



# Genetic Divergence in Linseed (*Linum usitatissimum* L.). Germplasm

A. Y. Patel<sup>a++\*</sup>, P. B. Wadikar<sup>a#</sup>, P. D. Kulkarni<sup>a++</sup>  
and V. M. Nakhate<sup>a++</sup>

<sup>a</sup> Department of Genetics and Plant Breeding, College of Agriculture, Latur, (VNMKV, Parbhani), India.

## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

## Article Information

DOI: <https://doi.org/10.9734/ijpss/2025/v37i75599>

## Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/140363>

Short Research Article

Received: 10/05/2025

Accepted: 15/07/2025

Published: 17/07/2025

## ABSTRACT

Mahalanobis  $D^2$  statistic was used to study the genetic diversity between and within the forty genotypes of linseed (*Linum usitatissimum* L.) at experimental farm department of Genetics and Plant Breeding field at College of Agriculture, Latur (Maharashtra) during Rabi 2023-24 which were sown in RBD Design at 30 cm x 5 cm spacing. The observations were recorded on ten quantitative characters namely days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight (g), harvest index, oil content (%) and seed yield per plant. The data recorded on these characters was utilized for estimation of mean, variability, genetic advance, and genetic diversity by  $D^2$  method. Forty genotypes were grouped into four clusters using Tocher's method. Cluster I had the highest number of genotypes (27) followed by cluster II (10), cluster IV (02) and cluster III included 1 genotype cluster. The intra cluster distance ( $D^2$ ) ranges from 10.86 to 12.89, whereas inter cluster

<sup>++</sup> M.Sc Student;

<sup>#</sup> Associate Professor;

<sup>\*</sup>Corresponding author: E-mail: [akhilpatel4959@gmail.com](mailto:akhilpatel4959@gmail.com);

**Cite as:** Patel, A. Y., P. B. Wadikar, P. D. Kulkarni, and V. M. Nakhate. 2025. "Genetic Divergence in Linseed (*Linum usitatissimum* L.). Germplasm". *International Journal of Plant & Soil Science* 37 (7):540-48. <https://doi.org/10.9734/ijpss/2025/v37i75599>.

distance  $D^2$  ranges from 14.70 to 22.36. The maximum inter cluster distance ( $D^2 = 22.36$ ) was observed between cluster I and cluster IV. All four clusters identified through divergence analysis comprised genotypes of diverse origins, suggesting a lack of parallelism between genetic diversity and geographical distribution. There is considerable potential for achieving improvement through hybridization and selection by making crosses between accessions belonging to different clusters.

**Keywords:** Cluster analysis; genetic diversity; hybridization; linseed.

## 1. INTRODUCTION

“Linseed (*Linum usitatissimum* L.) with a chromosome number of  $2n = 30$ , is one of the most significant *rabi* oilseed crops and belongs to the genus *linum*, a latin word meaning very beneficial” (Naik et al., 2020). “It is an annual crop from the Linaceae family under the order malpighiales, and is commonly referred to as “Alsi.” its probable origin is south west Asia, especially India. *Linum usitatissimum* is the only cultivated species of its genus and has been under cultivation for approximately 6000–7000 years, making it one of the oldest domesticated crops” (Paul et al., 2020). “All parts of the linseed plant are useful, and its oil content ranges between 33% and 45%” (Jaishri, 2021). “It is considered the richest plant-based source of omega-3 (36-57%) and omega-6 (18-24%) fatty acids, which are essential for human nutrition” (Paul et al., 2020). regular intake of 25 grams of linseed per day has been shown to lower the risk of breast cancer (Kaur et al., 2023; Mandal et al., 2025). Linseed grows best in cool climatic conditions, with ideal temperatures ranging from 10°C to 38°C, making October to November the most suitable sowing period. In Maharashtra, farmers have been cultivating linseed traditionally for generations, often using the same seed stock year after year without adopting scientific methods in most regions. With the increasing adoption of improved linseed varieties, these traditionally grown genotypes are gradually disappearing, despite carrying genetically valuable and diverse traits. One of the main reasons for low productivity is that linseed is often grown under the utera (relay cropping) system, in conditions of limited soil moisture and minimal input usage, leading to poor yields.

