International Journal of Current Agricultural Research Vol. 2, No.11, PP. 052-055, November, 2013
http://www.wrpjournals.com/journals/V/IJCAR

Full Length Research Article

STUDIES ON VARIABILITY AND HERITABILITY IN SESAME (*Sesamum indicum* L.)

***Narayanan, R. and Murugan, S.**

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar – 608002

Accepted 13th, October, 2013; Published 30th, November, 2013

Fifty sesame genotypes collected from various parts of Tamilnadu in main cropping season. The objective of the study was to estimate the phenotypic variability and the amount of heritability observed in each character. Analysis of variance revealed that there was highly significant difference among the 50 genotypes for all the characters studied ($p<0.01$). High Phenotypic Coefficient of Variation (PCV) was recorded for days to 50 per cent flowering, plant height, number of capsules plant-1, capsule length, number of branches plant-1, number of seeds capsule-1 and seed yield plant-1. High heritability value was observed for all the characters.

Key words: Sesame, phenotype, genotype, variability, heritability, D^2 analysis

INTRODUCTION

Sesame (*Sesamum indicum* L.) is a diploid species with 2n=26 chromosomes (Alemawu *et al., 1998*). It is a self pollinated crop and belongs to the family pedaliacea. It is often called the queen of oil seed crops. It is grown in tropical to the temperate zones from about 40° N latitude to 40° S latitude. It is grown in more than 50 countries in the world. India ranks first in production and one third of the world production. Nearly 30% of the sesame acreage in the world is in India alone (Bedigian and Harlan, 1986). It is a small farmers' crop in the developing countries (Gulhan *et al*., 2004). Its center of origin is thought to be in Africa, Ethiopia (Bedigian and Harlan, 1986). Sesame grows best on the areas which have an altitude of 500 to 800 meter above sea level (masl) and it can grow even upto1250 masl on well drained soils of moderate fertility. It is an annual, occasionally perennial crop. It needs a growing period of 70 to 150 days; usually 100 to 120 days (Nath *et al*., 2000). The optimum pH it requires ranges from 5.4 to 6.7. Good drainage is crucial, as sesame is very susceptible to short periods of water logging. It is intolerant of very acidic or saline soils. Periods of high temperature above 40°C during flowering reduce capsule and seed development. It requires from 600 to 1000 mm amount of water (Nath *et al*., 2000).

All of the world production area is found in developing countries with largest area in India, Maynmar, China, Nigeria, and Uganda (FAO, 1995). Total world production of sesame in 2005 was 9.35 million hectare and 3.7 million metric tons, 70% of which was produced in Asia and 26 % in Africa (FAO, 2008). Sesame seed is used for confectionery, as an important source of edible oil and as a spice. It is also used for pharmaceutical and skin care products and as a synergist for insecticides (Salunkhe and Desai, 1986). The seed contains 50 to 60% oil which has excellent stability due to the presence of natural antioxidants such as sesamolin, sesamin and sesamol (Brar and Ahuja, 1979). The fatty acid composition of sesame oil varies considerably among the different cultivars worldwide (Yermanos *et al*., 1972). The average productivity of sesame is low as compared to other oilseed crops due to the lack of high yielding cultivars, resistance to major insect pests and shattering problem. Since sesame has been treated as less input intensive crop, the role of breeding improved varieties has been considered as promising approach (Ashri, 1988). A potential high harvest, 3600 kg/ha was reported in Nigeria (Uzo and Ojiake, 1981). Selection is an integral part of breeding program by which genotypes with high productivity in a given environment are selected. However, selection for high yield is made difficult by the complex nature of trait in Sesame. Yield per unit area is the end product of components of several yield contributing characters (Singh and Singh, 1973; Sastri, 1974). The polygenic inheritance of yield components makes selection more difficult. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, there is another option to hasten the genetic improvement which is known as indirect selection for yield. So the phenotypic and genotypic variability study play of sesame crop characteristics was quite important for the improvement of the crop. Knowledge on the extent and pattern of genetic and phenotypic variability present in a population and heritability of characters is absolutely essential for improvement of the crop. Besides, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be useful for the breeding program. Little information is generated in sesame genetic diversity and phenotypic variability of land race collections. Therefore, this experiment was initiated to gather information on variability, heritability and genetic advance in 50 genotypes of sesame for 8 characters.

