PLANT SCIENCE TODAY
Vol x(x): xx–xx
https://doi.org/10.14719/pst.10589

eISSN 2348-1900

RESEARCH ARTICLE

Identification of elite breeding lines in linseed (*Linum usitatissimum* L.) through best linear unbiased prediction insights

Prasanta Kumar Majhi[1], Kishore Chandra Sahoo[2], Monika Ray[2*], Sukumar Tudu[2], Sujata Das[1], Subhakanta Samantaray[3], Abhishek Nanda[4] & Partha Pratim Behera[5]

[1]Department of Plant Breeding and Genetics, Odisha University of Agriculture and Technology, Bhubaneswar 751 003, Odisha, India
[2]Department of Agronomy, Odisha University of Agriculture and Technology, Bhubaneswar 751 003, Odisha, India
[3]Department of Agrometeorology, Odisha University of Agriculture and Technology, Bhubaneswar 751 003, Odisha, India
[4]Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology, Keonjhar 758 002, Odisha, India
[5]International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Hyderabad 502 324, Telangana, India

*Correspondence email - monikaray@ouat.ac.in

Received: 11 July 2025; Accepted: 01 January 2026; Available online: Version 1.0: 11 March 2026

Cite this article: Prasanta KM, Kishore CS, Monika R, Sukumar T, Sujata D, Subhakanta S, Abhishek N, Partha PB. Identification of elite breeding lines in linseed (*Linum usitatissimum* L.) through best linear unbiased prediction insights. Plant Science Today (Early Access). https://doi.org/10.14719/pst.10589

Abstract

Linseed or flaxseed (*Linum usitatissimum* L., 2n = 30, x = 15) is an annual herb belonging to the family Linaceae and tribe Lineae. It bears blue or white flowers and produces small, flat seeds ranging in colour from golden yellow to reddish brown, with a crisp texture and nutty flavour. The present investigation was conducted during the rabi season of 2021–2022 under the All India Coordinated Research Project (AICRP) on Linseed at Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology (OUAT), Keonjhar, Odisha, India. The experimental material comprised eight advanced breeding lines (F_8 generation) and three check varieties. The experiment was laid out in a randomized block design (RBD) with three replications. Data on seed yield and other agro-morphological traits were used to estimate genetic variability, heritability, genetic advance (GA) and trait correlations. Analysis of variance (ANOVA) revealed highly significant variation among the studied traits. Low to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for the advanced breeding lines. The highest GCV and PCV values were recorded for number of basal branches (NBB) per plant (14.66 % and 29.87 %), number of capsules per plant (NCP) (23.16 % and 23.91 %) and seed yield (SY) (17.99 % and 20.02 %). The highest broad-sense heritability was observed for plant height (PH) (0.97), days to maturity (DM) (0.96) and number of seeds per capsule (NSC) (0.93), whereas the lowest broad-sense heritability was recorded for NBB per plant (0.24). High heritability coupled with high GA as a percentage of mean was observed for NCP and SY, indicating the predominance of additive gene action for these traits. The highest significant positive correlation was observed between test weight (TW) and SY (0.67), followed by number of top branches and TW (0.45). Therefore, the results of the present investigation revealed the existence of substantial variability for SY and other agronomical traits, which can be exploited in future breeding programmes for the superior varieties.

Keywords: best linear unbiased prediction; correlation; genotypic coefficient of variation; genetic variability; heritability; linseed; phenotypic coefficient of variation

