Plant Archives Vol. 26, Supplement 1, 2026 pp. 136-141 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.020

GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR SELECTION IN ELITE BREEDING MATERIALS OF SESAME (*SESAMUM INDICUM* L.)

Dinkar[1], Sima Sinha[1]*, Namrata Dwivedi[2], Manisha Patel[1], Shubham Priyadarshi[3], Buddha Priya Mourya[4], Anish Kumar[1] and Ram Manish Kumar[5]
[1]Department of Plant Breeding and Genetics, B.A.U., Sabour, Bhagalpur, Bihar (813210), India
[2]Department of Genetics and Plant Breeding, R.V.S.K.V.V., Gwalior, Madhya Pradesh (474002), India
[3]Department of Horticulture (Vegetable and Floriculture), B.A.U., Sabour, Bhagalpur, Bihar (813210), India
[4]Department of Soil Science and Agricultural Chemistry, B.A.U., Sabour, Bhagalpur, Bihar (813210), India
[5]Department of Extension Education, B.A.U., Sabour, Bhagalpur, Bihar (813210), India
*Corresponding author E- mail: simasinha540@gmail.com

(Date of Receiving : 14-09-2025; Date of Acceptance : 19-11-2025)

ABSTRACT

The present investigation evaluated the extent of genetic variability, trait relationships, and the direct and indirect contributions of yield components in sesame across multiple environments and locations. Analysis of variance revealed significant differences among genotypes for all characters, confirming substantial genetic variability within the material studied. Environmental and locational influences were also evident for most traits, along with significant interactions, demonstrating the sensitivity of sesame genotypes to varying agro-ecological conditions. Estimates of phenotypic and genotypic coefficients of variation indicated that environmental factors contributed notably to trait expression. Moderate levels of genotypic variability were observed for key yield-related traits, including number of branches per plant, stem length to the first capsule, number of capsules per plant, and biological yield. Heritability estimates varied across characters, with only a few traits showing sufficient heritable variation to enable effective selection. Notably, days to flowering and number of branches per plant exhibited favourable combinations of heritability and genetic advance, suggesting additive gene action. Correlation analysis identified several traits that were positively associated with seed yield, whereas traits related to delayed maturity displayed negative relationships. Path coefficient analysis further demonstrated that biological yield, harvest index, and number of capsules per plant exerted meaningful direct effects on seed yield, highlighting their importance for selection in sesame improvement programmes.

***Keywords* :** Sesame, heritability, variability, significant, variation.

Introduction

Sesame (*Sesamum indicum* L.) is one of the oldest domesticated oilseed crops and is widely cultivated under a range of common names such as sesamum, gingelly, til, tila, simsim, and gergelim. A self-pollinated species with a chromosome number of 2n = 26, sesame belongs to the family Pedaliaceae and thrives in warm climates across the tropics and subtropics. Owing to its exceptionally high oil content, superior oil quality, and the presence of natural antioxidants such as sesamol, sesamin, sesamolin, and sesaminol it is often referred to as the "Queen of Oilseeds" (Vijayarajan *et al.*, 2007; Dinkar *et al.* 2024). Sesame seeds contain 46–50% oil, with 83–90% of the oil comprising polyunsaturated fatty acids (PUFAs). Additionally, they are rich in proteins (about 20%), lignans, tocopherols, phytosterols, phytates, and several micronutrients (Kamal-Eldin *et al.* 1995). In India, approximately 78% of sesame seed production is utilized for oil extraction. Of the extracted oil, nearly 73% is used in food preparations, 8.3% is converted to hydrogenated products, and 4.2% serves industrial purposes, including applications in paints, pharmaceuticals, and pesticides. Sesame oil is considered one of the healthiest vegetable oils due to its cardioprotective and anti-cancer properties, as well as its ability to reduce blood pressure and cholesterol levels. With 592 calories per 100 g of seeds, sesame is often regarded as an economical substitute for ghee. The residual oil cake is also valuable, containing 6.0–6.2% nitrogen, 2.0–2.2% phosphorus, and 1.0–1.2% potassium, making it a useful organic fertilizer. For breeders engaged in varietal improvement, understanding the contribution of individual yield-related traits is essential. Evaluating whether a trait influences yield positively or negatively, and whether its effect is direct or mediated through other characters, is crucial for making informed selection decisions. Correlation and path analysis therefore serve as valuable tools in identifying traits that can be effectively targeted to enhance overall grain yield. Genetic variability within a population forms the foundation of any successful breeding program. Partitioning this variability into heritable and non-heritable components using parameters such as genotypic and phenotypic variances, phenotypic and genotypic coefficients of variation, heritability, and genetic advance allows breeders to gauge the potential for genetic improvement. Selection of parents thus depends not only on desirable agronomic performance and yield-related traits but also on the magnitude and nature of genetic variability coupled with heritability estimates. Environmental conditions further influence these parameters, as heritability and genetic advance may vary across locations and seasons.