The assessment of genetic diversity is crucial as it provides a foundation for selecting suitable parents in hybridization programs aimed at crop improvement. Genotypes that are more genetically diverse, yet meet essential criteria of adaptability and performance, are more likely to exhibit greater hybrid vigor and produce a broad

range of variability in the segregating generations. The Mahalanobis  $D^2$  statistic, developed through multivariate analysis of quantitative traits, offers a powerful method for evaluating genetic divergence among genotype groups and identifying ideal parents for crossing in both self-pollinated and outbreeding crops.

## 2. MATERIALS AND METHODS

The experiment was conducted during *rabi* 2023-24 at experimental farm department of Genetics and Plant Breeding, College of Agriculture, Latur (VNMKV Parbhani) sown in a Randomized Block Design with two replications at a spacing of 30 x 5 cm. The experiment material comprised of 40 lines of linseed collected from Oilseeds Research Station (ORS), Latur. The analysis of genetic divergence was carried out by using Mahalanobis  $D^2$  statistics. The grouping of the genotypes into clusters was made as per Tocher's method. Five randomly competitive plants were taken from each environment for recording the data for all the traits viz. days to 50% flowering, days to maturity, plant height, number of capsules per plant, number of seeds per capsule, 1000 seed weight (g), harvest index, oil content and seed yield per plant.

## 3. RESULTS AND DISCUSSION

The variation among genotypes were highly significant for day to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight (g), harvest index (%), oil content (%) and seed yield per plant (g). Analysis of variance for these ten quantitative characters as presented in Table 1. The results revealed that mean sum of squares of genotypes were significant for all the characters under study, which indicated the existence of adequate amount of variability among the genotypes as given in Table 1, similar results were reported by Singh et al., (2019).

**Table 1. Analysis of variance for ten quantitative characters in linseed.**

Sr. No	Characters	Mean sum of squares		
		Replications (df=1)	Treatments (df=39)	Error (39)
1	Days to 50% flowering	2.11	7.67**	1.30
2	Days to maturity	2.45	22.69**	3.7
3	Plant height (cm)	11.40	51.07**	5.48
4	Number of branches per plant	0.098	0.79**	0.04
5	Number of capsules per plant	0.01	185**	7.8
6	Number of seeds per capsule	0.42	0.44**	0.19
7	1000 seed weight (g)	0.032	1.81**	0.14
8	Harvest index (%)	0.05	40.65**	1.28
9	Oil content (%)	0.63	8.12**	0.59
10	Seed yield per plant (g)	0.032	0.69**	0.12

\*and \*\* indicates significance at 5% and 1% respectively.

The estimates of GCV and PCV for different characters are given in Table 2 which revealed that high genotypic coefficient of variance (GCV) was highest for harvest index (17.96%) and number of branches per plant (17.54%). Phenotypic coefficient of variance (PCV) was highest for harvest index (18.26) and number of branches per plant (18.03). In general, the magnitude of the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. The characters with high value of GCV indicates high potential for selection, while the magnitude of the phenotypic coefficient of variation was higher than the genotypic coefficient of variation which indicates an influence of environment on the traits. Graphical representation of GCV and PCV for different characters is presented in Fig. 1.

