



Plant Archives

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

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.319>

ESTIMATION OF GENETIC VARIABILITY, CHARACTER ASSOCIATION AND PATH ANALYSIS FOR YIELD AND ITS RELATED TRAITS IN SESAME MUTANTS (*Sesamum indicum* L.)

Lavanya H. M.^{1*}, Anisa M. Nimbal², Parameshwarappa S. G.³, Prabhavathi N. Rao⁴,
Malavika M.⁵ Kirankumar Karikatti¹ and Arman Syed¹

¹Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad - 580005, Karnataka, India.

²Department of Genetics and Plant Breeding and Head, AICRP on Sesame and Niger, M.A.R.S., University of Agricultural Sciences, Dharwad- 580005, Karnataka, India.

³ Department of Genetics and Plant Breeding and Deputy Director of Research, College of Agriculture, University of Agricultural Sciences, Dharwad - 580005, Karnataka, India.

⁴Department of Plant Pathology, AICRP on Sesame and Niger, M.A.R.S., University of Agricultural Sciences, Dharwad- 580005, Karnataka, India.

⁵ AICRP on Sesame and Niger, M.A.R.S., University of Agricultural Sciences, Dharwad- 580005, Karnataka, India.

*Corresponding author E-mail: lavanyahm183@gmail.com

(Date of Receiving : 17-04-2026; Date of Revision : 10-06-2026; Date of Acceptance : 01-07-2026)

ABSTRACT

Sesame (*Sesamum indicum* L.) an indigenous oldest oilseed crop of India is valued for its highest quality oil and recognised as “Queen of Oilseeds”. Knowledge of genetic variability and trait associations play vital role in sesame breeding for its productivity enhancement in sesame, thus the present investigation was undertaken to estimate estimating genetic variability, correlation and path coefficient analysis by evaluating sesame mutants during summer, 2025. Analysis of variance indicated highly significant differences among genotypes for all traits, confirming sufficient variability for selection. High genotypic and phenotypic coefficient of variation were observed for number of capsules per plant and seed yield per plant, while moderate values were noted for number of primary branches and capsules on the main stem. High heritability coupled with high genetic advance was recorded for number of primary branches, capsules on main stem, total capsules per plant and seed yield, indicating predominance of additive gene action. Correlation analysis revealed strong positive associations of seed yield with number of primary branches, capsules per plant, seeds per capsule, capsule length and 1000 seed weight. Path analysis showed positive direct effect of capsules on main stem, seeds per capsule, height to first capsule, capsule length, days to 50% flowering and oil content on seed yield, whereas plant height and days to maturity exerted negative direct effects.

Keywords : Correlation, Genetic variability, Path analysis, Seed yield, Sesame.

Introduction

Sesame (*Sesamum indicum* L.) one of the earliest oilseed crop known to Indians and is being cultivated for centuries, especially in Asia and Africa (Jhakar *et al.*, 2026). Sesame is referred to as the ‘Queen of oilseeds’ due to its highest oil quality, and strong resistance to oxidation (Subrahmaniyan *et al.*, 2024). Sesame seeds contain 40–62% oil, 15–25% protein, 13.4–25.0% carbohydrates and 9.8% digestible fiber

(Dravie *et al.*, 2020) and provide significant health benefits. Presence of lignan compounds sesamin and sesamol serve as a potent source of antioxidants that fight against oxidative stress. Sesame crop can be grown in both subtropical and tropical regions (Dinkar *et al.*, 2026) and has rich genetic diversity. Due to its drought tolerant nature and adaptability to high temperature it is suitable for dryland farming (Tripathi *et al.*, 2013). Sesame is often cultivated on poor and

marginal lands, thus enhancing seed yield appears to be major and a challenging task for breeders. Further productivity of sesame crop is limited by the scarcity of region specific high yielding varieties and the farmer's limited awareness of the availability of such varieties. These challenges underscore the need for targeted research to improve sesame yield as a primary goal of breeding programme. Crop yield is a complex trait and polygenic nature, thus difficult to directly enhance the yield. Therefore present investigation was carried out with the aim to assess the genetic variability and the most reliable yield attributing traits via correlation and path coefficient analysis as information on variability and heritability help to formulate selection criteria for improvement of seed yield and its component traits and heritability estimates along with genetic advance through light on predicting the gain under selection (Islam *et al.*, 2024). The knowledge on character association between yield and its components and their direct and indirect impact on grain yield are helpful for selection process (Pawar *et al.*, 2025)) thus are the guiding tools to breeders over the years.

