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Assessment of Genetic Divergence for Quantitative Traits in Linseed (*Linum usitatissimum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. Author PDA designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Authors PBW and SS managed the analyses of the study. Authors PMT, PRK and AAS managed the literature searches. All authors read and approved the final manuscript.

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Abstract

Background: Linseed (*Linum usitatissimum* L.) is an important oilseed crop for which the identification of genetically diverse parents can support breeding for yield and related traits.
Aim: The present investigation was conducted in the field of Genetics and Plant Breeding at the College of Agriculture, Latur (Maharashtra), during *Rabi* 2024-2025. The aim of this study was to assess the extent of genetic divergence among 40 linseed genotypes for ten quantitative traits and to identify diverse parents for future breeding programmes.
Study design: A Randomised Block Design with two replications was used.
Place and Duration of Study: Department of Genetics and Plant Breeding, College of Agriculture, Latur (VNMKV, Parbhani), Maharashtra, India, during *Rabi* 2024-2025.
Methodology: Forty genotypes of linseed were evaluated for ten quantitative traits, viz., 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),

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harvest index (%), oil content (%) and seed yield per plant (g). Genetic diversity was assessed using the Mahalanobis D² statistic, and the genotypes were clustered using Tocher's method.
Results: The 40 genotypes were grouped into 8 clusters, indicating considerable genetic diversity. The highest contribution towards genetic divergence was made by 1000-seed weight, followed by plant height, number of capsules per plant and number of branches per plant. The maximum inter-cluster distance was observed between Cluster VII and Cluster VIII, suggesting wide genetic variability and greater heterosis potential.
Conclusion: The presence of substantial genetic divergence among linseed genotypes suggests the predominance of additive gene action and the effectiveness of selection for these traits. Crosses between genotypes from widely divergent clusters, particularly those from Cluster VII and Cluster VIII, are likely to produce transgressive segregants and may be utilised in future breeding programmes for yield and related trait improvement.

Keywords: Linseed; genetic divergence; cluster analysis; heritability; genetic advance; seed yield; oil content.

1. Introduction

Linseed (*Linum usitatissimum* L.), also known as flaxseed, is a major oilseed crop of agricultural importance. Vavilov identified two centres of origin for linseed: the oilseed type originated in Southwest Asia, while the fibre type evolved in the Mediterranean region. Oilseeds are essential components of global agriculture, providing vegetable oils and proteins for human diets, animal feed, and various industrial purposes. Major oilseed cropsinclude soybean (*Glycine max*), sunflower (*Helianthus annuus*), groundnut (*Arachis hypogaea*), and linseed (*Linum usitatissimum L.*). India is one of the world's leading oilseed-producing nations, contributing nearly 19% of the global oilseed area and about 10% of total world production. In the Indian agricultural sector, oilseeds rank next to cereals in importance and occupy around 14% of the country's gross cropped area.

Linseed (*Linum usitatissimum* L.) is a major *Rabi* oilseed crop with a chromosome number of 2n = 30 and belongs to the genus Linum and the family Linaceae. It is an annual, self-pollinated, non-edible oilseed crop commonly known as Alsi. At present, linseed is cultivated across Asia, Europe, the Americas, and Africa for both oil and fibre. In Southwest Asia, including Turkistan, Afghanistan, India, Nepal, and Canada, it is predominantly grown for oil, whereas in Russia, Egypt, and north-western Europe it is mainly cultivated for its superior quality fibre used in the production of linen fabrics and other products.

Genetic diversity forms the foundation of biodiversity and includes variation within species, among species, and across ecosystems. Crop diversity is a crucial component of agricultural production systems, playing a vital role in ensuring food security.

The sustainability and future success of global agriculture depend on its capacity to adapt by developing crop varieties suited to sustainable farming practices while maintaining high productivity to meet the demands of a growing population.

Recent large-scale and accession-based evaluations have documented substantial agro-morphological and yield-related variation in linseed germplasm, supporting systematic characterisation of diverse materials for breeding use (Kaur *et al.*, 2024; Singh *et al.*, 2024).

At the trait level, genomic analysis of thousand-seed weight has further demonstrated a complex genetic basis for this yield component and the utility of association mapping for its genetic dissection in linseed (Saroha *et al.*, 2023).