Since grain yield is a complex quantitative trait governed by numerous genes and significantly influenced by environmental interactions, direct selection based solely on yield can be unreliable. Instead, an understanding of how different component traits interact and contribute to the final yield is essential. When correlation analysis is complemented by path coefficient analysis, it enables breeders to dissect the direct and indirect effects of individual characters on yield, thereby providing a clearer picture of trait interrelationships. Such combined analyses guide the selection of promising traits and facilitate the development of high-yielding sesame varieties through informed and strategic breeding.

Materials and Methods

The present study was conducted using 22 sesame genotypes, including three checks two national checks (TKG-22 and GT-10) and one zonal check (JTS-8). The evaluation was carried out across three locations: BAC Sabour, BPSAC Purnea, and ARI Patna during the summer seasons of 2024 and 2025. Fourteen yield and yield-contributing traits were assessed. Observations were recorded from five randomly selected, competitive plants per genotype in each replication for the following quantitative parameters: days to 50% flowering, days to maturity, plant height at maturity, stem length to the first capsule, number of branches per plant, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, 1000-seed weight, biological yield per plant, seed yield per plant, harvest index, and oil percentage. The mean values for these traits were subjected to analysis of variance to determine their significance, following the procedure outlined by Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed using the method proposed by Burton (1952). Broad-sense heritability (h^2) was estimated according to Burton and DeVane (1953). Genetic advance, representing the expected improvement under selection, was calculated using the approach described by Johnson *et al.* (1955). Correlation coefficients among traits were derived using the method suggested by Singh and Chaudhary (1985) to assess the strength and direction of relationships between yield and its component characters. To further quantify the direct and indirect effects of these traits on grain yield, path coefficient analysis was performed following the methodology of Dewey and Lu (1959), with grain yield considered as the dependent variable and the associated traits treated as causal variables. This comprehensive analysis provided insights into the genetic variability, interrelationships, and trait contributions to yield, thereby aiding in the selection of promising genotypes for sesame improvement.

Results and Discussion

Analysis of variance (ANOVA) was performed on mean data for 14 characters to evaluate experimental precision and treatment effects (Table 1). The pooled ANOVA showed that mean squares attributable to genotypes were significant for all traits, confirming the presence of considerable genetic variability among the sesame genotypes under investigation. Significant environmental effects were also observed for most traits, except capsule length, capsule width, and number of seeds per capsule, 1000-seed weight, biological yield per plant, harvest index, and oil percentage, indicating differential environmental influence on trait expression. Similarly, locations exhibited significant differences for all traits except capsule length, confirming sufficient variation among locations and validating their suitability for multi-location experimentation. The significant location × environment interaction for all traits further underscored the strong interplay between site-specific and environmental factors. Comparable findings were reported by Aboelkassem *et al.* (2021), Kumar *et al.* (2022), and Ranjithkumar *et al.* (2022) in sesame.

The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Table 2) consistently showed higher PCV values than GCV values for all traits, indicating that environmental factors contributed notably to the observed variability. PCV ranged from 3.938% (oil percentage) to 27.517% (number of branches per plant), while GCV varied between 2.859% (oil percentage) and 18.598% (number of branches per plant). Higher PCV values were observed for number of branches per plant (27.517%), stem length to the first capsule (21.497%), and biological yield per plant (23.22%). Although none of the traits exhibited high GCV, moderate GCV values were noted for stem length to the first capsule (14.109%), number of branches per plant (18.598%), number of capsules per plant (10.969%), and biological yield per plant (15.498%). Similar trends in PCV and GCV were documented by Sasipriya *et al.* (2018), Kumar *et al.* (2022), Singh *et al.* (2024), and Ranjithkumar *et al.* (2022).