Understanding heritability and the expected genetic advance is essential for breeders to adopt an appropriate breeding strategy. Hence, it is important to assess the extent of genetic variability, heritability, and genetic advance as per cent of mean presented in Table 2, while Graphical representation is in Fig. 2. High heritability coupled with high genetic advance as per cent of mean which indicated that heritability is most likely due to additive gene effects and simple phenotypic selection may be effective. The estimates of heritability, genetic advance and genetic advance as percent mean is given in Table 3, in which maximum heritability was observed for days to 50 % flowering (98.3%), harvest index and 1000 seed weight. The estimates of genetic advance ranged from 0.54 per-cent to 18.97 per-cent at (5%) level of significance with the highest estimates in case of number of capsules per plant (18.97 %). The

estimates of genetic advance as per cent of mean ranged from 5.82 per-cent to 36.42 per cent at 5 (%) level of significance with the highest estimates in case of harvest index (36.42 %). In this study, high heritability and genetic advance as per centage of the mean (>20) were recorded for number of branches per plant, harvest index (%) and Seed yield per plant (g). Similar findings were reported by Meena et al. (2020), Terfa et al. (2020), Thakur et al. (2020), Triveni et al. (2024) and Korra et al. (2024).

The genetic diversity of selected parents is not always based on factors such as geographic diversity or place of release or ploidy level. Thus, for characterization of germplasm for genetic divergence for selection of suitable and diverse genotypes should be based on second statistical procedures, such as D<sup>2</sup> statistics and non-hierarchical Euclidean cluster analysis. All 40 linseed genotypes were classified into four distinct and non-overlapping clusters using Tocher's method. The primary objective of forming these clusters is to determine the intra and inter-cluster distances, which act as a guideline for selecting genetically diverse parents. "Mahalanobis D<sup>2</sup> statistics was used for quantitative assessment of genetic divergence for yield and its contributing characters among 40 linseed genotypes. Performing this, all the linseed genotypes are grouped into four clusters on the basis of their relation and closeness of different genotypes with respect to their D<sup>2</sup> values. Intra cluster distances depicts us the divergence among the genotypes within the cluster whereas inter cluster distances represent the relation of divergence between the clusters" (Triveni et al., 2024).

**Table 2. Estimates of variability parameters for ten characters for yield and yield contributing characters in linseed.**

Sr. No	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (h <sup>2</sup> ) (%)	Genetic Advance as % of mean
			Min	Max				
1	Days to 50% flowering	51.52	37	58	8.90	8.75	96.8	17.74
2	Days to maturity	99.02	91	105	3.40	3.11	83.7	5.86
3	Plant height (cm)	62.14	37	79.8	12.48	12.18	95.3	24.50
4	Number of branches per plant	3.48	2	5	18.03	17.54	94.6	35.15
5	Number of capsules per plant	54.85	19.8	76	17.53	17.15	95.7	34.58
6	Number of seeds per capsule	7.84	6.2	8.8	6.01	4.50	56.2	6.96
7	1000 seed weight (g)	7.73	6	10	12.55	12.32	96.3	24.90
8	Harvest index (%)	24.68	18	32.12	18.26	17.96	96.8	36.42
9	Oil content (%)	33.72	30.24	37.9	5.97	5.75	92.7	11.40
10	Seed yield per plant (g)	4.39	2.6	5.8	13.39	12.08	81.4	22.45