Agro-morphological D² analysis under rainfed conditions has likewise identified clear inter-genotypic divergence in linseed, supporting multivariate diversity assessment for the selection of divergent breeding materials (Mandal *et al.*, 2025).

Complementary evidence from recent line × tester analysis has shown genetic variation for seed yield and component traits among linseed parents and hybrids, emphasising the importance of parental choice in breeding programmes (Kshirsagar *et al.*, 2026).

Recent phenotypic evaluations have also reported variation across yield-associated and biochemical characters in linseed, supporting continued assessment of quantitative variability when identifying breeding materials (Shubham *et al.*, 2026).

Morphological characterisation under DUS descriptors has likewise separated linseed germplasm into distinct clusters, indicating that standardised agro-morphological characterisation can complement multivariate diversity assessment for identifying differentiated materials (Paliwal *et al.*, 2024).

Recent work using multi-environment evaluation, large germplasm core-collection analysis, and SSR markers has further documented structured diversity across linseed and Linum materials, providing complementary evidence for the characterisation and selection of genetically differentiated germplasm (Bezil *et al.*, 2026; Gouy *et al.*, 2025; Raut *et al.*, 2026).

A study-specific gap remains in quantifying the extent and pattern of genetic divergence among the 40 linseed genotypes under the present experimental conditions and in identifying divergent parental combinations from the measured quantitative traits.

1.1 Objective

The objective of the present study was to assess the extent of genetic divergence among 40 linseed genotypes for ten quantitative traits and to identify diverse parents for future breeding programmes.

2. Material and Methods

2.1 Experimental Site and Season

The present investigation was conducted during the Rabi season of 2024–25 at the experimental farm of the Department of Genetics and Plant Breeding, College of Agriculture, Latur (VNMKV, Parbhani), Maharashtra, India. The experiment was undertaken to evaluate genetic variability and divergence among linseed (*Linum usitatissimum* L.) genotypes for quantitative characters associated with crop performance, seed yield and oil content.

2.2 Experimental Material and Design

The experimental material consisted of 40 linseed genotypes collected from Indira Gandhi Krishi Vishwavidyalaya, Raipur. All 40 genotypes were evaluated under the same experimental conditions. The experiment was laid out in a Randomised Block Design (RBD) with two replications. A spacing of 30 × 5 cm was maintained during the experiment.

The use of two replications allowed the experimental material to be compared within the Randomised Block Design and provided the basis for assessing differences among the 40 genotypes for the quantitative characters studied.

2.3 Recording of Observations

Five randomly selected competitive plants were used for recording observations on the quantitative characters included in the study.

The 40 linseed genotypes were evaluated for ten 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), seed yield per plant (g), harvest index (%) and oil content (%).

These observations constituted the experimental data used for assessing variability and genetic divergence among the evaluated linseed genotypes.

2.4 Analysis of Variance and Variability Parameters

The data recorded for the ten quantitative characters were subjected to analysis of variance to determine the extent of variation among the 40 linseed genotypes. Under the Randomised Block Design with two replications, the analysis included variation attributable to replications, treatments and experimental error. The corresponding degrees of freedom were 1 for replications, 39 for treatments and 39 for error. The significance of treatment differences was assessed at the 5% and 1% levels.

For each of the ten characters, the mean and range of observations were considered together with the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as a percentage of the mean.

2.5 Genetic Divergence and Cluster Analysis

Genetic divergence among the 40 linseed genotypes was assessed using the Mahalanobis D^2 statistic based on the quantitative characters evaluated in the experiment. The multivariate divergence analysis was used to determine the extent of genetic differentiation among the genotypes by considering the studied characters collectively.

On the basis of genetic divergence, the genotypes were grouped into clusters according to Tocher's method. The resulting clusters were used to describe the distribution of genetic diversity among the 40 genotypes. Cluster mean values for the ten quantitative characters were examined to compare the performance of the different clusters for individual traits.

3. Results and Discussion

The analysis of varianc e clearly demonstrated the existence of substantial genetic variability among the 40 linseed genotypes for most of the quantitative traits studied, as presented in Table 1. The presence of highly significant differences for flowering time, maturity, plant height, yield components, seed yield and oil content indicates that effective selection can be practised for the improvement of these characters. Similar observations have been reported by Singh *et al.* (2019) and Tyagi *et al.* (2014).

