

# ASSESSMENT OF CORRELATION, PATH ANALYSIS AND GENETIC VARIABILITY IN SESAME (*Sesamum indicum* L.) ACCESSIONS BASED ON MORPHOLOGICAL AND CAPSULE SHATTERING RELATED CHARACTERS

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## ABSTRACT

The present research work was conducted with thirty five sesame accessions to study sixteen characters and the analysis of variance revealed highly significant differences among the genotypes for all sixteen characters. This indicates the presence of wide genetic variability among the genotypes. High values of PCV and GCV were noted for capsule number per plant, split of capsule before drying, opening of capsule before drying and seed yield per plot. A high heritability coupled with high genetic advance was found in capsules per plant, capsule split and open before drying and seed yield per plot. For most of the character pairs, genotypic correlations were higher than phenotypic correlations. Seed yield showed a highly significant and positive correlation with number of capsules per plant, branches per plant, capsule length, seed weight per capsule and number of seeds per capsule. The highest positive direct effect on seed yield was exhibited by capsules per plant followed by 1000- seed weight and capsule width at narrower side. The 35 genotypes formed eight conglomerates. The average inter-cluster distance varied from 299.29 (between cluster II and VI) to 1622.41(between cluster V and VII).

## INTRODUCTION

Sesame (*Sesamum indicum* L.) is a self pollinated crop with  $2x = 2n = 26$  chromosomes. It belongs to the family *Pedaliaceae*, containing 60 species organized into 16 genera (Ashri 1989; Zhang *et al.*, 2013). The genus comprises of 36 species (Kobayashi, 1981) of which *S.indicum* is one of the oldest oilseed crops grown in India. It has been regarded as a crop of insignificant importance compared to other oil seed crops like groundnut and soybeans probably due to its low harvest index, lack of wider adaptability, susceptibility to diseases, seed shattering at maturity, indeterminate growth habit and non-synchronous maturity. Most of the commercial sesame varieties grown are of indeterminate growth habit with continuous flowering bearing dehiscent capsules (Weiss, 1971; Ashri, 1989). Development of semi shattering sesame genotypes has not received much attention with very few reports till date (Uzun *et al.*, 2013). So rectification of the defect is a way to achieve the improvement of the crop. For this assessment of genetic diversity and effect of different traits to yield is very important. Genetic improvement for seed yield by selection through correlated response entailing several contributing factors which influence seed production both directly and indirectly will be most appropriate. Studies on sesame genetic variability help to combine desirable genes from genetically diverse parents through hybridization followed by selection in segregating generations (Raghuwanshi

and Duhoon, 2005). Keeping the above points in view, this study was carried out to recognize and categorize 35 sesame accessions to choose germplasm with diverse agronomic performances and yield potential with specific reference to capsule shattering characters.

## MATERIALS AND METHODS

The present investigation included 35 sesame accessions which included 26 advanced breeding lines of diverse genetic origin (*i.e* derived from different crosses) and 9 released varieties. Of these 14 were white seeded, 10 brown seeded and 11 were black seeded types. The crop was grown during 2015 kharif in Central Research Station, OUAT, Odisha. The field lay out was done in randomized block design with three replications. The average maximum and minimum temperature during the period was 34°C and 22.9°C respectively. The soil of experimental area was sandy loam with a pH of 5.5 to 6.5. Each entry was represented by a 4 row plot of 2.0 m length with a row-to-row spacing of 0.30 m. All the recommended agronomic package of practices was followed during the conduct of experiment. A total of sixteen characters for yield and its components as well as capsule characters related to shattering were studied. Observations were recorded on twelve quantitative traits, *viz.* days to flowering, days to maturity, plant height, number of branches per plant, number of capsules

