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Genetic variability, heritability and genetic advance studies in sesame (*Sesamum indicum* L.)

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Abstract

This trial conducted on 27 elite lines were used for the studies of genetic variability, heritability and genetic advance as % of mean with 12 yield and attributing traits. The experiment was operated at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). The field lay out was done in Randomized Block Design with three replications. Highly significant differences found for all 11 traits except yield/plot. No. of seeds per capsule followed by internode length and seed yield (kg/ha) observed moderate level of GCV and PCV values indicating relatively moderate contribution of these characters towards genetic variability. Heritability in broad sense were high (80%) for three (internode length followed by oil content and no. of seeds per capsule) characters. The genetic advance % of mean were high in internode length followed by no. of seeds/capsules and seed yield/ha. High heritability coupled with high genetic advance as per cent over mean was also observed for characters such as internode length followed by no. seeds per capsule. Based on the study, heritability was mostly due to additive gene action. Selection for highly heritable and high genetic advance as per cent of mean traits may be effective for the improvement of sesame.

Keywords: PCV, GCV, heritability, genetic advance, sesame

Introduction

Sesame (*Sesamum indicum* L.) also known as Til or Gingelly etc. It is oldest and ancient oilseed crops known to man. Seeds and its oil are being utilized as important food ingredients. The name, sesame, derives from the Arabic word "simsim".

It is cultivated extensively from tropical regions to the temperate region of the world.. It is referred as "Queen of oilseeds" due to its resistance to oxidation and rancidity, also plays an important role as an industrial food crop because of its high nutritional value. The seeds of sesame contains (40 to 63% oil and 25% protein). Sesame seed oil has long shelf life due to the presence of lignans (Sesamin, Sesamol, Sesamolol) Kiruthika *et al.* (2018) [9], which have remarkable antioxidant function, resisting oxidation and has a significant amount of oleic and linoleic acids (Abate and Mekbib, 2015) [1]. Sesame seed is consumed as a source of calcium, potassium, tryptophan and methionine. Sesame oil has highest antioxidant content and contains several fatty acids such as oleic acid (43%), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%) (Yogranjan *et al.* 2015) [22].

Genetic variation survives for agronomically vital characters in sesame but its production is still very low in India. Traditional sesame landraces as well as related wild species are an important source of genetic diversity for breeders and form the backbone of agricultural production. Selection for high yielding types with wider adaptability shall help in increasing the production both locally and globally. But the performance of crop is affected by such factors as climatic, nutrients, water availability, inter and intra specific competitions, pest and diseases, as well as socio-cultural and socioeconomic factors. The knowledge of genetic variability in germplasm will help in the selection and breeding of high yielding, good quality cultivars that will increase production. It is necessary to study variability in respect of quantitative characters with reference to genetic parameters such as genotypic and, phenotypic variances, heritability (broad sense) and genetic advance. According to Johnson *et al.* (1955) [8], high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone.

Materials and Methods

The experimental material consists of 27 genotypes collected from All India Coordinated Research Project on Sesame & Niger (ICAR), JNKVV Campus, Jabalpur, Madhya Pradesh. They were selected on the basis of duration, suitable for Kharif season and yield. The field lay out was done in Randomized Block Design with 3 replications. Each entry was represented by a 08 row per plot of 2.4 m length with a Row-to-Row spacing of 30 cm and plant to plant spacing of 10 cm. The experiment was conducted in a well prepared field during *khariif* 2016-17 at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). The crop was raised under recommended package of practices along with prophylactic protection measures. Observations were recorded on Days to 50% flowering, Internode length, Number of capsules per plant, Capsule Length, Plant height (cm), Days to maturity, Plant stand per plot, Number of seeds per capsule, 1000-seed weight(g), Oil

Content, Seed Yield per Plot (gm) and seed yield (kg/ha). The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme (1967) [12]. The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane (1953), Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean basis as described by Allard (1960) [2] and Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955) [18].

Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes in respect of all the traits (Table 1) thereby indicating presence of wide genetic diversity.