Introduction

The annual herb linseed or flaxseed (*Linum usitatissimum* L., 2n = 30, x = 15) belongs to the family Linaceae and the tribe Lineae. The crop has blue or white flowers and produces small, flat seeds ranging in colour from golden yellow to reddish brown, with a crisp texture and nutty flavour (1, 2). The genus *Linum* is composed of approximately 230 species; however, cultivated linseed is the only species of economic importance in the genus and is one of the oldest plants cultivated for fibre and oil, with high industrial and nutraceutical value (3, 4). Flaxseed and linseed are synonyms, both referring to the same plant. Flaxseed is the common name used when the crop is intended for human consumption, while linseed is the term used when it is intended for industrial purposes (5, 6). More than 50 countries cultivate this crop, mainly in the Northern Hemisphere. Canada dominates the global market as the leading exporter of flaxseed, followed by India, China, the United States and Ethiopia. When it comes to land used for growing flaxseed, India ranks first, accounting for 23.8 % of the total. However, in terms of production, India ranks third, contributing 10.2 % of the total global output (7). Linseed is presently cultivated in several countries, with production (lakh tonnes) recorded in Kazakhstan (9.7), Russia (6.08), Canada (4.89), China (3.53), the U.S.A. (1.38), India (1.36), Ethiopia (0.88), France (0.46), Afghanistan (0.41) and the UK and Northern Ireland (0.35). Approximately, 50.4 % of the global linseed production is contributed by Asian regions. Among individual countries, the highest production of linseed is recorded in Kazakhstan, followed by Russia (8). Rajasthan, Himanchal Pradesh, Madhya Pradesh, Maharashtra, Chhattisgarh, Bihar, Jharkhand, Karnataka, Odisha, Uttar Pradesh and Assam are the important linseed-growing states in India and about 97 % of the total area under flaxseed cultivation in the country is concentrated in these states (8, 9). Flaxseed is believed to have originated in India and has long served as a vital crop. Flaxseed is still used both as a food and a medicine in India. Flax seeds are associated with numerous health benefits, including improved digestion and a reduced risk of cardiovascular disease, type 2 diabetes and cancer (10–12). The antioxidant activity of brown flax seeds is slightly higher than that of yellow flaxseeds. Owing to its high concentration of beneficial nutrients such as alpha-linolenic acid (ALA), fibre, protein and phytoestrogens, flaxseed has gained popularity as a health-promoting food. Flaxseeds contain approximately 55 % ALA, followed by 28–30 % protein and 35 % fibre (13–15).

The development of high-yielding linseed genotypes with better and acceptable oil quality and higher seed yield has always been a major objective of linseed breeding programmes worldwide. Generating information on genetic variability, relationships among traits and mechanisms of inheritance is a key requirement for the genetic improvement of any crop plant. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Genetic variability within a population is important for biodiversity, as the absence of variability reduces the ability of a population to adapt to environmental changes, thereby increasing its vulnerability to extinction. Therefore, understanding genetic variation and the mode of inheritance of both quantitative and qualitative traits is of prime importance in planning effective breeding programmes (16, 17). Assessment of variability for yield and other characters becomes absolutely essential before planning an appropriate breeding strategy for genetic improvement (17). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the extent of variability present in the germplasm (17–19). Furthermore, understanding the magnitude and direction of correlation among yield and associated traits, along with heritability and genetic advance (GA), provides valuable tools for predicting the resultant effect of selection for desired plant types. Some genetic studies related to variability, correlation and other genetic parameters in linseed have previously been conducted using limited genetic materials (20–22). Knowledge of heritability helps plant breeders predict the behaviour of succeeding generations and make desirable selections. Thus, GA is another important selection parameter that aids breeders in selection programmes, as it indicates the magnitude of the expected genetic gain from one cycle of selection. In addition, the pattern of variation was evaluated using principal component analysis (PCA) by simultaneously examining all the attributes. Principal component analysis has proven beneficial in identifying associations among traits, determining dominant principal components (PCs) that significantly impact on plant characteristics and evaluating genetic diversity (23). Understanding the magnitude and direction of correlation among various quantitative traits helps to develop and impart suitable selection strategies for genetic improvement of targeted traits (21). Therefore, the present investigation was conducted using eight advanced breeding lines of linseed to estimate the levels of genetic coefficient of variation, heritability and GA based on best linear unbiased prediction (BLUP) analysis, with the objective of developing appropriate selection indices for increased production with improved quality.

Materials and Methods

Experimental location, materials, layout and observations recorded

The present investigation was conducted during rabi 2021–2022 at the Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology (OUAT), Keonjhar, Odisha, India. The geographical position of the research station lies between 21°01′ N and 22°10′ N latitude and 85°11′ E and 86°22′ E longitude, with an altitude of 480 m above mean sea level. The experimental material of the study comprised eight advanced breeding lines (F_8 generation), namely OL-2013-14-2022-1, OL-2013-14-2022-2, OL-2013-14-2022-3, OL-2013-14-2022-4, OL-2013-14-2022 -5, OL-2013-14-2022-6, OL-2013-14-2022-7, OL-2013-14-2022-8 along with three check varieties (Padmini, Arpita and Indra Alsi-32). These breeding lines were developed at the All India Coordinated Research Project (AICRP) on Linseed, RRTTS, OUAT, Keonjhar, Odisha.