The estimates of heritability (h^2), genetic advance (GA) and genetic advance as a percentage of the mean (GAM) for ten quantitative traits in forty linseed genotypes are presented in Table 2.

These parameters provide valuable information regarding the nature of gene action and the effectiveness of selection for trait improvement. The heritability estimates ranged from 0.34 for number of seeds per capsule to 0.90 for harvest index. High heritability was observed for harvest index (0.90), plant height (0.88), number of capsules per plant (0.85), 1000-seed weight (0.80), and number of branches per plant (0.79), indicating that these traits were less influenced by environmental factors and largely controlled by genetic factors. Moderate heritability was recorded for oil content (0.65), seed yield per plant (0.62), and days to 50% flowering (0.56), suggesting that selection for these traits would be moderately effective. In contrast, days to maturity (0.43) and number of seeds per capsule (0.34) exhibited low heritability, indicating a greater environmental influence and lower efficiency of direct selection. Similar results were obtained by Johnson *et al.* (1955) and Singh *et al.* (2019).

Among the clusters, Cluster I exhibited the highest intra-cluster distance (31.47), followed by Cluster II (23.04), suggesting the presence of relatively higher genetic variability among genotypes within these clusters, as presented in Table 4. The intra-cluster distances of Clusters III, IV, V, VI, VII, and VIII were zero, indicating that each of these clusters consisted of a single genotype and therefore showed no internal divergence. The inter-cluster distances ranged from 55.65 to 401.20, indicating a wide range of genetic diversity among the clusters. The maximum inter-cluster distance was observed between Cluster VII and Cluster VIII (401.20), followed by Cluster IV and Cluster VIII (255.68) and Cluster V and Cluster VIII (249.96). These high D^2 values indicate that the genotypes belonging to these clusters are highly genetically divergent. Similar results were obtained by Kumar *et al.* (2018) and Tewari *et al.* (2023).

The cluster mean values presented in Table 3 indicate substantial variability among the eight clusters for all ten characters studied, suggesting the existence of considerable genetic diversity among the forty linseed genotypes. The mean value for days to 50% flowering ranged from 47.00 days (Cluster VI) to 56.00 days (Cluster IV). Early-flowering genotypes are desirable for escaping terminal drought and fitting into multiple cropping systems. Days to maturity varied from 85.50 days in Cluster VI to 104.50 days in Cluster IV. Plant height ranged from 35.10 cm (Cluster VI) to 72.60 cm (Cluster III). Plant height contributes significantly to biomass production and lodging resistance. The number of branches per plant varied between 2.40 (Cluster V) and 3.45 (Cluster II). The highest mean number of capsules per plant was observed in Cluster III (45.00), followed by Cluster VIII (42.10). The number of seeds per capsule ranged from 7.20 (Cluster V) to 9.30 (Cluster VIII). The highest 1000-seed weight was recorded in Cluster VII (9.65 g). Harvest index varied from 20.41% (Cluster V) to 43.28% (Cluster II). Oil content ranged from 29.90% (Cluster VII) to 34.45% (Cluster IV). Cluster IV exhibited the highest oil content, followed by Cluster VI (33.13%) and Cluster III (32.75%). These findings suggest that traits with higher contributions should be prioritised in selection and hybridisation programmes to maximise genetic improvement.

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	11.25	16.33**	4.48
2	Days to maturity	15.31	32.49**	12.90
3	Plant height (cm)	0.96	72.26**	4.42
4	Number of branches per plant	0.16	0.47**	0.05
5	Number of capsules per plant	0.18	77.80**	5.97
6	Number of seeds per capsule	0.012	0.34**	0.16
7	1000 seed weight (g)	0.22	1.03**	0.10
8	Seed yield per plant (g)	0.08	0.56**	0.13
9	Harvest index (%)	8.81	47.37**	2.39
10	Oil content (%)	0.025	6.41**	1.34