Broad-sense heritability estimates ranged from 19.9% for harvest index to 64.5% for days to 50% flowering. Only days to 50% flowering showed high heritability. Moderate heritability was recorded for stem length to the first capsule, number of branches per plant, capsule length, capsule width, number of seeds per capsule, plant height at maturity, 1000-seed weight, biological yield per plant, days to maturity, oil percentage, and seed yield per plant. No trait exhibited the desirable combination of high heritability and high genetic advance. However, days to 50% flowering displayed high heritability coupled with moderate genetic advance, implying predominant additive gene action. Moderate heritability along with high genetic advance was observed for number of branches per plant and biological yield per plant, suggesting the potential effectiveness of selection for these traits. These findings align with the results of Roy *et al.* (2022), Kumar *et al.* (2022), and Ranjithkumar *et al.* (2022).

Seed yield per plant showed a highly significant and positive correlation (Table 3) with number of branches per plant (0.676**), number of capsules per plant (0.545**), capsule length (0.298**), capsule width (0.339**), number of seeds per capsule (0.589**), 1000-seed weight (0.325**), and biological yield per plant (0.633**). Significant negative correlations were observed with days to 50% flowering (–0.649**), plant height at maturity (–0.434**), harvest index (–0.292**), days to maturity (–0.608**), and stem length to the first capsule (–0.117*). Correlations for the remaining traits were non-significant. These results corroborate findings reported by Sasipriya *et al.* (2018), Aboelkassem *et al.* (2021), Ranjithkumar and Bisen (2022), and Kumar *et al.* (2022). Path coefficient analysis (Table 4) revealed that biological yield per plant and harvest index exerted high positive direct effects on seed yield per plant, while number of capsules per plant contributed a moderate direct effect. These results indicate that direct selection for these traits would be effective. Since correlation analysis alone cannot always reveal true causal relationships, path analysis serves as a useful tool to partition total correlations into direct and indirect effects. Similar conclusions were reported by Sasipriya *et al.* (2018), Kumar *et al.* (2022), and Srikanth *et al.* (2022).

Table 1: Pooled Analysis of Variance (ANOVA)

Source of Variations	**MSS**							
	Replication	**Locations**	**Environments**	**Location X Environment**	**Interactions**	**Overall Sum**	**Genotypes**	**Error**
df	2	2	1	2	10	17	21	357
DFF	0.44	98.27**	4.78**	47.91**	4.23	155.64**	2459.72**	1238.04
SLFC	4.67	7154.21**	235.47**	16592.33**	32.18	24018.86**	11275.40**	13127.96
NBPP	0.14	7.98**	1.39**	19.25**	1.08	29.85**	180.10**	189.75
NCPP	7.11	4315.41**	218.27**	14469.86**	136.80	19147.45**	20293.85**	38299.10
CL	0.07	0.04	0.00	1.69**	0.42	2.22*	13.20**	24.00
CW	0.00	0.01**	0.00	0.45**	0.01	0.47**	0.71**	0.80
NSPC	2.46	38.00*	5.34	31.08*	41.80	118.69	3471.75**	5550.73
PHM	128.91	2067.22**	804.93**	9794.49**	100.00	12895.54**	25053.23**	33817.88
TSW	0.06	0.31**	0.00	0.16**	0.15	0.68**	8.13**	5.58
BYPP	16.01	2474.06**	39.15	4688.22**	499.51	7716.95**	62945.33**	69238.95
HI	0.18	132.13**	0.04	185.28**	11.31	328.94**	196.72**	610.34

DM	0.48	1438.37**	8.06**	4932.38**	2.89	6382.18**	6484.63**	7009.36
OIL %	2.20	28.62**	1.35	22.22**	14.75	69.14**	729.19**	588.72
SYPP	0.00	16.41**	0.40*	14.20**	0.60	31.62**	170.57**	250.20

DFF- Days to fifty per cent flowering, SLFC- Stem length to first capsule, NBPP- Number of branches per plant, NCPP- Number of capsules per plant, LC- Length of capsule, WC- Width of capsule, NSPC, Number of seed per capsule, PHM- Plant height at maturity, 1000 SW- 1000 seed weight, BYPP- Biological yield per plant, HI- Harvest index, DM- Days to maturity, Oil%- Oil percentage and SYPP- Seed yield per plant

