

Original Research Article

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Genetic Variability, Heritability and Genetic Advance in Sesame (*Sesamum indicum* L) Genotypes

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ABSTRACT

Sesamum (*Sesamum indicum* L) is the most cultivated oil crop in India. It has great diversity across the Indian biota. The existing variability would be utilized for the commercial purpose of sesame. The purpose of the study is to evaluate the morphological characterization and variability available in the sesame genotypes available in Tamil Nadu. Fifteen sesame genotypes were grown during Rabi Summer 2018 at Agricultural College and Research Institute, Kudumiyamalai (TNAU) for the estimation of genotypic and phenotypic coefficient of variation along with heritability and genetic advance. Eight biometrical and morphological traits were recorded for fifteen genotypes. High PCV and GCV are recorded for the traits viz., number of branches per plant, seed yield per plant and total number of capsules per plant. High heritability and genetic advance was observed for the characters number of branches per plant, number of capsules per plant, seed yield per plant, plant height, plot yield, 1000 seed weight and number of seeds per capsules. The traits with high heritability and high genetic advance as percent of mean are governed by the additive gene action where simple selection is effective for breeding programmes.

Keywords

Sesame genotypes,
GCV, PCV,
Heritability,
Genetic advance

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Introduction

Sesamum (*Sesamum indicum*. L) is the ancient oil seed crop widely cultivated in Asia and Africa. The cultivated species of sesame, *Sesamum indicum*. L is proved to be domesticated in India around 5000B.C based on the archeological evidence of charred sesame found in Harappa civilization (Ali Al-

Somain *et al.*, 2017; Bedigian, 2003). The wild relatives and probable progenitor of sesame would be *Sesamum malabaricum*, rooted its origin in India, are the appropriate reason for the varying diversity found in India, despite the fact that the majority of the wild species of the genus *Sesamum* are native to sub-Saharan Africa. Sesamum, the favored oil crop, has much utility because of the edible

seed and quality oil content used in various Indian cuisines for its flavorsome. Sesamum seed contains 20% proteins high amounts of (83% - 90%) unsaturated fatty acids, mainly linoleic acid (37% - 47%), oleic acid (35% - 43%), palmitic (9% - 11%) and stearic acid (5% - 10%) with trace amount of linolenic acid, and also high oil content (46% - 50%), 20% proteins, carbohydrates (Pal, Khanum, and Bawa, 2010). Apart from these, a group of special health benefitting compounds called lignans (sesamin, sesamol, sesaminol and sesamolol), tocopherol, phytosterols, phytates and some other micronutrients are also present (Bedigian, (2003); Brar and Ahuja, (1980); Fukuda *et al.*, (1985); Pathak *et al.*, (2014). Sesame is said to be a drought tolerant crop because of its long tap root system which makes it a promising oil crop for tropical and subtropical. Though India ranks first in acreage and production in sesame, the low productivity has always made sesame to be a marginal crop (NMOOP, 2015).

Low yield level is due to lack of wider adaptability, non-synchronous maturity, non-availability of superior high yielding varieties with built in resistance to biotic and abiotic stresses and presence of pre and post fertilization barriers (Rao *et al.*, 2002). Lack of sufficient researches unlike cereals is also a reason for under development of this crop. India being rich in the genetic variability of genus, *Sesamum*, exploiting of variability would come hand in hand in the improvement of genetics background of the crop. Enriching the details of the genetic diversity available in the genus *Sesamum* of Indian origin greatly helps in the selection of parent base material for hybridization and development of high yielding varieties suitable to various geographical situations. The present study aimed in analyzing of genotypic and phenotypic variability, heritability and genetic advance of biometrical morphological

characters of fifteen sesame genotypes which could provide a wide magnitude of genetic parameters for selection in sesame breeding programme.

Materials and Methods

In this present study, fifteen genotypes were selected including 11 advance sesame culture of Tamilnadu Agricultural University and one local variety and three checks varieties (Table 1). The experiment was conducted in Agricultural College and Research Institute (Tamil Nadu Agricultural University), Kudumiyamalai, Pudukkottai District of Tamil Nadu during Rabi Summer 2018. The genotypes were sown in Randomized Block Design (RBD) with 2 replications in 4 rows of length 5 meter and breadth of 0.3 meter covering an area of 6m² for a genotype. The plants are grown with inter-row spacing of 30 cm and inter plant spacing with 30 cm (30 cm x 30 cm). All the recommended Agronomic practices like thinning, weeding were practiced for raising the healthy plants. Five plants were randomly selected and biometrical observations were recorded on eight quantitative characters *viz.*, days to fifty per cent flowering, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, thousand seed weight(gm), seed yield per plant (g) and plot yield (g). Observations on each characters contributed to the genetic diversity of the sesame genotypes were calculated using mean, variability (PCV and GCV), heritability and genetic advance.