per plant, capsule length, capsule width at broader side, capsule width at narrower side, number of seeds per capsule, seed weight per capsule, 1000-seed weight and seed yield per plant. Observations were also recorded on four capsule shattering related traits, viz. capsule split before drying of capsules, capsule split after drying of capsules, capsule open before drying of capsules and capsule open after drying of capsules. Days to flowering, days to maturity and seed yield were recorded on plot basis and observations on other characters were taken from a sample of five randomly chosen competitive plants per plot and averaged for per plant values. Analysis of variance (ANOVA) was carried out on the basis of replication wise plot mean values for individual characters. The total variance was partitioned into components ascribable to replications, genotypes and error by adopting standard analysis of variance technique for RBD design (Panse and Sukhatme, 1954). The phenotypic and genotypic coefficients of variation (%) for different traits were estimated by Burton (1968) method and heritability (in broad sense) for different traits was estimated using the components of variance as suggested by Hanson *et al.* (1956). The expected genetic advance or genetic gain due to selection for different quantitative traits was estimated using the formula suggested by Johnson *et al.* (1955). Using the variance and covariance components, the genotypic and phenotypic correlations between two characters (X and Y) were computed following Al-Jibouri *et al.* (1958). The path coefficients were obtained by solving simultaneous equations which give the basic relationship between correlations and path coefficients in a system of correlated causes (Dewey and Lu, 1959). Genetic divergence was computed by using Mahalanobis generalized distance or  $D^2$  statistic as described by Rao (1952). In all the  $D^2$  combinations, the characters were ranked on the basis of their contribution to  $D^2$ . Grouping of genotypes into different clusters was done according to Tocher's method (Rao, 1952).

## RESULTS AND DISCUSSION

The analysis of variance and F-test revealed highly significant differences among the genotypes for all sixteen characters (Table 1). This indicates the presence of wide genetic variability among the genotypes. The variation of different traits under study revealed the measure of free variability in the population of different genotype, which would reflect the unforeseen impact of potential variability on yield. High values of PCV and GCV were noted for capsule number per plant, split of capsule before drying, opening of capsule before drying and seed yield per plot. None of the reports indicated higher values of PCV and GCV simultaneously for the traits stated above except for capsule number per plant. However, higher value of both PCV and GCV for number of primary branches was reported by Chandra Mohan (2011) and Ahadu (2012); capsules per plant by Chowdhary *et al.* (2010), seeds per capsule by Parameswarappa *et al.* (2009), Ahadu (2012) and Gadisa *et al.* (2015). For all characters, PCV was higher than GCV. Similar type of results is reported by Sengupta and Dutta (2004). This implies that these characters had interacted with the environment to some extent for their expression.

In the present study heritability was higher (>80%) in all the 16 characters studied. High heritability for one or more characters was also reported by Tripathi *et al.* (2013) and Bharathi *et al.* (2014). But, contradictory results have been found in some cases, which might be due to the number of genotypes studied, variability present in the population and the type of environment in which the varieties were evaluated. The genetic gain (as percentage of mean) was higher for capsules per plant, splitting and opening of capsules before drying and seed yield, thus points to the predominance of additive effects and can be taken as unit characters for effective selection. Low genetic advance for days to flowering was reported by Babu *et al.* (2005) and seeds per capsule by Reddy

**Table 1: Genetic parameters for seed yield and its components and some capsule shattering related characters in sesame**

Characters	Range		Mean	SE	Coefficient of variation (CV %)	Coefficients of variability		Heritability (broad sense) $h^2$ %	Genetic advance as percentage of mean (gam)
	Minimum	Maximum				GCV	PCV		
DF	33.33	42.67	37.74	0.502	2.34	6.63	6.77	96.02	11.44
DM	70	87	78.55	0.595	1.33	6.82	6.86	98.75	11.93
B/P	2	6	3.98	0.281	12.39	29.95	30.79	94.61	51.28
C/P	13.33	75	26.96	1.904	12.54	48.08	48.62	97.78	83.67
PH	69	150.7	114.56	5.925	9.09	16.37	17.19	90.68	27.44
CL	1.84	2.88	2.44	1.102	7.35	9.53	10.43	83.45	15.32
CW-1	5.38	9.35	7.253	0.076	1.84	12.03	12.08	99.23	21.1
CW-2	3.98	7.82	6.105	0.15	4.33	14.35	14.57	97.06	24.88
CS-1	0	1.99	0.71	0.048	11.88	88.34	88.6	99.4	155.01
CS-2	0.84	2.99	2.17	0.054	4.35	17.96	18.14	98.09	31.31
CO-1	0	1.5	0.44	0.08	32.44	94.23	96.08	96.2	162.67
CO-2	0.82	2.69	1.66	0.083	8.84	33.07	33.46	97.68	57.53
SN/C	27.2	68.2	49.05	0.687	9.63	21.21	21.93	93.57	36.11
SW/C	0.1	0.34	0.197	0.008	7.5	28.19	28.52	97.69	49.04
TSW	1.7	4.13	2.867	0.06	3.7	17.85	17.97	98.59	31.19
SY/P	0.07	0.32	0.137	0.01	12.88	42.21	42.86	96.99	73.17