Table 2: Estimates of Genetic variability parameters for grain yield and its contributing traits

S. No.	Characters	σ^2g	σ^2p	GCV	PCV	h^2 (Broad Sense)	Genetic Advance	Genetic Adv. as % of Mean
1	DFF	6.315	9.782	6.338	7.889	64.5	4.159	10.49
2	SLFC	27.786	64.559	14.103	21.497	43	7.124	19.059
3	NBPP	0.447	0.978	18.598	27.517	45.7	0.931	25.893
4	NCPP	47.727	155.008	10.969	19.767	30.8	7.897	12.538
5	CL	0.031	0.098	6.627	11.773	31.7	0.205	7.685
6	CW	0.002	0.004	7.28	10.993	43.9	0.057	9.932
7	NSPC	8.321	23.869	4.812	8.151	34.9	3.508	5.853
8	PHM	61.016	155.744	8.866	14.165	39.2	10.072	11.432
9	TSW	0.021	0.036	5.254	6.966	56.9	0.223	8.164
10	BYPP	155.747	349.694	15.498	23.222	44.5	17.157	21.306
11	HI	0.425	2.135	7.505	16.812	19.9	0.6	6.901
12	DM	16.064	35.698	4.478	6.675	45	5.539	6.188
13	OIL %	1.837	3.487	2.859	3.938	52.7	2.027	4.276
14	SYPP	0.412	1.113	9.489	15.591	37	0.805	11.896

σ^2g-Genotypic variance, σ^2p- Phenotypic variance, GCV-Genotypic coefficient of variance, PCV- Phenotypic coefficient of variance, DFF-Days to fifty per cent flowering, SLFC- Stem length to first capsule, NBPP- Number of branches per plant, NCPP- Number of capsules per plant, LC- Length of capsule, WC- Width of capsule, NSPC, Number of seed per capsule, PHM- Plant height at maturity, 1000 SW- 1000 seed weight, BYPP- Biological yield per plant, HI- Harvest index, DM- Days to maturity, Oil%- Oil percentage and SYPP- Seed yield per plant

Table 3: Pooled phenotypic correlation between yield and yield attributing characters

	DFF	SLFC	NBPP	NCPP	CL	CW	NSPC	PHM	TSW	BYPP	HI	DM	OIL%	SYPP
DFF	1	-0.207**	-0.685**	-0.643**	-0.271**	0.231**	-0.570**	0.627**	0.0093	-0.676**	0.345**	0.645**	-0.0383	-0.649**
SLFC		1	0.184**	0.269**	-0.0827	0.0749	0.154**	-0.128*	-0.113*	0.124*	-0.0685	-0.233**	-0.0574	-0.117*
NBPP			1	0.523**	0.274**	-0.394**	0.618**	-0.655**	0.078	0.522**	-0.400**	-0.602**	0.124*	0.676**
NCPP				1	0.375**	-0.255**	0.506**	-0.551**	0.018	0.521**	-0.389**	-0.616**	0.149**	0.545**
CL					1	-0.365**	0.224**	-0.395**	0.0292	0.399**	-0.334**	-0.236**	0.0816	0.298**
CW						1	-0.306**	0.244**	0.0138	-0.384**	0.237**	0.212**	0.0155	0.339**
NSPC							1	-0.685**	0.207**	0.750**	-0.252**	-0.605**	0.165**	0.589**
PHM								1	0.0231	-0.752**	0.411**	0.686**	-0.138**	-0.434**
TSW									1	0.0441	0.067	0.017	0.0917	0.325**
BYPP										1	-0.693**	-0.637**	0.0717	0.633**
HI											1	0.349**	0.0617	-0.292**
DM												1	-0.0694	-0.608**
OIL%													1	0.148

*Significant at 5 % level, **Significant at 1 % level, DFF- Days to fifty per cent flowering, SLFC- Stem length to first capsule, NBPP- Number of branches per plant, NCPP- Number of capsules per plant, LC- Length of capsule, WC- Width of capsule, NSPC, Number of seed per capsule, PHM- Plant height at maturity, 1000 SW- 1000 seed weight, BYPP- Biological yield per plant, HI- Harvest index, DM- Days to maturity, Oil%- Oil percentage and SYPP- Seed yield per plant