Statistical analysis

Phenotypic and genotypic variances were estimated according to the formula given by Lush (1940), PCV and GCV were computed based on the methods given by Burton (1952). The coefficients of variation were categorized as proposed by Sivasubramanian and

Madhava Menon (1973). The heritability was computed based on the methods given by Lush (1949). Genetic advance and genetic advance as percentage of mean were estimated according to the formula given by Johnson *et al.*, (1955). Statistical analysis was done by using INDOSTAT software.

Results and Discussion

Mean performance of sesame genotypes based on morphological characters

Based on the mean performances, the genotype COS 14017 (W) which showed early flowering and it could be used in breeding programmes as early flowering was desirable for the benefits that come along with it such as early duration, escape from undesirable characters. In the present study, the genotype COS 14017 (W) was identified as early flowering and early maturing type than the other varieties studied (Table 2). The present study revealed that the genotype COS 14001 had higher mean value for plant height and COS 13015 has higher number of branches per plant, indicating that it could be used in breeding programmes for increasing plant height and number of primary branches per plant. The genotype COS 14001 exhibited high means value for number of capsules per plant followed by COS 14026(W) respectively (Table 2). High mean value for capsule length was recorded in COS14017 (DW) and COS 13015 highest number of seeds per capsule. TMV 7 showed high mean value for 1000 seed weight, recorded high mean value for seed yield per plant followed by the genotypes TMV 7 (Table 2). These genotypes can be used as donors in plant breeding programmes. The genotypes COS14017 and COS14018 were found to be the monopodial sesame genotype along with the seed characters. High yield was found to be recorded in COS13006 followed by COS 13015. The genotype COS 13015 was recorded for high yielding variety

with maximum recorded for number of seeds per capsule ranging upto 84 seeds per capsules and these capsules are 4 and 6 loculed (Table 2). These sesame genotypes can advanced as high yielding varieties in plant breeding programmes.

Genetic variability, phenotypic and genotypic co-efficient of variation

In the present study, all the quantitative characters that were studied *viz.*, days to fifty per cent flowering, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, thousand seed weight, seed yield per plant and plot yield shows significance difference for all the genotypes under study which indicates that there are sufficient genetic variation exist among the genotypes which could eligible for further breeding programmes. The variation analysis of different quantitative traits under study showed that the Phenotypic Coefficient of Variation (PCV) is higher than the Genotypic Coefficient of Variation (GCV) among the genotypes with the minimum environmental interference exhibiting greater performance (Table 3). The traits number of branches per plant (Gidey *et al.*, 2013; Saha *et al.*, 2012; Sudhakar *et al.*, 2007) followed by seed yield per plant (Sudhakar *et al.*, 2007; Sumathi and Muralidharan, 2011) and total number of capsules per plant (Parameshwarappa, *et al.*, 2009; Singh, *et al.*, 2018) showed higher PCV and GCV estimates. It indicated that there was greater diversity for these traits in sesame. Hence, direct selection based on these traits would be effective for the improvement of this crop. The PCV and GCV are medium for plant height, number of seeds per capsule, thousand seed weight and plot yield. Days to maturity had low PCV and GCV estimates indicating low scope of selection for improvement. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse

populations. In the present study, high heritability was observed for the characters number of capsules per plant, seed yield per plant, plot yield, plant height, number of seeds per capsule, Total number of branches per plant and thousand seed weight (Dash *et al.*, 2018; Mahalakshmi K. Patil *et al.*, 2017). This indicates that selection for these characters would give the best results for selecting sesame genotypes with these traits with high heritability. Days to 50% flowering has medium heritability. Relative comparison of heritability estimates along with genetic advance as percent of mean would give an idea about the nature of gene action governing a particular character, improving the effectiveness selection which is estimated based upon the heritability, genetic variability and selection intensity (Allard, 1960). High genetic advance as percentage of mean was