DF (Days to Flowering), DM (Days to maturity), B/P(Branches per plant), C/P(Capsules per plant), PH(Plant height), CL(Capsule length), CW-1(Capsule Width at Broader Side), CW-2(Capsule Width at narrower Side), CS-1(Capsule split before drying), CS-2(Capsule split after drying), CO-1(Capsule Open Before drying), CO-2(Capsule split after drying), SN/C (Seed number per capsule), SW/C (Seed weight per capsule), TSW(Thousand seed weight), SY/P(Seed yield per plot)

Table 2: Phenotypic (above the diagonal) and genotypic (below the diagonal) correlation coefficients among yield and capsule shattering characters in sesame

Characters	DF	DM	B/P	C/P	PH	CL	CW-1	CW-2	CS-1	CS-2	CO-1	CO-2	SN/C	SW/C	TSW	Y/P
DF																
DM	0.386*															
B/P	-0.308															
C/P	-0.364	-0.379														
PH	0.308	0.055	0.157													
CL	-0.188	0.136	0.192	0.178												
CW-1	-0.209	0.064	0.102	0.422*	0.087											
CW-2	0.106	0.092	0.067	0.198	-0.061	0.365*										
CS-1	0.154	0.165	0.271	0.241	-0.087	0.176	0.214									
CS-2	0.234	0.16	-0.018	-0.112	0.117	0.311	0.019	0.046								
CO-1	0.137	0.295	0.072	-0.021	-0.17	0.001	0.147	0.132	0.863**	0.466**						
CO-2	-0.044	0.13	-0.126	-0.079	0.104	0.066	-0.146	-0.187	0.067	0.475**	0.355*					
SN/C	0.022	-0.072	0.474**	0.496**	-0.07	0.079	0.096	0.167	0.486**	0.07	0.335*	0.044				
SW/C	-0.158	0.02	0.302	0.413*	-0.139	0.368*	0.045	0.088	0.351*	0.065	0.279	0.245	0.473**			
TSW	-0.297	-0.053	0.308	0.468**	-0.08	0.343*	0.218	0.231	0.08	-0.166	0.072	0.149	0.155	0.416*		
Y/P	-0.342	-0.335	0.604**	0.957**	0.092	0.491**	0.18	0.319	0.281	-0.139	0.046	-0.027	0.419*	0.469**	0.699**	

\* and \*\* indicate significance at 5% and 1% levels probability respectively

et al. (2001). A high heritability coupled with high genetic advance was found in capsules per plant, capsule split and open before drying and seed yield per plot, which indicated the presence of additive gene effects for these characters. Similar reports of high heritability coupled with high genetic advance for one or more character has been reported (Yirgalem et al., 2012; Mahmoud and Zeinab, 2015). This indicates that the selection in the desired direction will be quite effective for these four traits.

In respect of most of the character pairs, genotypic correlations were higher than phenotypic correlations (Table 2). In case of genotypic correlation, highest positive significant association (0.957) was found between capsule per plant and seed yield per plot whereas lowest positive significant association (0.335) was found between seed number per capsule and capsule opening before drying. In case of phenotypic correlation, highest positive significant association (0.933) was found between seed yield per plot and capsule per plant whereas lowest positive significant association (0.349) was found between seed weight per capsule and capsule length. This indicates that the environmental cause of correlation has affected the genetic cause, thereby reducing the use of genotypic correlation in crop improvement program. Days to flowering showed positive association with days to maturity, plant height, capsule breadth and seed number per capsule. Similar results were reported by Solanki and Gupta (2003). Seed yield showed a highly significant and positive correlation with number of capsules per plant, branches per plant, capsule length, seed weight per capsule and number of seeds per capsule. Similar results were obtained by Siddiqui et al. (2005), Sumathi et al. (2007), Yirgalem et al. (2012), Shekhawat et al. (2013) and Mahmoud and Zeinab (2015) in sesame. These results are in parallel with the research findings of Thakur et al. (2015) in greengram and Khan et al. (2015) in cowpea.