Table 1: Analysis of Variance for 12 quantitative and qualitative characters in Sesame

S. No.	Characters	Mean Sum of Square		
		Replication	Treatments	Error
		Degree of freedom	26	52
1	Days to 50% flowering	5.2716	40.6648***	7.4639
2	Internode length cm	0.3738	4.4715***	0.1359
3	No. of Capsules/ Plant	1.9259	76.4957***	26.2208
4	Capsule length (cm)	0.0181	0.1242***	0.0128
5	Plant height (cm)	0.1446	117.5497***	32.3674
6	Days to maturity	3.8148	15.1624***	2.5199
7	Plant stand per plot	5.2438	60.9829***	15.3881
8	No. of seeds per capsules	1.1481	46.2650***	2.1353
9	1000 seed weight(g)	0.0015	0.0251***	0.0063
10	Oil Content (%)	2.152	38.9042***	1.1893
11	Seed Yield/ plot(g)	359.4197	372.109	218.8132
12	Seed Yield (kg/ ha.)	2490.4568	22779.7734***	3354.6748

Variance components and coefficients of variation

Higher values of PCV and GCV were noted for internode length, no. of seeds per capsule and seed yield (kg/ha) while high value PCV and low value of GCV recorded for no. of capsules per plant (Table 2). The similar results were reported by Reddy *et al.* (2001) [14], Solanki and Gupta (2004) [17], Banerjee and Kole (2006) [5], Parameshwarappa *et al.* (2009) [13], Sumathi and Muralidharan (2010) [19], Akbar and Shinwari (2011) [3], Gidely *et al.* (2012) [6], Ismaila and Usman (2012) [7], Narayanan and Murugan (2013) [11], Teklu

et al. (2014) [20], Abate and Mekbib (2015) [1], Sabel *et al.* (2015) [15], Saxena and Bisen (2017) [16] for internode length, no. of capsules per plant, no. of seeds per capsule and seed yield (kg/ha). For all characters, PCV was higher than GCV with narrow difference indicates that environment influenced considerably in expression of these traits. Similar type of results is reported by Gidely *et al.* (2012) [6], Ismaila and Usman (2012) [7], Sabel *et al.* (2015) [15] and Abate and Mekbib (2015) [1].

Table 2: Mean, Range, Genotypic and Phenotypic coefficient of variation for 12 quantitative and qualitative characters in Sesame

S. No.	Characters	Grand mean (\bar{X}) + SE (m)	Range		Coefficient of Variation		C.V. (%)
			Min.	Max.	GCV	PCV	
1	Days to 50% flowering	52.02 ± 1.58	45.00	59.67	6.39	8.27	5.25
2	Internode length cm	6.59 ± 0.21	3.67	10.20	18.24	19.08	5.59
3	No. of Capsules/ Plant	57.52 ± 2.96	45.67	66.67	7.12	11.40	8.90
4	Capsule length (cm)	2.27 ± 0.07	1.90	2.70	8.49	9.84	4.98
5	Plant height (cm)	88.58 ± 3.28	79.83	102.27	6.02	8.80	6.42
6	Days to maturity	89.37 ± 0.92	86.67	94.67	2.30	2.90	1.78
7	Plant stand per plot	175.48 ± 2.26	167.33	187.00	2.22	3.15	2.24
8	No. of seeds per capsules	20.81 ± 0.84	10.67	26.33	18.43	19.72	7.02
9	1000 seed weight(g)	3.23 ± 0.05	3.10	3.47	2.45	3.47	2.45
10	Oil Content (%)	46.17 ± 0.63	36.47	51.20	7.68	8.04	2.36
11	Seed Yield/ plot(g)	377.80 ± 8.54	355.00	395.67	1.89	4.35	3.92
12	Seed Yield (kg/ ha.)	564.46 ± 33.44	420.67	754.33	14.26	17.56	10.26