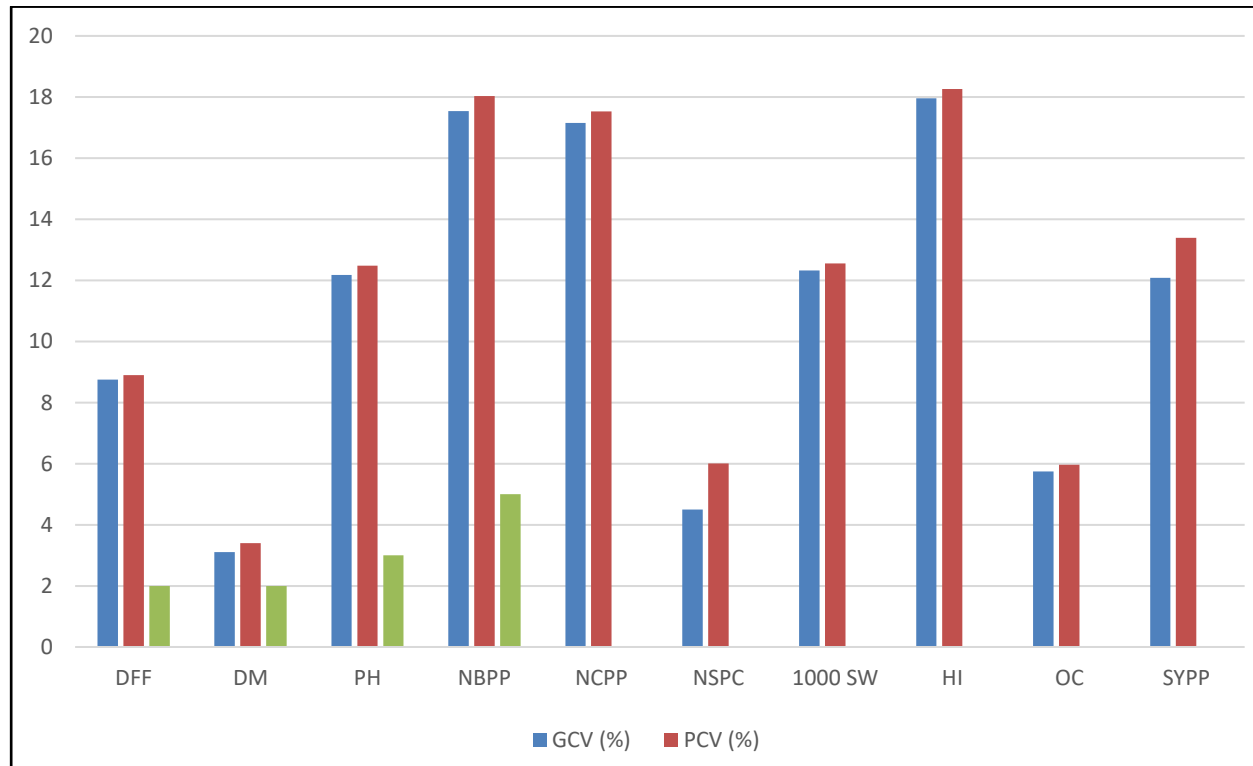
GCV- Genotypic coefficient of variation; PCV- Phenotypic coefficient of variation