The cause and relationship between seed yield and other 11 characters were investigated both at phenotypic and genotypic level. It was found that seed yield was very much influenced by capsules per plant, 1000-seed weight, branches per plant, days to maturity, capsule width and seed weight per capsule. The highest positive direct effect on seed yield per plot was exhibited by capsules per plant (0.735) followed by 1000-seed weight (0.267) and capsule width at narrower side (Table 3). The positive direct effect of one or more of these characters was reported by Renuka et al. (2011), and Shekhawat et al. (2013). It is evident from both direct and indirect effects of the component characters at phenotypic and genotypic levels that selection would be more effective when based on characters like capsule per plant, capsule width at narrower side and 1000-seed weight.

The grouping of the 35 genotypes by the Tocher's optimization criterion formed eight conglomerates (Table 4). Cluster I was the largest with 14 genotypes followed by cluster II with 8 genotypes. Cluster IV showed the maximum intra-cluster distance ( $D^2 = 247.89$ ). The average inter-cluster distance varied from 299.29 (between cluster II and VI) to 1622.41 (between cluster V and VII). Relative contribution of different characters to total divergence (Table 5) revealed that capsule width at broader side has the highest (22.44%) contribution to total divergence followed by seed yield (12.67%) and least

**Table 3: Direct and indirect effects of component traits on yield at the phenotypic level in sesame**

TRAITS	DF	DM	B/P	C/P	PH	CL	CW-1	CW-2	SN/C	SW/C	TSW	Phenotypic correlation with seed yield (rp)
Days to flowering (DF)	-0.079	0.001	-0.036	-0.160	-0.005	-0.001	0.013	0.017	-0.001	-0.002	-0.079	-0.329
Days to maturity (DM)	-0.029	0.002	-0.033	-0.275	-0.001	0.001	-0.004	0.015	0.004	0.000	-0.014	-0.332
Branches per plant (B/P)	0.025	-0.001	0.106	0.389	-0.003	0.001	-0.006	0.010	-0.028	0.003	0.079	0.576
Capsules per plant (C/P)	0.016	-0.001	0.056	0.735	-0.003	0.003	-0.002	0.031	-0.029	0.005	0.122	0.933
Plant height (PH) (cm)	-0.020	0.000	0.016	0.117	-0.019	0.001	0.008	-0.007	0.003	-0.001	-0.018	0.078
Capsule length (CL) (cm)	0.012	0.000	0.018	0.284	-0.001	0.009	-0.014	0.053	-0.005	0.004	0.081	0.441
Capsule width at broader side (CW-1) (mm)	0.015	0.000	0.011	0.028	0.002	0.002	-0.063	0.132	-0.006	0.000	0.057	0.180
Capsule width at narrower side (CW-2) (mm)	-0.008	0.000	0.007	0.142	0.001	0.003	-0.051	0.162	-0.010	0.001	0.061	0.308
Seeds per capsule (SN/C)	-0.001	0.000	0.048	0.348	0.001	0.001	-0.006	0.025	-0.062	0.005	0.040	0.398
Seed weight per capsule (SW/C) (g)	0.011	0.000	0.031	0.299	0.002	0.003	-0.003	0.014	-0.028	0.011	0.109	0.451
1000-seed weight (TSW) (g)	0.022	0.000	0.031	0.337	0.001	0.003	-0.013	0.037	-0.009	0.005	0.267	0.680

Residual = 0.163, R<sup>2</sup> = 97.34%; NB: bold figures indicate direct effects**Table 4: Intra-(diagonal) and inter-cluster average d<sup>2</sup> among 35 genotypes**

Cluster	I (14)	II (8)	III (4)	IV (4)	V (2)	VI (1)	VII (1)	VIII (1)	Genotypes in cluster
I	226	386.23	405.93	321.73	726.13	351.35	474.29	834.42	OSC-17, OSC-20, OSC-28, OSC-56, OSC-96, OSC-134, OSC-333, OSM-195, OSM-212, OSM-221, TKG-22, RT-54, AMRIT, KANAK
II		192.14	318.21	617.05	639.29	299.29	684.97	430.17	OSC-26, OSC-47, OSC-79, OSC-83, OSM-152, NIRMALA, UMA
III			152.67	767.54	326.03	365.82	909.42	811.97	OSC-21, OSC-98, OSC-366, PRACHI
IV				247.89	1149.79	622.48	557.8	1072.21	OSC-172, OSC-303, OSC-442, OSC-493
V					246.81	573.36	1622.41	1445.41	OSC-32, OSC-389
VI						0	459.72	587.45	USHA
VII							0	771.27	KALIKA
VIII								0	OSM-170