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

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^2)	Genetic Advance as % of mean
			Min	Max				
1	Days to 50% flowering	51.75	47.00	56.00	06.23	04.70	0.56	07.31
2	Days to maturity	98.66	85.50	104.5	04.82	03.17	0.43	04.29
3	Plant height (cm)	51.90	35.10	72.60	11.93	11.22	0.88	21.74
4	Number of branches per plant	03.22	02.40	03.45	15.97	14.27	0.79	26.28
5	Number of capsules per plant	39.84	26.00	45.00	16.24	15.04	0.85	28.68
6	Number of seeds per capsule	08.30	07.20	09.30	06.05	03.57	0.34	04.35
7	1000 seed weight (g)	07.30	04.70	09.65	10.34	09.29	0.80	17.19
8	Seed yield per plant (g)	04.32	03.69	04.95	13.66	10.81	0.62	17.62
9	Harvest index (%)	24.61	20.41	43.28	20.26	19.26	0.90	37.72
10	Oil content (%)	32.24	31.89	34.45	06.10	04.93	0.65	08.22

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation

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

Traits	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	51.53	53.00	55.50	56.00	54.00	47.00	52.00	50.50
Days to maturity	99.22	96.50	98.00	104.5	89.00	85.50	102.5	99.00
Plant height (cm)	51.85	52.05	72.60	43.30	53.30	35.10	55.40	53.10
No. of branches per plant	03.26	03.45	03.10	03.40	02.40	02.80	03.10	02.70
Number of capsules per plant	40.54	37.85	45.00	26.00	37.60	40.80	29.40	42.10
Number of seeds per capsules	08.32	08.50	08.30	08.10	07.20	08.40	08.70	09.30
1000 seed weight (gm)	07.22	07.55	07.70	07.70	08.95	07.20	09.65	04.70
Seed yield per plant	04.32	04.63	03.90	04.20	03.69	04.95	04.55	04.00
Harvest index (%)	23.70	43.28	22.21	24.31	20.41	25.55	23.15	24.21
Oil content (%)	32.21	32.40	32.75	34.45	32.36	33.13	29.90	31.89

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

Cluster	I	II	III	IV	V	VI	VII	VIII
Cluster I	**5.61**	11.29	8.53	8.85	8.39	8.30	11.69	10.32
Cluster II		**4.80**	13.98	11.38	13.87	12.83	14.91	15.10
Cluster III			**0.00**	13.15	9.50	14.20	12.41	12.34
Cluster IV				**0.00**	7.60	9.90	8.34	15.99
Cluster V					**0.00**	10.67	7.46	15.81
Cluster VI						**0.00**	14.96	11.13
Cluster VII							**0.00**	20.03
Cluster VIII								**0.00**

4. Conclusion

Based on the combined results of variability, heritability, genetic divergence, correlation and path coefficient analyses, the traits, namely harvest index, 1000-seed weight, number of capsules per plant, number of seeds per capsule and oil content, were identified as the most important selection criteria for improving seed yield in linseed. Genotypes RLC-176, RLC-143, R-3785, RLC-173, Kiran and R-2596, which formed solitary clusters, may be considered valuable and genetically divergent parents for future hybridisation programmes. Overall, the study established the presence of substantial genetic variability and divergence among the evaluated linseed genotypes. Harvest index, 1000-seed weight, number of capsules per plant, number of seeds per capsule and oil content were identified as the most important yield-determining traits. The divergent genotypes belonging to Clusters VI, VII and VIII, particularly RLC-176, RLC-173 and Kiran, can be effectively utilised in future breeding programmes for developing superior linseed varieties combining high yield, earliness and enhanced oil content.

5. Limitations

The study was conducted during one rabi season at a single experimental location with two replications. Consequently, the observed genetic parameters and cluster relationships reflect the evaluated material under the reported experimental conditions. Wider multi-location and multi-season evaluation would be required to assess the stability of genotype performance and divergence patterns across environments.