Table 4: Pooled direct and indirect effect of different yield attributing characters on seed yield per plant (Residual effect=0.374)

	DFF	**SLFC**	**NBPP**	**NCPP**	**CL**	**CW**	**NSPC**	**PHM**	**TSW**	**BYPP**	**HI**	**DM**	**OIL %**	**Phenotypic correlated with SYPP**
DFF	**-0.0181**	0.0037	0.0124	0.0116	0.0049	-0.0042	0.0103	-0.0114	-0.0002	0.0122	-0.0063	-0.0117	0.0007	-0.649**
SLFC	0.0106	**-0.0513**	-0.0094	-0.0138	0.0042	-0.0038	-0.0079	0.0066	0.0058	-0.0063	0.0035	0.012	0.0029	-0.117*
NBPP	-0.0259	0.007	**0.0378**	0.0274	0.0104	-0.0149	0.031	-0.0248	0.003	0.0311	-0.0151	-0.0228	0.0047	0.676**
NCPP	-0.1818	0.076	0.2045	**0.2828**	0.1061	-0.0721	0.1996	-0.2124	0.0051	0.2321	-0.1099	-0.1741	0.0421	0.545**
CL	0.0144	0.0044	-0.0146	-0.0199	**-0.0531**	0.0194	-0.0119	0.021	-0.0016	-0.0212	0.0177	0.0125	-0.0043	0.298**
CW	-0.0098	-0.0032	0.0167	0.0108	0.0155	**-0.0423**	0.0129	-0.0103	-0.0006	0.0162	-0.01	-0.009	-0.0007	0.339**
NSPC	0.0146	-0.004	-0.021	-0.0181	-0.0057	0.0078	**-0.0256**	0.0176	-0.0053	-0.0192	0.0065	0.0155	-0.0042	0.589**
PHM	-0.0437	0.0089	0.0457	0.0524	0.0276	-0.017	0.0478	**-0.0697**	-0.0016	0.0525	-0.0287	-0.0478	0.0096	-0.434**
TSW	-0.0004	0.0053	-0.0037	-0.0009	-0.0014	-0.0007	-0.0098	-0.0011	**-0.0473**	-0.0021	-0.0032	-0.0008	-0.0043	0.325**
BYPP	-0.5395	0.0987	0.5562	0.0555	0.3183	-0.3065	0.4285	-0.3007	0.3352	**0.7986**	-0.553	-0.5085	0.0173	0.633**
HI	0.1407	-0.0279	-0.1628	-0.2583	-0.1361	0.0966	-0.1025	0.1676	0.0273	-0.4721	**0.4074**	0.142	0.0251	-0.292**
DM	-0.0074	0.0027	0.0069	0.0071	0.0027	-0.0024	0.0069	-0.0079	-0.0002	0.0073	-0.004	**-0.0115**	0.0008	-0.608**
OIL %	-0.0022	-0.0033	0.0072	0.0086	0.0047	0.0009	0.0096	-0.008	0.0053	0.0042	0.0036	-0.004	**0.058**	0.148*

DFF- Days to fifty per cent flowering, SLFC- Stem length to first capsule, NBPP- Number of branches per plant, NCPP- Number of capsules per plant, LC- Length of capsule, WC- Width of capsule, NSPC, Number of seed per capsule, PHM- Plant height at maturity, 1000 SW- 1000 seed weight, BYPP- Biological yield per plant, HI- Harvest index, DM- Days to maturity, Oil%- Oil percentage and SYPP- Seed yield per plant

Conclusion

The overall findings of the study demonstrate substantial genetic variability among the sesame genotypes evaluated across multiple environments and locations. The significant effects of genotypes, environments, and their interactions indicate that both genetic and non-genetic factors played important roles in shaping trait expression. The consistently higher phenotypic variability compared to genotypic variability across traits further reflects the influence of environmental conditions on performance. Although heritability estimates varied widely, only a few traits exhibited sufficiently high heritable variation to support effective selection. Traits such as days to 50% flowering, number of branches per plant, and biological yield per plant showed moderate to high heritability with appreciable genetic advance, suggesting a predominance of additive gene action and their suitability for direct selection. Correlational analyses identified several key traits that were positively associated with seed yield, including number of branches per plant, number of capsules per plant, capsule dimensions, number of seeds per capsule, seed weight, and biological yield. Conversely, flowering and maturity duration, as well as certain growth attributes, were negatively associated with yield. Path coefficient analysis confirmed that biological yield, harvest index, and number of capsules per plant exerted meaningful direct effects on seed yield, highlighting them as the most influential determinants. Collectively, these findings provide valuable guidance for selecting promising traits and designing effective breeding strategies aimed at enhancing sesame productivity.