Heritability and genetic advance

The heritability in broad sense values were ranged from 38.99 (no. of capsules per plant) to 91.41 (internode length). High heritability estimates were observed for Internode length, Oil content, No. of seeds per capsules (Table 3). Hence these traits might be governed by additive genes indicating that direct selection would be effective from present genotypes. These results are in accordance with the findings of Babu *et al.* (2005) [4], Gidely *et al.* (2012) [6], Teklu *et al.* (2014) [20], Parameswarappa *et al.* (2009) [13], Narayanan and Murugan (2013) [11], Behra (2016), Saxena and Bisen (2017) [16],

Tripathy *et al.* (2016) [21], Sumathi and Murlidharan (2009), Kiruthika *et al.* (2018) [9] for one or more characters. The Moderate heritability estimates were recorded in capsule length, seed yield/plot, seed yield/ha and 1000 seed weight. Moderate to high heritability indicates that though the character is least influenced by the environmental effects, the selection for improvement of such trait may not be useful, because h^2_b is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistatic) variance.

Table 3: Heritability (%) in broad sense, genetic advance and genetic advance in percent of mean for 12 quantitative and qualitative characters in Sesame

S.N.	Characters	Heritability (Broad Sense)	Genetic Advance	Genetic Advance % of Mean
1	Days to 50% flowering	59.72	5.3	10.18
2	Internode length cm	91.41	2.37	35.93
3	No. of Capsules/ Plant	38.99	5.27	9.16
4	Capsule length (cm)	74.42	0.34	15.09
5	Plant height (cm)	46.73	7.5	8.47
6	Days to maturity	62.58	3.35	3.74
7	Plant stand per plot	49.69	5.66	3.23
8	No. of seeds per capsules	87.32	7.38	35.47
9	1000 seed weight(g)	50.04	0.12	3.57
10	Oil Content (%)	91.36	6.98	15.12
11	Seed Yield/ plot(g)	65.87	6.41	1.70
12	Seed Yield (kg/ ha.)	65.87	134.54	23.83

The result expressed that genetic advance % of mean (Table 3) high in internode length followed by no. of seeds/capsules and seed yield/ha. These findings were found in agreement with the result reported by Babu *et al.* (2005) [4], Gidely *et al.* (2012) [6], Teklu *et al.* (2014) [20], Parameswarappa *et al.* (2009) [13], Narayanan and Murugan (2013) [11], Saxena and Bisen (2017) [16], Tripathy *et al.* (2016) [21], Sudhakar *et al.* (2007), Reddy *et al.* (2001) [14], Mubashir *et al.* (2007), Ismaila and Usman (2012) [7] for one or more traits and genetic advance % of mean moderate for oil content (15.12%) followed by capsule length (15.09%) and days to 50% flowering (10.18%) similar result obtained for one or more traits by Babu *et al.* (2005) [4], Gidely *et al.* (2012) [6], Teklu *et al.* (2014) [20], Parameswarappa *et al.* (2009) [13], Narayanan and Murugan (2013) [11], Saxena and Bisen (2017) [16], Tripathy *et al.* (2016) [21], Abate and Mekbib (2015) [1], Sumathi and Murlidharan (2009) else trait are showed low genetic advance % of mean. The high value of genetic advance was showed that the character was governed by additive genes and selection will be rewarding for improvement of such trait.

High heritability coupled with high genetic advance as per cent over mean was also observed for characters such as internode length and no. seeds per capsule (Table 3), this indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance and selection may be effective. Similar results were reported by Gidely *et al.* (2012) [6], Teklu *et al.* (2014) [20], Parameswarappa *et al.* (2009) [13], Narayanan and Murugan (2013) [11], Saxena and Bisen (2017) [16] and Tripathy *et al.* (2016) [21] for one or more traits. High heritability coupled with moderate genetic advance as % of mean recorded for oil content. Similar result reported by Abate and Mekbib (2015) [1]. Moderate heritability coupled with high genetic advance as % of mean recorded for seed yield (kg/ha). Parallel result confirmed by Teklu *et al.* (2014) [20].

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