Materials and Methods

The present experiment was carried out at AICRP on Sesame and Niger, UAS, Dharwad during summer 2025. The study material consisted of 43 advanced mutant lines and six check varieties namely, DS-5, TKG-22, DSM-17-1-1, DS-51, DS-61 and DSS-9. The experiment was laid out in a randomized complete block design with two replications and each genotype was sown in two rows of 3 m length by maintaining a spacing of 30 cm $\times$ 7.5 cm between rows. Standard agronomical practices were followed to raise good crop. Observations were recorded on five randomly selected plants in each genotype for the following characters viz., days to 50 % flowering, days to maturity, number of primary branches per plant, plant height (cm), height to first capsule (cm), number of capsules on the main stem, total number of capsules per plant, number of seeds per capsule, capsule length (cm), 1000 seed weight (g) and seed yield per plant (g). The genotypic and phenotypic coefficients of variation were estimated as per the method of Burton and Devane (1953). Broad sense heritability and genetic advance as per cent of mean was computed following methods suggested by Hanson *et al.* (1956) and Johnson *et al.* (1955). Correlation and path analysis were carried out as per the methods given by Singh and Chaudhary (1977) and Dewey and Lu (1959). statistical analysis was done using R software 4.5.2 on the data of traits mean recorded on 5 randomly plants for yield and its attributable traits.

Results and Discussion

Any plant breeding programme aims to develop high yielding genotypes by improving important traits over the existing ones. Therefore, presence of genetic variability in sesame mutant lines provide valuable opportunity in selecting superior genotypes. Thus, assessing the extent of variability, heritability and genetic advance for different traits is essential.

Analysis of variance revealed highly significant differences among the tested genotypes for all the yield and yield contributing traits studied indicating the presence of high magnitude of variability (Table 1) suggesting a strong potential for effective selection (Islam *et al.*, 2024). Based on the *per se* performance of all the genotypes, a broad range was observed for all the yield and its related traits. This indicates the presence of sufficient variability and providing considerable scope for yield improvement through selection. Similar observations have been made in earlier research work conducted by Ranjithkumar *et al.* (2022) and Mitkari *et al.* (2023).

The estimates phenotypic coefficient of variation was higher than genotypic coefficient of variation with minimal difference between them for all the twelve quantitative characters, indicating effect of environment on expression of these characters (Table 2). High value of GCV and PCV values were recorded for number of capsules per plant (21.4 % and 24.1%) and seed yield per plant (20.8 % and 26.7 %) respectively. Moderate values of PCV and GCV were observed for number of primary branches per plant (12.5% and 13.3%) and number of capsules on main stem (12.2% and 13.8%) respectively. These values indicate that the presence of considerable variability among characters under study. Similar kind of results were also substantiated by Khuntia *et al.*, (2024), Bhattacharya *et al.* (2025) and Hatkar *et al.* (2025).

For selection of genotypes, extent of heritability and genetic advance are widely considered as important parameters and information of genetic variability along with heritability estimates provides more reliable basis for understanding the effectiveness of selection (Burton 1952). The high estimate of heritability was observed for all the characters such as days to 50 per cent flowering (77.9 %), days to maturity (66.6 %), number of primary branches per plant (88.1%), plant height (73.8 %), height to first capsule (85.0%), number of capsules on main stem (78.7%), number of capsules per plant (78.5%), number of seeds per capsule (80.9 %), capsule length (64.0%), 1000 seed weight (88.9 %), oil content (84.7 %) and seed yield per plant (60.5%). The result of our

study was found consistent with the findings of Parameshwarappa *et al.* (2010), Khuntia *et al.* (2024).

Genetic advance as per cent of mean was showed range from 0.049% to 32.70%. A high genetic advance as per cent of mean was witnessed for number of primary branches per plant (24.1 %), number of capsules on main stem (22.3 %), number of capsules per plant (39.0 %) and seed yield per plant (33.3 %). Moderate genetic advance was recorded by height to first capsule (14.6 %), number of seeds per capsule (15.6 %) and 1000 seed weight (12.6 %). This reflects presence of additive gene action thus indicate direct selection for these characters would be effective. Similar findings were reported by Patidar *et al.* (2020), Mitkari *et al.* (2023) and Khuntia *et al.* (2024). Further, combination of high heritability coupled with high genetic advance for the traits indicate their amenability in effective improvement through direct phenotypic selection (Akkiligungta *et al.*, 2024).