Acknowledgement

Authors are thankful to Dr. D.R. Singh, Vice Chancellor, Bihar Agricultural University, Sabour who providing us fund timely and all kinds of support. We acknowledge Programme Co-coordinator (Sesame) Dr. Anand Vishwakarma and Dr. Rajani Bisen for their extended support time to time.

References

Aboelkassem, K.M., Ahmed, A.A. and Hassan, T.H.A. (2021). Genetic variability and path coefficient analysis of some Sesame (*Sesamum indicum* L.) genotypes for seed yield and their components. *Journal of Plant Production, Mansoura University*, **12 (4),** 733-783.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proceedings of 6th International Grassland congress, **1**, 277-283.

Burton, G.N. and Devane, E.M. (1953). Estimating Heritability in Fall Fescue (*Festuca arundiancea* L.) from Replicated Clonal Materials. *Agronomy Journal*, **45**, 478-481.

Dinkar, Sinha, S., Singh, A.K., Chandra, K., Gupta, T.D. (2024). Different approaches for genetic improvement of sesame (*Sesamum indicum* L.) for enhancing yield in India, A Review. *Journal of Oilseed Research*, **41(2),** 105-116.

Dewey, D.R. and Lu, K.H (1959) A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51(9),** 515- 518.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability of Soybeans. *Agronomy Journal*, **47**, 314-318.

Kamal-Eldin, A., Pettersson, D. and Appelqvist, L.Å. (1995). Sesamin (a compound from sesame oil) increases tocopherol levels in rats fedad libitum. *Lipids*, **30(6),** 499-505.

Kumar, V., Sinha, S., Singh, R.S. and Singh, S.N. (2022). Assessment of genetic variability, correlation and path analysis in sesame (*Sesamum indicum* L.). *Electronic journal of plant breeding*, **13(1),** 208-215.

Kumar, V., Sinha, S., Sinha, S. and Singh, S.N. (2022). Characterization of diverse sesame (*Sesame indicum* L.) panel through morphological and molecular marker analysis. *Journal of Oilseed Research,* **39(2),**77-85

Panse, V.G. and Sukhatme, P.V. (1985). Statistical Measures for Agricultural Workers, Indian council of agricultural research, New Delhi, **17,** 318-328.

Ranjithkumar, G. and Bisen, R. (2022). Correlation and path Analysis for seed yield and its contributing traits in sesame (*Sesamum indicum* L.). *Biological Forum-An International Journal*, **14(1),** 1292-1295.

Ranjithkumar, G., Bisen, R. and Kumar, V. (2022). Genetic variability studies for yield and its attributing traits in dark brown sesame (*Sesamum indicum* L.). *International Journal of Plant and Soil Science,* **34(8),** 43-49.

Roy, B., Pal, A.K. and Basu, A.K. (2022). The estimation of genetic variability and genetic divergence of some advanced lines of sesame based on morphological traits. *Plant Science Today,* **9(2),** 281-287.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical Methods in quantitative genetic analysis. Kalyani publisher, New Delhi

Singh, A.K., Sinha, S., Satyendra., Sinha, S., Dinkar. and Singh, P.K. (2024). Genetic variability, correlation and path analysis for selection in elite breeding material of sesame (*Sesamum indicum* L.). *Journal of Oilseed Research*, **41(2),** 132-137.

Sasipriya, S., Eswari, K.B. and Balram, M. (2018). Correlation and path co efficient analysis for seed yield and its components in sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*, **9(4),** 1594-1597.

Srikanth, K. and Ghodke, M.K. (2022). Correlation and path analysis in sesame (*Sesamum Indicum* L.) genotypes. *International Journal of Plant & Soil Science*, **34(18),** 228-235.

Vijayarajan, S., Ganesh, S.K. and Gunasekaran, M. (2007). Generation mean analysis for quantitative traits in sesame (*Sesamum indicum*) crosses. *Genet. Mol. Biol*, **30(1),** 80-84.