Corresponding author: Narayanan, R.
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar – 608002

MATERIALS AND METHODS

Experimental Site Description

The experiment was conducted at the Plant Breeding Experimental Farm, Faculty of Agriculture, Annamalai University which is located at Chidambaram, India. The site is located at 11° 24' N latitude and 79°44' E longitude. The altitude of Annamalai Nagar is + 5.79 meter above sea level. The mean annual temperature is 30°C. The minimum annual temperature is 24°C and the maximum annual temperature is 32°C.

Experimental Materials

The experimental material consisted of 50 genotypes or local collections from different regions which are the major growing regions of South India. The accessions were obtained from Tamilnadu

Table 1. List of genotypes studied

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1.	N 8	11.	JLT 28	21.	AKT 101	31.	USHA	41.	PRACHI
2.	DS 1	12.	JT 7	22.	PHULE TIL 1	32.	UMA	42.	THILOTHAMA
3.	RT 103	13.	TKG 21	23.	TR 127	33.	NIRMALA	43.	CHANDANA
4.	T 78	14.	CO 1	24.	TKG 22	34.	TC 289	44.	GAUTAMA
5.	TILAK	15.	GT 1	25.	TKG 55	35.	T12	45.	TMV 6
6.	VINAK	16.	GT 2	26.	JTS 8	36.	T 13	46.	TMV 3
7.	MADHAVI	17.	GT 10	27.	RT 46	37.	T 4	47.	VRI 1
8.	E 8	18.	KAPLI	28.	PKDS 11	38.	THILATHARA	48.	TMV 5
9.	RT 125	19.	TG 25	29.	PKDS 12	39.	PUNJAB TIL 1	49.	SVPR 1
10.	JLT 7	20.	PRAGATI	30.	KANAK	40.	RT 54	50.	TMV 4

Agricultural University, Coimbatore and from Regional Research Stations of Virdhachallam and Tindivanam.

Experimental Design

The trial was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was planted in a plot size of 6 m^2 (5rows, 6 m row length, 45 cm between rows and 15 cm between plants with in row). Other cultural practices like weeding, plant protection and production were followed as recommended for the area.

Data Collection

The following data were collected from the central two rows both per plot and per plant basis.

- Days to 50 per cent flowering - number of days from planting to a stage when 50% of the plants in a plot produced flower and expressed in days.
- Plant height – the aerial part of the stem above ground was measured at the time of harvest and expressed in cm.
- Number of capsules $plant^{-1}$ – the number of capsules was recorded at the time of harvest.
- Capsule length – the length of five randomly selected capsules were measured and averaged to get the unbiased mean value and expressed in cm.
- Number of branches $plant^{-1}$- was measured at the time of harvest.
- Number of seeds per capsule - five random capsule were selected and the number of seeds were counted and averaged to get the unbiased mean value
- 100 seed weight– 100 seeds were randomly selected and weighed and expressed in grams.
- Seed yield $plant^{-1}$–five plants were randomly selected and their full plant yield was estimated and expressed in grams.

Data analysis

Analysis of variance (ANOVA) was conducted using Indostat statistical package.

Estimation of variance components

The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane (1953) as follows:-

Environmental variance (σ^2e) = MSe

$$\text{Genotypic variance } (\sigma^2 g) = \frac{MSg - MSe}{r}$$

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

$$\text{Environmental variance } (\sigma^2 e) = MSE$$

$$\text{Phenotypic coefficient of variation (PCV)} = \sqrt{\frac{\sigma^2 p}{\bar{x}}}\ X\ 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \sqrt{\frac{\sigma^2 g}{\bar{x}}}\ X\ 100$$

Where,

$\bar{x}$= grand mean of a character.

Estimation of heritability in broad sense

Broad sense heritability (h2) expressed as the percentage of the ratio of the genotypic variance (σ^2g) to the phenotypic variance (σ^2p) and was estimated on genotype mean basis as described by Allard (1960) as:

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p}\ X\ 100$$

Estimation of genetic advance

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) as:

$$\text{Genetic advance (GA)} = \frac{K\sqrt{\sigma^2 p\ X \sigma^2 g}}{\sigma^2 p}$$

Where,

k = the standardized selection differential at 5% selection intensity (K = 2.063).