observed in number of branches, number of capsules per plant, seed yield per plant (Bharathi, *et al.*, 2014; Gidey *et al.*, 2013), plant height, plot yield, 1000 seed weight and number of seeds per capsules. Low genetic advance as percentage of mean was observed in case of Days to 50% flowering. High heritability coupled with high genetic advance was observed for the characters number of branches, number of capsules per plant, seed yield per plant, plant height, plot yield, 1000 seed weight and number of seeds per capsules (Thirumala Rao *et al.*, 2013). This showed that these characters were controlled by additive gene action and revealed better scope for improvement of these characters through direct selection. Low heritability and low genetic advance is noted for days to 50% flowering where excising of selection would impart no advantage.

Table.1 List of genotypes studied under the experiment

Sl. No.	Genotypes
1.	COS13006
2.	COS13015
3.	COS14001
4.	COS14017(W)
5.	COS14017(DW)
6.	COS14018
7.	COS14025
8.	COS14026
9.	COS14026(W)
10.	COS16007
11.	COS16009
12.	GT10
13.	TMV 7
14.	SVPR 1
15.	NAYAKARPATTI LOCAL

W – white; DW – dull white

Table.2 Mean Performance of yield and yield related traits of fifteen sesame genotypes

Genotype	Days to fifty percent flowering	Plant height	Total No. of branches per plant	Total	No. of seeds per capsule	Thousand seed weight(g)	Seed yield per plant(g)	Plot yield(g)
		(cm)		No. of capsules per plant				
COS13006	41.0	133.30	3.7	173.50	73.0	3.165	19.65	640.5
COS13015	34.0	123.00	6.1	240.10	82.0	3.435	19.30	594.5
COS14001	36.0	148.00	5.1	240.20	62.4	3.500	16.70	510.0
COS14017(W)	32.0	122.80	1.0	158.50	73.0	2.955	20.30	530.0
COS14017(DW)	33.0	122.00	4.5	150.50	73.4	2.940	20.85	550.0
COS14018	33.0	136.30	1.0	171.00	68.2	3.365	20.55	598.0
COS14025	37.0	137.00	4.0	200.25	62.4	3.510	19.45	594.0
COS14026	34.0	106.55	1.7	161.10	70.9	2.785	15.15	422.0
COS14026(W)	33.0	97.80	1.8	108.30	72.0	3.115	13.80	527.0
COS16007	36.0	92.00	4.1	186.00	60.4	3.225	13.60	560.0
COS16009	41.0	132.80	4.6	227.60	65.4	2.680	12.75	545.0
GT10	36.0	87.20	3.8	202.50	68.2	2.615	10.10	420.0
TMV 7	36.0	120.80	5.0	135.80	50.4	3.840	11.60	540.0
SVPR 1	34.0	104.70	4.5	122.60	66.8	2.600	10.95	535.0
NAYAKARPATTI LOCAL	35.0	105.00	6.0	116.45	76.4	2.415	9.10	410.0

Table.3 Estimation of Variability, heritability and Genetic Advance

<i>Characters</i>	<i>mean</i>	<i>Range</i>	<i>PCV (%)</i>	<i>GCV (%)</i>	<i>Heritability (h²)</i>	<i>Heritability (%)</i>	<i>GA(% of Mean (%))</i>
Days to 50 % flowering	35.40	32-41	8.779	6.226	0.503	50.3	9.10
Plant height	117.95	87.2-148	15.535	15.302	0.970	97.0	31.10
Total No. of branches per plant	3.79	1-6.1	45.605	42.461	0.867	86.7	81.43
Total No of capsules per plant	172.96	108.3 - 240.2	24.945	24.840	0.992	99.2	51.00
No. of seeds per capsule	68.33	50.4 - 82	11.338	10.882	0.921	92.1	21.51
1000 seed weight	3.08	2.415 - 3.84	14.146	12.414	0.770	77.0	22.44
Seed yield per plant	15.59	9.1 - 20.85	26.950	26.822	0.990	99.0	55.00
Plot yield	531.73	410 - 640.5	12.907	12.775	0.980	98.0	26.05

High heritability coupled with high genetic advance was observed for the characters seed yield per plant, number of seeds per capsule, number of capsules per plant, number of branches per plant, plant height. This showed that these characters were controlled by additive gene action and revealed better scope for improvement of these characters through direct selection.

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