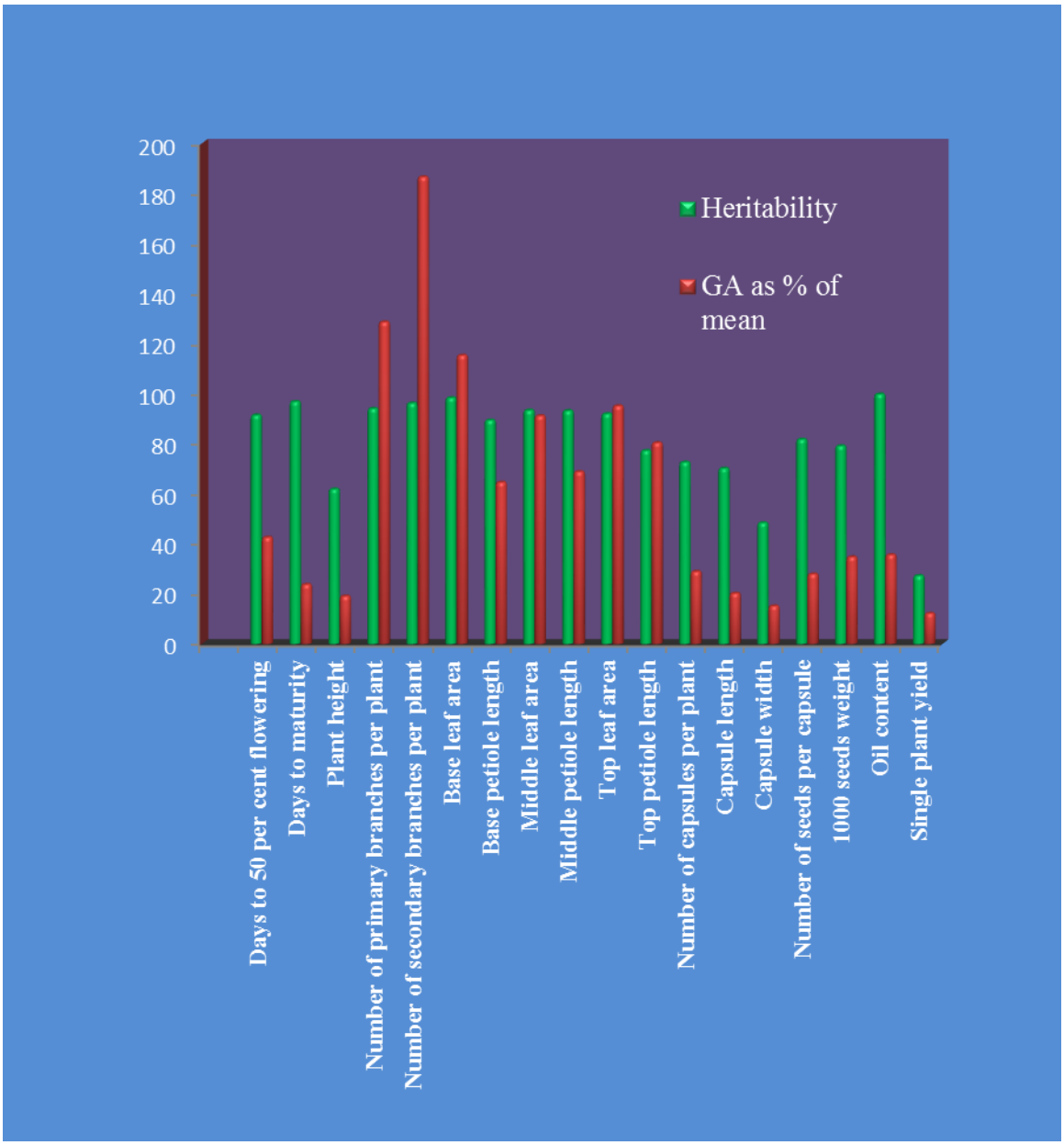

Fig. 2. Estimation of Heritability and Genetic advance as per cent mean for eighteen traits of *Sesamum indicum L*