RESULTS AND DISCUSSION

In the present study highly significant differences among sesame genotypes were observed for all traits studied. These findings indicate the presence of large genetic variation among the tested sesame genotypes. Similarly, Arameshwarappa *et al*. (2009) recorded significant differences among 151 sesame genotypes for days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of capsules/plant, capsule length and number of seeds/capsule, oil content and seed yield/plant. Sumathi and Muralidharan (2010) also reported that thirty hybrids of eleven sesame genotypes and observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, capsule breadth, number of seeds per plant, 100 seed weight, seed yield per plant and oil content and analysis of variance confirmed highly significant

differences among genotypes for all the characters without capsule breadth indicating considerable amount of genetic variation in the experimental materials.

Variance components and coefficients of variation

Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances and phenotypic (PCV) and Genotypic Coefficients of Variation (GCV) are given in Table3. The genetic coefficient of variation ranged from 23.07% for100 seed weight to 62.63% for seed yield plant^{-1}. At the same time the range for phenotypic coefficient of variation was from 29.56% for 100 seed weight to 69.56% for seed yield plant^{-1}. In this study the GCV values were lower than that of PCV, indicating that the environment had an important role in the expression of these characters. Generally quantitative characters or agronomic traits are highly influenced by environment. Similarly, Phenotypic coefficient of variation and genotypic coefficient of variation values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium (Deshmukh *et al*.,1986). Based on this delineation, all the eight characters had high genotypic (GVC) and phenotypic (PCV) coefficients of variation. This finding indicates that selection may be effective based on these characters and their phenotypic expression would be a good indication of genetic potential. There is larges cope for selection based on these characters and the diversity in genotypes provides huge potential for future breeding program.

Similar finding was reported by Sumathi and Muralidharan (2010) for number of primarybranches/plant and seed yield. Arameshwarappa *et al*. (2009) reported similar results considering number of capsules/plant, number of primary branches/plant and number of seeds/capsule where high PCV and GCV values were recorded except for number of capsules/plant that had medium GCV. Solanki and Gupta (2003) and Saravanan and Nadarajan (2003) recorded high coefficient of variation for number of capsules per plant and branches per plant. Furthermore, Vasline *et al*. (2000) reported high coefficient of variation for number of capsules per plant. The difference between PCV and GCV was high for all the eight characters namely days to 50 per cent flowering, plant height, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, number of branches plant^{-1}, 100 seed weight and seed yield plant^{-1}. High difference between PCV and GCV shows high influence of the environment on the characters whereas low difference shows low influence of the environment on the characters. Similar results were found by Arameshwarappa *et al*. (2009).

Heritability and genetic advance

Heritability estimate for characters under study is given in Table 3. Heritability values are helpful in predicting the expected progress to be achieved through the process of selection. Genetic coefficient of variation along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Wright, 1921). Heritability ranged from 49.14% for number of capsules plant^{-1} to 90.17% for number of branches plant^{-1}. According to Singh (2001), heritability values greater than 80% are very high, values from 60 to79% are moderately high, values from 40 to 59% are medium and values less than 40% are low. Accordingly, the characters, like number of branches plant^{-1} and seed yield plant^{-1} had very high heritability. This indicates that selection will be the best step for selecting sesame genotypes having these traits with very high heritability. This is because there would be a close correspondence between the accessions and the phenotype due to the relative small contribution of the environment to the total variability. Similar results were reported by Sumathi and Muralidharan (2009, 2010) for days to maturity. All the remaining characters revealed moderate to high heritability. The range for genetic advance as percent of mean was from 7.02% for 100 seed weight to 44.87%for seed yield plant^{-1} (Table 3). Number of seeds capsule^{-1} (33.82%), plant (31.74%) had moderate genetic advance as a percent mean. The lowest genetic advance as percent of mean was observed for 100 seed weight (7.02%), followed by capsule length (14.98%). This low estimate of genetic advance as apercent mean arises from low estimate of phenotypic variance and heritability. Selection based on those traits with a relatively high GAM will result in the improvement of the performance of the genotypes for the traits. The character, capsule length had moderate heritability and genetic advance on the contrary to the findings of Rajaravindran *et al*. (2000) and Paramasivam (1980). 100 seed weight and capsule length showed very high values of heritability and low to moderate genetic advance as percent of mean. These results are in conformity with the findings of Reddy *et al*. (2001) and Sudhakar *et al*. (2007).