**Table 3. Cluster mean among four clusters for ten characters for forty genotypes of Linseed.**

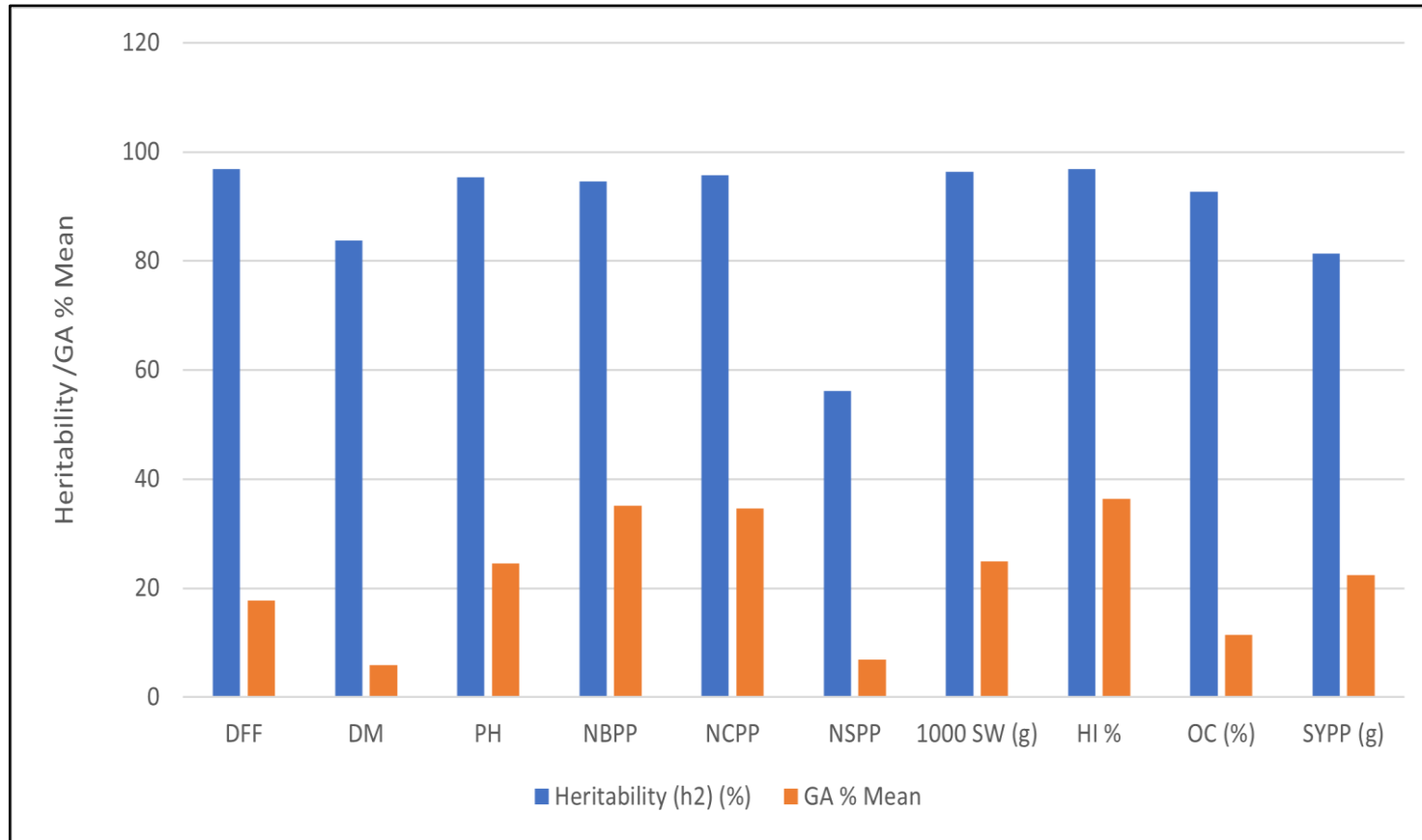
Traits	Cluster I	Cluster II	Cluster III	Cluster IV
Days to 50% flowering	52.33	53.40	39.00	37.50
Days to maturity	99.39	98.75	95.50	97.25
Plant height (cm)	62.80	63.15	58.30	50.15
No. of branches plants	3.30	3.95	2.90	4.03
Number of capsules per plant	50.79	66.8	48.20	53.35
Number of seeds per capsule	7.66	8.30	7.30	8.45
1000 seed weight (gm)	7.55	8.09	6.10	9.32
Harvest index (%)	22.61	29.84	18.25	30.26
Oil content (%)	33.07	35.28	31.47	35.98
Seed yield per plant (gm)	4.2	4.85	3.60	5.10

**Table 4. Intra and Inter cluster distances (D) among four clusters for forty Linseed genotypes.**

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	<b>11.16</b>	14.70	17.31	22.36
Cluster II		<b>10.86</b>	22.31	19.02
Cluster III			<b>0.00</b>	22.30
Cluster IV				<b>12.89</b>



**Fig. 1. Bar graph representing genotypic and phenotypic coefficient of variation in linseed**



**Fig. 2.** Bar graph representing heritability and genetics advance as % of mean for all characters of linseed

The average intra and inter cluster  $D^2$  values are presented Table 4. The intra cluster distance ( $D^2$ ) ranges from 10.86 to 12.89, whereas inter-cluster distance  $D^2$  ranges from 14.70 to 22.36. Maximum inter cluster distance ( $D^2 = 22.36$ ) was observed between cluster I and cluster IV, followed by cluster II and III ( $D^2 = 22.31$ ), cluster III and cluster IV ( $D^2 = 22.30$ ). The minimum inter cluster distance ( $D^2 = 14.70$ ) was between clusters I and II. Indicating that the genotypes falling in the clusters I and IV were highly divergent from each other implying a large amount of diversity within and between groups, which could be exploited in a breeding programme. The minimum inter cluster distance ( $D^2 = 14.70$ ) was between clusters I and II indicating that this cluster is less divergent. The cluster means for the ten characters are presented in Table 4. Similar result was found in Kumar *et al.* (2018), Patial *et al.* (2019), Samantara *et al.* (2020), Tewari *et al.* (2020) and Thakur *et al.* (2021).