The genotypic correlation coefficients (Table 3) for most of the characters recorded higher values than their corresponding phenotypic values indicating that although inherent associations exist among the traits, the lower phenotypic correlation values may be attributed due to the masking or modifying effects of the environment, which alter the true genetic relationships among traits. Genotypic correlation analysis revealed a highly significant and positive genotypic association of seed yield per plant with number of capsules on main stem (0.99), number of capsules per plant (0.99), capsule length (0.97) and 1000 seed weight (0.97), number of primary branches per plant (0.93) and number of seeds per capsule (0.93). These observations are in consonance with the previous reports of others for 1000 weight (Teklu *et al.*, 2014), number of seeds per capsule (Kalaiyarasi *et al.*, 2019), number of primary branches per plant, capsule length (Patil *et al.*, 2018) and number of capsules per plant (Srikanth and Ghodke, 2022).

Inter correlation analysis among the traits revealed that the number of primary branches per plant exhibited a highly significant positive correlation with number of capsules on main stem, number of capsules per plant, number of seeds per capsule, capsule length and 1000 seed weight, indicating their strong mutual association. The number of capsules on main stem also showed a highly significant and positive relationship with number of capsules per plant, number of seeds per capsule, capsule length and 1000 seed weight. Similarly, number of capsules per plant was highly and positively correlated with number of capsules on main stem, number of seeds per capsule, capsule length and 1000 seed weight, reflecting their close

interdependence. The number of seeds per capsule exhibited highly significant positive correlation with number of capsules on main stem, number of capsules per plant, capsule length and 1000 seed weight. Likewise, capsule length recorded a highly significant positive correlation with number of capsules on main stem, number of capsules per plant and 1000 seed weight, signifying their concurrent improvement potential. In addition, 1000 seed weight exhibited a highly significant positive association with number of capsules on main stem, number of capsules per plant and capsule length. The strong associations among number of branches, capsule traits, 1000-seed weight and plant height suggest that simultaneous improvement of these characters may effectively enhance productivity. Similar observations were reported by Kumari, confirming the association between these traits and their collective impact on yield.

Path coefficient analysis (Table 4) demonstrated that at genotypic level, the highest direct effect on seed yield per plant was recorded by number of capsules on main stem (1.218) followed by capsules length (0.730), number of seeds per capsule (0.353), days to 50 per cent flowering (0.237) and height to first capsule (0.127). Path coefficient analysis revealed that days to 50% flowering, height to first capsule, number of capsules on main stem, number of seeds per capsule, capsule length and oil content exhibited positive direct effect at both genotypic and phenotypic level. Similar results were reported by other researchers, for number of seeds per capsule and capsule length by Srikanth and Ghodke (2022), for days to 50% flowering and oil content by Patel *et al.*, (2023), for number of capsules on main stem by Meenakumari *et al.* (2015) and for height to first capsule by Ibrahim and Khidir (2012). At genotypic level, number of primary branches, number of capsules per plant and 1000 seed weight exhibited negative direct effect on seed yield per plant but showed positive indirect effects on seed yield per plant through number of capsules on main stem, number of seeds per capsule and capsule length. Similar results were reported by Kalaiyarasi *et al.* (2019) and Kehie *et al.* (2020). Therefore, these traits would be considered as principal traits during selection programme for the improvement of yield. Conversely, days to maturity and plant height showed negative direct effect on seed yield per plant. These results are in accordance with Srivalli *et al.* (2025) and Jaiswal and Bisen (2021). The magnitude of residual effect at both genotypic and phenotypic level was very low, suggesting that the selected characters in this study are important determinants for improving yield in sesame.

Conclusion

Sesame crop is widely cultivated on poor and marginal lands with low input technologies. Enhancing the productivity is the major concern to bring notable improvement in the seed yield. Therefore, it is essential to understand presence of genetic variability as well as the relationship of independent variables along with its magnitude on dependent trait. In this context from the

present study it is concluded that there is ample genetic variability among the sesame genotypes for traits viz., number of primary branches per plant, number of capsules on main stem, number of capsules per plant, number of seeds per capsule, capsule length and 1000 seed weight and thus provide great scope for plant breeders during selection and improvement programme.