Table 2. Estimates of range, mean, genetic components of variance of sesame genotypes

Trait	Range	Mean	SE	σ^2p	σ^2g	σ^2e
Days to 50 percent flowering	39.20 - 62.43	46.66	7.23	14.8	13.48**	1.32
Plant height	38.16 - 145.06	68.52	5.57	20.22	11.74**	46.48
Number of capsules plant^{-1}	27.73 - 101.33	61.53	2.59	19.82	39.74**	10.08
Capsule length	1.76 - 8.73	2.5	1.44	8.99	5.88**	3.11
Number of seeds capsule^{-1}	46.56 - 76.73	61.86	2.46	21.61	32.47**	9.14
Number of branches plant^{-1}	2.30 - 6.83	6.5	0.76	13.32	12.01**	21.31
100 seed weight	1.61 - 2.99	2.9	0.69	4.37	3.66*	0.71
Seed yield plant^{-1}	3.35 - 7.01	6.67	0.62	24.19	0.61	0.58

Table 3. Estimates of PCV, GCV, heritability, Genetic advance of sesame genotypes

Trait	PCV (%)	GCV (%)	h^2	GA
Days to 50 percent flowering	54.41	41.18	57.30	23.08
Plant height	63.59	48.46	58.06	31.74
Number of capsules plant^{-1}	62.96	44.14	49.14	28.62
Capsule length	42.40	34.29	65.41	14.98
Number of seeds capsule^{-1}	65.74	49.94	57.70	33.82
Number of branches plant^{-1}	51.61	49.01	90.17	26.05
100 seed weight	29.56	23.07	60.87	7.02
Seed yield plant^{-1}	69.56	62.63	81.07	44.87

According to Johnson *et al*. (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study showed that high heritability coupled with high expected genetic advance as percent of mean for plant height, number of capsules plant^{-1}, number of seeds capsule^{-1}, number of branches plant^{-1} and seed yield plant^{-1}. These characters were controlled by additive gene effects and phenotypic selection for these characters would likely to be effective than other characters measured (Sumathi and Muralidharan, 2009). Similar result to the present finding was reported

by Reddy *et al*. (2001) and Krishnaiah *et al*. (2002) for number of primary branches/plant. The result of genetic variability, heritability and genetic advance as percentage of mean confirmed that the characters plant height, number of capsules plant^{-1}, number of seeds capsule^{-1}, number of branches plant^{-1} and seed yield plant^{-1} were important. The greater variability in these characters would give a prime scope for the development of high yielding through selection in the segregating generation.

REFERENCES

Alemawu, G., Terefe, G., Zewdie K. and Weyassa, B. 1998. Lowland oil crops: A three-decade research experiences in Ethiopia. Research Report No. 31, Institute of Agricultural Research, Addis Abeba, pp: 13-18.

Allard, R.W. 1960. Principles of Plant Breeding, John Willey and Sons. Inc., New York Pages: 485.

Arameshwarappa, S.G., Palakshappa, M.G., Salimath, P.M. & Parameshwarappa, K.G. 2009. Studies on genetic variability and character association in germplasm collection of sesame (*Sesamumindicum* L.). Karnataka Journal of Agric. Sci., 22: 252-254.

Ashri, A. 1988. Sesame breeding: Objectives and approaches. In: Oil crops: sunflower, linseed and sesame. Proceedings of 4th Oil Crops Network. Njoro, Kenya.

Bedigian, D. and Harlan, J.R. 1986. Evidence for cultivation of sesame in the ancient world. Economic Botany, 40: 137-154.

Brar, G.S. and Ahuja, K.L. 1979. Sesame: its culture, genetics, breeding and biochemistry p. 245-313. In: Malik, C.P. (ed.). Annual Review of Plant Science, Kalyani publishers, New Delhi.