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Declaration of AI Use

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Competing Interests

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

Bezil, M., Magudeeswari, P., Keisham, M., Behera, A., Kumar, A., Tyagi, W., & Rai, M. (2026). Genetic diversity, combining ability and stability analysis of linseed (Linum usitatissimum) under acidic soil conditions in the North-Eastern Region of India. *Agricultural Research, 15*, 670–681. https://doi.org/10.1007/s40003-025-00903-1

Gouy, M., Bogard, M., Mohamadi, F., & Demenou, B. (2025). Optimizing core collections for genetic studies: A worldwide flax germplasm case study. *Frontiers in Plant Science, 16*, 1675815. https://doi.org/10.3389/fpls.2025.1675815

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agronomy Journal, 47*(10), 477–483. https://doi.org/10.2134/agronj1955.00021962004700100008x

Kaur, V., Gomashe, S. S., Yadav, S. K., Singh, D., Sheela, Chauhan, S. S., Kumar, V., Jat, B., Tayade, N. R., *et al.* (2024). Leveraging genetic resource diversity and identification of trait-enriched superior genotypes for accelerated improvement in linseed (*Linum usitatissimum* L.). *Scientific Reports, 14*, 20266. https://doi.org/10.1038/s41598-024-71044-8

Kshirsagar, P. B., Pole, S. P., Dhuppe, M. V., Wadikar, P. B., Ganjure, R. R., & Chinmay, R. (2026). Genetic analysis of seed yield and component traits through line × tester analysis in linseed. *Plant Cell Biotechnology and Molecular Biology, 27*(7–8), 499–508. https://doi.org/10.56557/pcbmb/2026/v27i7-810929

Kumar, S., Sharma, A., Purushottam, & Chauhan, M. P. (2018). Diversity analysis in linseed (*Linum usitatissimum* L.). *International Journal of Current Microbiology and Applied Sciences, 7*(2), 790–794. https://doi.org/10.20546/ijcmas.2018.702.100

Mandal, R. K., Mallikarjun, Suresh, K., Choudhary, V. K., Choudhary, H. C., & 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. https://doi.org/10.9734/jabb/2025/v28i22001

Paliwal, S., Tripathi, M. K., & Sikarwar, R. S. (2024). Elucidating diversity of linseed (Linum usitatissimum) germplasms by applying DUS guideline to examine morphological features. *Plant Cell Biotechnology and Molecular Biology, 25*(5–6), 76–86. https://doi.org/10.56557/pcbmb/2024/v25i5-68702

Raut, V. K., Ngangkham, U., Yadav, A., Kaur, V., Malav, P. K., Saroha, A., Singh, G. P., Wankhede, D. P., & Singh, M. (2026). Cross-species transferability and genetic diversity analysis in Linum species using microsatellite markers. *Scientific Reports, 16*, 13358. https://doi.org/10.1038/s41598-026-42744-0

Saroha, A., Gomashe, S. S., Kaur, V., Pal, D., Ujjainwal, S., Aravind, J., Singh, M., Rajkumar, S., Singh, K., Kumar, A., & Wankhede, D. P. (2023). Genetic dissection of thousand-seed weight in linseed (*Linum usitatissimum* L.) using multi-locus genome-wide association study. *Frontiers in Plant Science, 14*, 1166728. https://doi.org/10.3389/fpls.2023.1166728

Shubham, Singh, D., Choudhary, R., Verma, K., Srivastav, R., & Ali, T. (2026). Assessment of genetic variability divergence, biochemical influence on growth and yield parameter in linseed (Linum usitatissimum L.). *Journal of Advances in Biology & Biotechnology, 29*(5), 865–878. https://doi.org/10.9734/jabb/2026/v29i53963

Singh, R., Saffeullah, P., Ahmad, S., & Umar, S. (2024). Linseed (*Linum usitatissimum* L.) accessions depict genetic variations in growth and yield characteristics, biochemical parameters, antioxidant potential, and secoisolariciresinol diglucoside content. *Genetic Resources and Crop Evolution, 71*, 4441–4464. https://doi.org/10.1007/s10722-024-01914-7

Singh, V. K., Kerkhi, S. A., Singh, S. P., & 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. https://www.phytojournal.com/archives/2019/vol8issue2/PartM/8-2-172-913.pdf

Tewari, N., Shankar, K., Singh, M., & Singh, D. K. (2023). Study of genetic divergence in linseed genotypes. *Journal of Oilseeds Research, 40*(Special Issue). https://doi.org/10.56739/jor.v40iSpecialissue.145323

Tyagi, A. K., Sharma, M. K., Mishra, S. K., Kerkhi, S. A., & Chand, P. (2014). Estimates of genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) germplasm. *Progressive Agriculture, 14*(1), 37–48.

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