Table 1: Analysis of variance for twelve quantitative characters in sesame genotypes

Sl. No	Sources of variation	Mean sum of squares		
		Treatments (df=48)	Replications (df=1)	Error (df=48)
1	Days to 50 per cent flowering	7.63**	0.09	0.95
2	Days to maturity	32.50**	8.00	6.52
3	Number of primary branches	0.65**	0.01	0.04
4	Plant height (cm)	66.99**	23.61	10.10
5	Height to first capsule (cm)	36.40**	0.83	2.95
6	Number of capsules on main stem	24.87**	5.12	2.97
7	Number of capsules per plant	458.62**	44.45	55.34
8	Number of seeds per capsule	45.91**	10.98	4.84
9	Capsule length (cm)	0.03**	0.01	0.01
10	1000 seed weight (g)	0.09**	0.01	0.01
11	Oil content (%)	3.73**	0.06	0.31
12	Seed yield per plant (g)	5.17**	0.20	1.27

* - Significant at 5% probability level ** - Significant at 5% and 1% probability level

Table 2: Genetic variability parameters for yield and yield related characters in sesame genotypes

Traits	Mean	Range		Coefficient of variation		H2b (%)	GAM (%)
		Minimum	Maximum	GCV (%)	PCV (%)		
DFF	52.4	48.5	56.5	3.5	4.0	77.9	6.3
DM	102.7	94.0	108.5	3.5	4.3	66.6	5.9
NPB	4.4	3.5	6.2	12.5	13.3	88.1	24.1
PH (cm)	106.5	93.9	116.1	5.0	5.8	73.8	8.9
HFC (cm)	53.3	45.1	62.5	7.7	8.3	85.0	14.6
NCM	27.1	20.1	36.0	12.2	13.8	78.7	22.3
NCP	66.4	44.5	126.9	21.4	24.1	78.5	39.0
NSC	53.7	39.0	68.0	8.4	9.4	80.9	15.6
CL (cm)	2.5	2.3	2.9	4.5	5.7	64.0	7.5
TSW (g)	3.1	2.7	3.8	6.5	6.9	88.9	12.6
OC (%)	41.68	37.7	44.2	3.1	3.4	84.7	5.9
SYP (g)	6.7	3.7	11.9	20.8	26.7	60.5	33.3

DFF-Days to 50% flowering; **DM**- Days to maturity; **NPB**- Number of primary branches; plant; **PH**: Plant height (cm); **HFC**: Height to first capsule (cm); **NCM**- Number of capsules on main stem; **NCP**- Number of capsules per plant; **NSC**- Number of seeds per capsule; **CL**- Capsule length (cm); **TSW**-1000 seed weight (g); **OC**-Oil content (%); **SYP**- seed yield per plant (g)

Table 3: Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient for twelve quantitative traits in sesame genotypes

	DFF	DM	NPB	PH	HFC	NCM	NCP	NSC	CL	TSW	OC	SYP
DFF	1.00	0.17	-0.01	0.37**	0.11	0.02	0.08	0.00	-0.05	0.04	-0.03	0.05
DM	0.20*	1.00	0.16	0.16	0.29*	-0.05	-0.17	-0.13	0.04	-0.14	0.44**	-0.16
NPB	-0.001	-0.03	1.00	0.13	-0.12	0.95**	0.87**	0.92**	0.95**	0.96**	-0.13	0.93**
PH	0.32*	0.13	0.14	1.00	0.40**	0.33*	0.30*	0.17	0.35**	0.28*	0.27	0.21
HFC	0.08	0.23*	-0.06	0.38**	1.00	0.04	-0.04	-0.02	-0.04	0.08	0.45**	-0.03
NCM	0.04	0.02	0.64**	0.31**	-0.001	1.00	0.96**	0.90**	0.95**	0.96**	0.06	0.99**
NCP	0.08	-0.12	0.72**	0.33**	-0.02	0.87**	1.00	0.88**	0.93**	0.96**	-0.06	0.99**
NSC	0.02	-0.05	0.65**	0.22*	-0.01	0.85**	0.84*	1.00	0.91**	0.99**	-0.14	0.93**
CL	-0.06	0.03	0.58**	0.29**	-0.03	0.78**	0.76**	0.79**	1.00	0.91**	-0.19	0.97**