A considerable inter-cluster variation was observed among the cluster means for the characters presented in Table 3. studied *viz.*, days to 50 per-cent flowering, days to maturity, plant height, branches per plant, number of capsules per plant, seeds per capsule, 1000 seed weight (g), harvest index (%), oil content (%) and seed yield per plant. The cluster mean for days to 50 per cent flowering varied from 37.50 (IV) to 53.40 (II), the cluster mean for days to maturity ranged between 95.50 (III) to 99.39 (I), the cluster mean for plant height was from 50.15 (IV) to 63.15 (II), the cluster mean for branches per plant ranged from 2.90 (III) to 4.03 (IV), the cluster mean for capsules per plant varied from 48.20 (III) to 66.80 (II), the cluster mean for seeds per capsule varied from 7.30 (III) to 8.45 (IV), the cluster mean for 1000 seed weight (g) ranged from 6.10 (III) to 9.32 (IV), the cluster mean for harvest index (%) ranged from 18.25 (III) to 30.26 (IV), the cluster mean for oil content ranged from 31.47 (III) to 35.98 (IV) and the cluster mean for yield per plant ranged from 3.60 (III) to 5.10 (IV). The results indicate that the harvest index contributed the most (26.28%) to genetic divergence among the forty linseed genotypes. traits like days to 50% flowering (14.87%), 1000 seed weight (14.49%), and number of capsules per plant (13.46%) also played major roles in divergence. However, traits such as seed yield per plant (0.26%) and number of seeds per capsule (0.13%) had a low impact. These findings suggest that traits with higher

contributions should be prioritized in selection and hybridization programs to maximize genetic improvement. This result is in accordance with the findings of Kasana *et al.*, (2018) and Rizvi *et al.*, (2018).

#### 4. CONCLUSION

The variability among genotypes was highly significant for all the characters. The highest magnitude of genotypic coefficient of variation was observed for harvest index followed by number of branches per plant. Phenotypic coefficient of variance (PCV) was highest for harvest index followed by number of branches per plant and number of capsules per plant. Heritability estimates were highest for days to 50 per cent flowering, followed by harvest index (%). In terms of genetic advance as a percentage of mean, the highest value was recorded for harvest index (%), followed by the number of branches per plant. The cluster mean values revealed marked differences across clusters for each character. Notable inter-cluster variability was observed for traits such as days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seeds per capsule, 1000 seed weight, harvest index, oil content, and seed yield per plant. Therefore, genotypes chosen for hybridization should ideally be selected from clusters that exhibit the greatest genetic distance. Hybridization among accessions from different clusters identified in this study could lead to considerable genetic improvement by following appropriate selection strategies in the segregating generations.

#### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

#### REFERENCES

- Dalvi, V. T., Wadikar, P. B., Thombare, R. A., Jadhav, R. S., & Gaiwal, K. B. (2022). Genetic divergence studies for quantitative