Burton, G.W. and De Vane, E.H. 1953. Estimating heritability in Tall Fescue from replicated clonal material. Agronomy Journal, 45: 481-487.

Deshmukh, S.N.N., Basuand, M.S. & Reddy, P.S. 1986. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian J. Agric. Sci., 56: 515-518.

FAO Production Year Book. 1995. Food and Agriculture Organization of the United Nations-Rome, vol. 49. p. 113.

FAOSTAT. (2008). FAOSTAT statistical service.Food and Agriculture, Organization of the United Nations, Rome, Italy.

Gulhan Ercan, Melih Taskin and KenanTurgut. 2004. Analysis of genetic diversity in Turkish sesame (*Sesamum indicum* L.) populations using RAPD markers. Genetic Resources and Crop Evolution 51: 599–607.

Johnson, H.W., Robinson, H.F. & Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. Agronomy Journal, 47: 314-318.

Krishnaiah, G., Reddy, K.R. & Sekar, M.R. 2002. Variability studies in sesame. Crop Res., 24: 501-504.

Nath, R., Chakraborty, P. K. & Chakraborty, A. 2000. Effect of microclimatic parameters at different sowing dates on capsule production of sesame (*Sesamum indicum* L.). In: A Tropical Humid Region. Journal of Agronomy and Crop Science, 184: 247–252.

Paramasivam, K., 1980. Genetic analysis of yield and yield components in F2 and F3 generations of sesame (*Sesamumindicum* L.). M.Sc. Thesis, School of Graduate Studies of Tamil Nadu Agriculture University, Coimbatore, India.

Rajaravindran, G., Kingshlin, M. & Shunmagavalli, N. 2000. Heritability and genetic advance in sesame (*Sesamum indicum* L.). Sesame Safflower Newslett., 15: 23-25.

Reddy, P.A.V., Sekar, M.R., Ranganatha, A.R.G. & Dhanraj, A. 2001. Genetic variability and heritability for seed yield and its components in sesame (*Sesamum indicum* L.). J. Oilseeds Res., 18: 173-175.

Salunkhe, D.K. & Desai, B.B. 1986. Post Harvest biotechnology of oilseeds. CRC Press, Boca Raton, Florida. p. 105-117.

Saravanan, S. & Nadarajan, N. 2003. Combining ability studies in sesame. Crop Res., 25: 319-324.

Sastri, A.B. 1974. Path analysis of yield components in Tobacco. Indian Journal of Genetics, 34: 57-58.

Singh, B.D. 2001. Plant Breeding: Principles and Methods. Kalyani Publishers, New Delhi, India, pp: 896.

Solanki, Z.S. & Gupta, D. 2003. Variability and character association among quantitative characters of sesame. J. Oilseeds Res., 20: 276-277.

Sudhakar, N., Sridevi, 0. & Salimath, P.M. 2007. Variability and character association analysis in sesame, *Sesamum indicum,* L.J. Oilseeds Res., 24: 56-58.

Sumathi, P. & Muralidharan, V. 2009. Genetic analysis of the hybrids involving monosystem/shy branching accessions in sesame (*Sesamemun indicum* L.).Electron. J. Plant Breed., 1: 65-69.

Sumathi, P. & Muralidharan, V. 2010. Analysis of genetic variability, association and path analysis in the hybrids of sesame (*Sesamum indicum* L.). Trap. Agric.Res. Ext., 13: 63-67.

Uzo, J.O. & Ojiake, G.V. 1981. Breeding and selection method for sesame on the basis of assessment of major Nigerian sesame strains, F1 hybrids and segregating generations. In: sesamestatus and improvement. Proceedings of expert consultation, Rome.

Vasline, Y.A., Saravanan, K. & Ganesan, J. 2000. Studies on variability heritability and genetic advance for certain characters in mutant populations of sesame (*Sesamum indicum* L.). Sesame Safflower Newslett., 15: 39-43.

Wright, S. 1921. Correlations and causations. J. Agric. Res., 20:557-558.

Yermanos, D.M., Hemstreet, S., Saeeb, W. & Huszar, C.K. 1972. Oil content and composition of the seed in the world collection of sesame introductions. Journal of American Oil Chemistry Society, 49:20-23.

****