**Table 5: Contribution of yield and its components to genetic divergence**

Character	AverageD <sup>2</sup>	% contribution to Total divergence
Days to flowering	16.74	3.86
Days to maturity	53.04	12.22
Branches per plant	13.13	3.03
Capsules per plant	29.83	6.87
Plant height (cm)	11.27	2.60
Capsule length (cm)	6.19	1.43
Capsule width at broader side (mm)	97.36	22.44
Capsule width at narrower side (mm)	36.10	8.32
Seeds per capsule	12.86	2.96
Seed weight per capsule (g)	48.28	11.13
1000-seed weight (g)	54.15	12.48
Seed yield per plot (kg)	54.98	12.67
TOTAL	433.93	100

by capsule length (1.43%). Crosses between genotypes of cluster V with genotypes of cluster VII may give rise to high yielding segregants (Shekhawat *et al.*, 2014). It is also observed that the clustering pattern of genotypes did not show any parallelism with their genetic origin. Such grouping of genotypes from different genetic origin may be attributed to the unidirectional selection practiced by the breeder in a particular location. However Murty and Arunachalam (1996) have reported that genetic drift and selection, both natural and artificial in different environments could cause greater diversity among genotypes than geographic distances.

Probably due to above two factors, the genotypes originating from the different crosses have been clustered together. The use of genotypes from cluster V and VII as parents in a hybridization program will give rise to high yielding segregants possessing semi shattering capsule characters. Intercrossing of such genotypes involved in these clusters would be useful for generating variability for the respective characters, and their rational improvement for increasing the seed yield per plant. These morphological characters need to be substantiated further with molecular markers for confirming the genetic differences among the genotypes.

## REFERENCES

- Ahadu M, A. 2012. Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum* L.) genotypes. *Nature and Sci.* **10**:117-26.
- Al-Jibouri, H. A., Miller, P. A. and Robinson, H. F. 1958. Genotypic and environmental variances in an upland cotton cross of inter-specific origin. *Agron. J.* **50**: 633-636.
- Ashri, A. 1989. Sesame breeding. *Plant Breeding Review.* **16**: 179-228.
- Babu, D. R., Kumar, P. V. R. and Rani, C.V.D. 2005. Genetic variability, heritability and genetic advance of seed yield and its components in sesame (*Sesamum indicum* L.). *Res. on Crops.* **6**: 307-308.
- Bharathi, D., Rao, V.T., Mohan, Y., Chandra, B. D. and Venkanna, V. 2014. Genetic variability studies in sesame (*Sesamum indicum* L.). *Inter.J.Appl.Bio. Pharma.Tech.* **5**(4):31-33.