TSW	0.07	-0.05	0.65**	0.31**	0.09	0.85**	0.86**	0.91**	0.76**	1.00	-0.07	0.97**
OC	0.02	0.27*	-0.06	0.23*	0.27**	0.12	0.07	0.02	0.05	0.01	1.00	-0.10
SYP	0.08	-0.09	0.70**	0.28**	0.01	0.89**	0.95**	0.90**	0.81**	0.93**	0.04	1.00

* - Significant at 5% probability level ** - Significant at 5% and 1% probability level

DFE-Days to 50% flowering; **DM**- Days to maturity; **NPB**- Number of primary branches per plant; **PH**: Plant height (cm); **HFC**: Height to first capsule (cm); **NCM**- Number of capsules on main stem; **NCP**- Number of capsules per plant; **NSC**- Number of seed per capsule; **CL**- Capsule length (cm); **TSW**-1000 seed weight (g); **OC**-Oil content (%); **SYP**- Seed yield per plant (g).

Table 4: Genotypic and phenotypic path coefficient analysis for seed yield in sesame genotypes

Traits		DFE	DM	NPB	PH	HFC	NCM	NCP	NSC	CL	TSW	OC
DFE	G	0.237	-0.031	0.002	-0.125	0.014	0.028	-0.007	0.002	-0.034	-0.033	-0.001
	P	0.045	-0.006	-0.00001	-0.021	0.002	0.003	0.040	0.002	-0.007	0.019	0.0001
DM	G	0.040	-0.185	-0.053	-0.053	0.037	-0.060	0.015	-0.048	0.027	0.111	0.013
	P	0.009	-0.029	-0.0002	-0.008	0.005	0.002	-0.059	-0.004	0.004	-0.015	0.001
NPB	G	-0.002	-0.030	-0.327	-0.045	-0.016	1.153	-0.078	0.324	0.696	-0.746	-0.004
	P	-0.0001	0.001	0.005	-0.009	-0.001	0.057	0.337	0.050	0.073	0.187	-0.0003
PH	G	0.088	-0.029	-0.044	-0.338	0.051	0.404	-0.027	0.059	0.254	-0.218	0.008
	P	0.014	-0.004	0.001	-0.065	0.009	0.027	0.155	0.017	0.037	0.089	0.0012
HFC	G	0.026	-0.054	0.041	-0.136	0.127	0.043	0.003	-0.006	-0.028	-0.061	0.014
	P	0.004	-0.007	-0.0003	-0.025	0.023	-0.0003	-0.009	-0.001	-0.004	0.026	0.001
NCM	G	0.005	0.009	-0.309	-0.112	0.005	1.218	-0.086	0.317	0.695	-0.745	0.002
	P	0.002	-0.001	0.003	-0.020	-0.0001	0.089	0.409	0.066	0.099	0.247	0.001
NCP	G	0.019	0.031	-0.285	-0.100	-0.005	1.175	-0.089	0.313	0.680	-0.741	-0.002
	P	0.004	0.004	0.004	-0.021	-0.0004	0.077	0.471	0.065	0.096	0.249	0.0004
NSC	G	0.001	0.025	-0.299	-0.056	-0.002	1.094	-0.079	0.353	0.665	-0.765	-0.004
	P	0.001	0.002	0.004	-0.014	-0.0002	0.076	0.396	0.077	0.100	0.262	0.0001
CL	G	-0.011	-0.007	-0.312	-0.118	-0.005	1.161	-0.083	0.322	0.730	-0.706	-0.006
	P	-0.003	-0.001	0.003	-0.019	-0.001	0.069	0.357	0.061	0.128	0.218	0.0003
TSW	G	0.010	0.026	-0.315	-0.095	0.010	1.174	-0.086	0.350	0.667	-0.773	-0.002
	P	0.003	0.002	0.004	-0.020	0.002	0.076	0.405	0.070	0.096	0.289	0.00004
OC	G	-0.007	-0.081	0.044	-0.092	0.057	0.078	0.005	-0.051	-0.136	0.052	0.030
	P	0.001	-0.008	-0.0003	-0.015	0.006	0.011	0.034	0.002	0.006	0.002	0.005

Genotypic residual effect = 0.0773; Phenotypic residual effect = 0.0412; Note: Diagonal bold figures are the direct effect and the off diagonal are indirect effects.