- traits in linseed (*Linum usitatissimum* L.). *The Pharma Innovation Journal*, 11(12), 4953–4956.
- Jaishri, J. (2021). Genetic divergence and variability studies in yellow seeded and flax type linseed (*Linum usitatissimum* L.). M.Sc. Thesis, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. 1-83.
- Kasana, R. K., Singh, P. K., Tomar, A., Mohan, S. & Kumar, S. (2018). Selection parameters (heritability, genetic advance, correlation and path coefficient) analysis in linseed (*Linum usitatissimum* L.). *The Pharma Innovation Journal*. 7(6), 16-19.
- Kaur, V., Singh, M. & Wankhede, D. P. (2023). Diversity of *Linum* genetic resources, agro-morphological characterisation to novel genomic technologies-a review. *Frontiers in Nutrition*. 10, 11-65580.
- Korra, S., Guglothu, S. & Nalini, T. (2024). Analysis of genetic variability, heritability and genetic advance for yield and yield-related traits of linseed (*Linum usitatissimum* L.). *Journal of Advances in Biology & Biotechnology*. 27(10), 1596-1604.
- Kumar, S., Sharma, A. & Chaudhary, A. M. (2018). Diversity analysis in linseed. *Journal of Current Microbiology and Applied Sciences*, 7(2), 597–601.
- Mandal, R. K., Mallikarjun, Suresh, K., Choudhary, V., Choudhary, H., & Chetna. (2025). Studying Genetic Diversity in Genotypes of Linseed (*Linum usitatissimum* L.) Using Agro-morphological Traits for Rainfed Conditions. *Journal of Advances in Biology & Biotechnology*. 28(2), 411–418.
- Meena, A. K., Kulhari, S. & Kumar, M. (2020). Studies on genetic variability and character association in linseed (*Linum usitatissimum* L.). genotypes. *International Journal of Current Microbiology and Applied Sciences*. 9(7), 3949-3957.
- Naik, S. R., Anurag, A. P., Prakruthi, M. and Mahesh, M. S. (2020). Flax seeds (*Linum usitatissimum*) nutritional composition and health benefits. *Journal of Nutritional, Metabolism and Health Science*. 3(2), 35-40
- Patial, R., Paul, S., Sharma, D., Sood, V. K. & Kumar, N. (2019). Morphological characterization and genetic diversity of linseed (*Linum usitatissimum* L.). *Indian Society of Oilseeds Research*. 36(1), 8-16.
- Paul, S., Satasiya, P. & Kumar, A. (2020). Genetic variability, correlation and path coefficient analysis of introduced genotypes of linseed in mid hills of North West Himalayas. *Journal of Pharmacognosy and Phytochemistry*. 9(1), 1189-1192.
- Rizvi, A., Marker, S. & Choudhary, A. (2018). Multivariate analysis in linseed (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry*. 7(2), 528-531.
- Samantara, K., Mohapatra, S. R. & Pradhan, B. D. (2020). Assessment of genetic diversity in linseed (*Linum usitatissimum* L.). *International Journal of Current Microbiology and Applied Sciences*. 9(5), 508-513.
- Singh, V. K., Kerkhi, S. A, Singh, S. and Tomar, P. (2019). Study on genetic variability, heritability and Genetic advance for grain yield and yield component traits (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry*. 8(2), 761-765.
- Terfa, G. N. & Gurmu, G. N. (2020). Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.). genotypes for seed yield and other agronomic traits. *Oil Crop Science*. 5(3), 156-160.
- Tewari, N., Singh, A. & Husain, M. F. (2020). Assessment of genetic and geographic divergence in linseed (*Linum usitatissimum* L.). genotypes. *International Journal of Agriculture & Environmental Science*. – Volume 7.
- Thakur, R., Paul, S. & Satasiya, P. (2020). Genetic variability and path analysis for yield and its related traits in linseed (*Linum usitatissimum* L.). *International Journal of Current Microbiology and Applied Sciences*. 10, 2579-2586.
- Thakur, R., Paul, S., Thakur, G. & Kumar, A. (2021). Assessment of genetic diversity among linseed germplasm based on morphological traits. *Journal of Pharmacognosy and Phytochemistry*. 9(6), 1785-1790.
- Triveni, R. P., Agarwal, A. P. & Sharma, D. J. (2024). Assessment of genetic variability and correlation analysis for yield and yield associated

traits in linseed genotypes (*Linum usitatissimum* L.). *International Journal of*

*Advanced Biochemistry Research*. 934-936.

**Disclaimer/Publisher's Note:** The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

© Copyright (2025): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

*Peer-review history:*

*The peer review history for this paper can be accessed here:*

<https://pr.sdiarticle5.com/review-history/140363>