- Burton, G. W. 1968.** Heterosis and heterozygous in pearl millet forage production. *Crop Science*. **8**: 229-230.
- Chandra Mohan. 2011.** Genetic variability and character association studies in sesame (*Sesamum indicum* L.). *Crop Res.* **42 (1, 2 & 3)** : 259-262.
- Chowdhary, S., Datta, A. K., Saha, A., Sengupta, S., Paul, R., Maity, S. and Das, A. 2010.** Traits influencing yield in sesame (*Sesamum indicum* L.) and multi locational trials of yield parameters in some desirable plant types. *Indian J. Sci. Techn.* **3(2)**: 163-166.
- Dewey, D. R. and Lu, K. H. 1959.** A correlation and path analysis of components in crested wheat grass seed production. *Agron. J.* **51**: 515-518.
- Gadisa, H., Geleta, N., and Jaleta, Z. 2015.** Genetic variability, heritability and genetic advance for the phenotypic traits in sesame (*Sesamum indicum* L.) populations from Ethiopia. *Sci. Technol. Arts Res. J.* **4(1)**: 20-26.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956.** Biometrical studies of yield in segregating population in Korean lespedza. *Agron. J.* **48**: 268-272.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955.** Estimates of genetic and environmental variability in soybeans. *Agron. J.* **47**: 314-318.
- Khan, H., Viswanatha, K. P. and Sowmya, H. C. 2015.** Study of genetic variability parameters in cowpea (*Vigna unguiculata* L. Walp.) germplasm lines. *The Bioscan.* **10(2)**: 747-750.
- Kobayashi, T. 1981.** The wild and cultivated species in the genus *Sesamum*. Sesame: Status and improvement. Proceedings of Expert Consultation, Rome, Italy, 8-12 December, 1980. *FAO Plant Production and Protection Paper* 29 pp. 157-163.
- Mahmoud, M. W. Sh. and Zeinab, E. G. 2015.** Variability of yield and some morphological traits in sixteen sesame genotypes. *Egypt. J. Plant Breed.* **19(4)**:1031–1045.
- Murty, B. R. and Arunachalam, V. 1996.** The nature of genetic divergence in relation to breeding system in some crop plants. *Ind. J. Genet.* **26(A)**: 188-198.
- Nayar, N. M. and Mehra, K. L. 1970.** Sesame: Its uses: botany, cytogenetics, and origin. *Economic Botany.* **24**: 20-31.
- Panse, V. G. and Sukhatme, P.V. 1954.** Statistical methods for agricultural workers, Second Edn, ICAR, New Delhi.
- Parameswarappa, S. G., Palakshappa, M. G., Salimath, P. M. and Parameswarappa, K. G. 2009.** Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum* L.). *Karnataka J. Agric. Sci.* **22**: 252-254.
- Rao, C. R. 1952.** Advanced statistical methods in biometric research. *John Wiley & Sons, New York.*
- Raghuwanshi, K. M. S. and Duhoon, S. S. 2005.** Genetic diversity and adaptability in Indian germplasm collection of sesame (*Sesamum indicum* L.). *J. Oilseeds. Res.* **22(1)**: 29-36.
- Reddy, P. A. V., Sekhar, M. R., Ranganath, A. R. G. and Dhanraj, A. 2001.** Genetic variability and heritability for seed yield and its components in sesame (*Sesamum indicum* L.). *J. Oilseeds Res.* **18**: 173-175.
- Renuka, G., Lokesh, R and Ranganatha, A.R.G. 2011.** Trait association and path coefficient analysis for yield and yield attributing traits in sesame (*Sesamum indicum* L.). *EJPB.* **2(3)**: 448-452.
- Sengupta, S. and Dutta, A. K. 2004.** Genetic studies to ascertain selection criteria for yield improvement in sesame. *J. Phytological Res.* **17**: 163-166.
- Shekhawat, R. S., Rajput, S. S., Meena, S. K. and Singh, B. 2013.** Variation and character association for seed yield and related traits in sesame (*Sesamum indicum* L.). *Ind. Res. J. Genet. Biotech.* **5(3)**:186-193.
- Shekhawat, N., Jadeja, G. C., Singh, J. and Ramesh. 2014.** Genetic diversity analysis in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern Coss). *The Bioscan.* **9(2)**: 713-717.
- Siddiqui, M. A., Baig, K. S. and Patil, P. V. 2005.** Correlation and path analysis studies for yield and yield attributing characters in sesame (*Sesamum indicum* L.). *J. Res. ANGRAU.* **33**: 31-35.
- Solanki, Z. S. and Gupta. 2002.** Genetic divergence for seed yield and other characters in sesame. *J. Oilseeds Res.* **19**: 35-37.
- Sumathi, P., Muralidharan, V. and Mannivannan, N. 2007.** Trait association and path coefficient analysis for yield and yield attributing traits in sesame. *Madras agric. J.* **94**: 174-178.
- Thakur, D. K., Nag, S. K., Gendley, T. K. and Patel, R. K. 2015.** Character association and path coefficient analysis for seed yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *The Bioscan.* **10(4)**: 1947-1950.
- Tripathi, A., Bisen, R., Ahirwal, P., Paroha, S., Sahu, R. and Ranganatha, A. R. G. 2013.** Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. *The bioscan.* **8(4)**: 1387-1391.
- Uzun, B., Yol, E. and Furat, S. 2013.** Genetic advance, heritability and inheritance in determinate growth habit of sesame. *Aust.J.Cr.Sci.* **7**: 978-983.
- Weiss, E. A. 1971.** Castor, Sesame and Safflower. Leonard Hill books, London, P. 901.
- Yirgalem, T. G., Sentayehu, A.K. and Geremew, T.G. 2012.** Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. *Int. J. Plant Breed.Genet.* PP: 1-14.
- Zhang, H., Miao, H., Wei, L., Li, C., Zhao, R. and Wang, C. 2013.** Genetic analysis and QTL mapping of seed coat color in sesame (*Sesamum indicum* L.). *PLoS ONE.* **8(5)**: e63898.