DFE-Days to 50% flowering; **DM**- Days to maturity; **NPB**- Number of primary branches per plant; **PH**: Plant height (cm); **HFC**: Height to first capsule (cm); **NCM**- Number of capsules on main stem; **NCP**- Number of capsules per plant; **NSC**- Number of seed per capsule; **CL**- Capsule length (cm); **TSW**-1000 seed weight (g); **OC**-Oil content (%); **SYP**- seed yield per plant (g).

Acknowledgements

This study was supported by the Department of Genetics and Plant Breeding, AICRP on Sesame and Niger, Main Agricultural Research Station, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India. The author expresses sincere gratitude to the Chairman, Advisory Committee members, Head of the Department, Senior Technical Officer, labours and all other concerned personnel for their valuable guidance and support.

Conflict of interest

The authors hereby declare that no potential conflict of interest exists with respect to the research, authorship or publication of this article.

References

- Akkilgunt, P., Jatothu, J., & Sameer Kumar, C. V. (2024). Unveiling the sesame germplasm: A study of genetic variability for yield (*Sesamum indicum* L.). *Journal of Experimental Agriculture International*, **46**(8), 693–699.
- Bhattacharya, S., Kale, B., Chandramaniya, C. P., Priyanka, B., & Chhodavadiya, R. J. (2025). Deciphering genetic variability, character associations, and diversity analysis in sesame (*Sesamum indicum* L.) germplasms. [Journal name not provided], **25**(1), 898–911.
- Burton, G. W., & DeVane, D. E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. [Journal name not provided], 478–481.
- Burton, G. W. (1952). Quantitative inheritance in grasses. In *Proceedings of the 6th International Grassland Congress* (Vol. 1, pp. 277–283).
- Dewey, D. R., & Lu, K. H. (1959). A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51**, 515–518.
- Dinkar, S. S., Dwivedi, N., Patel, M., Priyadarshi, S., Mourya, B. P., Kumar, A., & Kumar, R. M. (2026). Genetic variability, correlation and path analysis for selection in elite breeding materials of sesame (*Sesamum indicum* L.). *Plant Archives*, **26**(1), 136–141.
- Dravie, E. E., Kortei, N. K., Essuman, E. K., Tettey, C. O., Boakye, A. A., & Hunkpe, G. (2020). Antioxidant, phytochemical and physicochemical properties of sesame seed (*Sesamum indicum* L.). *Scientific African*, **8**, e00349.

- Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agronomy Journal*, **48**(6), 268–272.
- Hatkar, R. M., Rathod, S. T., Sarode, S. B., Washimkar, G. S., & Wadikar, P. B. (2025). Genetic variability studies for yield and yield contributing traits in sesame (*Sesamum indicum* L.). *International Journal of Plant and Soil Science*, **37**(8), 259–266.
- Ibrahim, S. E., & Khidir, M. O. (2012). Genotypic correlation and path coefficient analysis of yield and some yield components in sesame (*Sesamum indicum* L.). [Journal name not provided], 664–670.
- Islam, M. N., Sultana, S., Rashid, M. U., & Rahim, M. A. (2024). Determination of the potentiality of different sesame (*Sesamum indicum* L.) genotypes. *Bangladesh Journal of Agriculture*, **49**(1), 52–67.
- Jaiswal, A., & Bisen, R. (2021). Estimation of correlation and path analysis between seed yield and various quantitative traits in black sesame (*Sesamum indicum* L.). *International Journal of Current Microbiology and Applied Sciences*, **10**(1), 893–901.
- Jakhar, D. S., Kumhar, S. R., Pandey, S., Geat, N., Choudhary, R., Bisen, R., & Vishwakarma, A. K. (2026). Unraveling trait relationships and their direct and indirect contributions to seed yield of sesame (*Sesamum indicum* L.) genotypes. *Journal of Advances in Biology & Biotechnology*, **29**(5), 612–619.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**, 314–318.
- Kalaiyarasi, R., Rajasekar, R., Lokeshkumar, K., Priyadarshini, A., & Mohanraj, M. (2019). Correlation and path analysis for yield and yield traits in sesame (*Sesamum indicum* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, **8**(11), 1251–1257.
- Kehie, T., Shah, P., Chaturvedi, H. P., & Singh, A. P. (2020). Variability, correlation and path analysis studies in sesame (*Sesamum indicum* L.) genotypes under foothill condition of Nagaland. *International Journal of Current Microbiology and Applied Sciences*, **9**, 2917–2926.
- Khuntia, J. B., Dash, A. P., Kar, R. K., Lenka, B., Pradhan, H., Samal, A., Pattanayak, S., Mishra, S., Pani, B., & Satapathy, S. (2024). Unveiling genetic variability and character associations in sesame. *Biochemical and Cellular Archives*, **24**(1).
- Kumari, P., & Shah, P. (2023). Trait association and path coefficient analysis for yield and yield attributing traits in sesame (*Sesamum indicum* L.). *Ecology, Environment and Conservation*, **29**, 242–249.
- Meenakumari, B., & Ganesamurthy, K. (2015). Studies on variability, correlation and path analysis in sesame (*Sesamum indicum* L.). *Advances in Applied Research*, **7**(2), 116–120.
- Mitkari, S. B., Wankhade, M. P., Ghuge, S. B., Kadam, K. V., & Deshmukh, S. S. (2023). Analysis of direct and indirect effect of yield contributing traits in sesame (*Sesamum indicum* L.). *The Pharma Innovation Journal*, **12**(12), 1341–1344.
- Parameshwarappa, S. G., Palakshappa, M. G., Salimath, P. M., & Parameshwarappa, K. G. (2010). Analysis of genetic divergence in sesame, *Sesamum indicum* L. [Journal name not provided], 227–230.
- Patel, N. B., Acharya, R. R., Macwana, S. M., Halladakeri, P., Parihar, A., & Parmar, D. J. (2023). Genetic variability, correlation and path analysis for seed yield and yield contributing traits in sesame (*Sesamum indicum* L.) germplasm. *The Pharma Innovation Journal*, **12**, 3781–3786.
- Patidar, B., Tripathi, D., Patidar, S., Patidar, M., Singh, Y., & Kumari, G. (2020). Genetic variability, heritability and genetic advance studies in sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy and Phytochemistry*, **9**(3), 1679–1683.
- Patil, M. K., & Lokesha, R. (2018). Estimation of genetic variability, heritability, genetic advance, correlations and path analysis in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy and Natural Products*, **4**(1), 1–5.
- Pawar, R., Devi, M. S., Bharathi, D., Jyosthna, M. K., & Sekhar, M. R. (2025). Trait interactions influencing yield in sesame (*Sesamum indicum* L.): A correlation and path analytical approach. *Andhra Pradesh Journal of Agricultural Sciences*, **11**(4), 325–330.
- Ranjithkumar, G., Bisen, R., & Kumar, V. (2022). Genetic variability studies for yield and its attributing traits in dark brown sesame (*Sesamum indicum* L.). *International Journal of Plant & Soil Science*, **34**(8), 43–49.
- Singh, R. K., & Chaudhary, B. D. (1977). *Biometrical methods in quantitative genetic analysis*. [Publisher details not provided].
- Srikanth, K., & Ghodke, M. K. (2022). Correlation and path analysis in sesame (*Sesamum indicum* L.) genotypes. *International Journal of Plant & Soil Science*, **34**(18), 228–235.
- Srivalli, K., Kumar, V. S., Madhuri, T., BhagavathaPriya, M., SreenivasaChari, Prabhakarareddy, G., & [Author details incomplete]. (2025). Assessment of genetic variability, correlation and path analysis for yield and yield components in sesame (*Sesamum indicum* L.). In *National Seminar on “Climate Smart Innovations to Address the Current Agronomic Challenges”*, 27–28 June 2025, ANGRAU, Regional Agricultural Research Station, Tirupati (pp. 107–109).
- Subrahmaniyan, K., Veeramani, P., Mahalingam, A., Ranjith, R., Harishma, P. H., & Abarajitha, P. (2024). A comprehensive review on nutritional and antioxidant properties of sesame (*Sesamum indicum* L.) seed oil with its therapeutic utilization as phytomedicine. *Annals of Phytomedicine*, **13**(2), 1–9. <https://doi.org/10.54085/ap.2024.13.2.26>
- Teklu, D. H., Kebede, S. A., & Gebremichael, D. E. (2014). Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. *Asian Journal of Agricultural Research*, **8**(4), 181–194.
- Tripathi, A., Bisen, R., Ravindra, P., Paroha, A. S., Sahu, R., & Ranganatha, A. R. G. (2013). Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. *An International Quarterly Journal of Life Sciences*, **8**, 1387–1391.