These lines were developed through systematic hybridization and selection under the linseed improvement programme. Each genotype differed in its pedigree and phenotypic expression. The experiment was laid out in a randomized block design (RBD) with three replications. The net plot size of the experiment was 5.0 m × 3.6 m with a spacing of 30 cm × 10 cm. All the agronomical practices were followed to raise an excellent crop with better yield performance. Agro-morphological observations were recorded for nine yield-attributing characters namely days to flowering (DF), days to maturity (DM), plant height (PH) (cm), number of primary branches (NPB), number of secondary branches (NSB), number of capsules per plant (NCP), number of seeds per capsule (NSC), test weight (TW) (g) and seed yield (SY) (kg/ha). The morphological data were recoded from five randomly selected plants from each replication.

Statistical analysis

Statistical analysis was performed using the RStudio environment with R version 4.1.2 (24, 25). Analysis of variance (ANOVA), variability parameters, along with correlation and path analysis, were carried out using the “variability” package based on methods reported in previous studies, the “Metan” package and Microsoft Excel 2010 (26–28). The phenotypic and genotypic coefficients of variability (PCV and GCV) for all characters were estimated using standard formulae (29). The BLUP mixed linear model, developed in earlier studies, was calculated by treating genotype, genotypic and interaction effects (GEIs) as random effects, while considering environment and replication effects as fixed effects (30). A two-tailed chi-square test with one degree of freedom was conducted using a likelihood ratio test (LRT) to assess the statistical significance of the random effects. The GCV and PCV values were categorized as low (0–10 %), moderate (10–20 %) and high (> 20 %) as suggested by a previous study (31). Broad-sense heritability was estimated for all characters as the ratio of genotypic variance to total variance, following earlier studies (32, 33). According to an earlier report, heritability estimates in cultivated plants were classified as low (0–30 %), moderate (30–60 %) and high (> 60 %) (34). Genetic advance for each character was estimated using the formula proposed in previous studies and

GA as percentage of mean (GAM) was categorized as low (0–10 %), moderate (10–20 %) and high (> 20 %) (35).

Results and Discussion

Analysis of variance of different yield attributing traits

The analysis of variance revealed the effects of genotype and replication on several traits of interest, namely DF, DM, PH, NPB, NSB, NCP, NSC, TW and SY (Table 1). The sources of variation, along with their degrees of freedom (df), mean sum of squares and significance levels based on *p*-values are presented in Table 1. The results indicated that the genotype factor was highly significant for most traits, suggesting substantial genetic variation within the population. Specifically, DF, DM, PH, NSB, NCP, TW and SY exhibited highly significant genotype effects ($p < 0.001$).

This suggests that the different genotypes had a strong influence on these traits, reflecting genetic diversity within the population. The significant effect on SY indicates that genetic differences among the genotypes likely influenced yield outcomes. The NPB did not show significant variation among genotypes ($p > 0.05$), suggesting that this trait might be more stable or less influenced by genetic differences in the evaluated population. Similarly, the NSC exhibited a non-significant genotype effect ($p > 0.1$), implying that this trait may not vary substantially across genotypes under the prevailing conditions.

The replication factor showed limited significant effects, which is expected in many agricultural trials, as replication primarily accounts for environmental or random variation between plots. However, SY exhibited a significant replication effect ($p < 0.01$), suggesting that environmental or experimental factors across different replicates had a significant impact on SY. This highlights the importance of accounting for replication in yield trials to ensure accurate assessment of genotype performance. For all other traits (DF, DM, PH, NPB, NSB, NCP, NSC and TW), the replication effect was not significant, indicating that the differences among replicates were minimal for these traits.

This suggests that these traits are relatively consistent across experimental replicates and less influenced by environmental or uncontrolled experimental factors. The error variation, representing unexplained variation or residuals, varied across traits but remains generally low. This indicates that the model, which includes genotype and replication effects, captured a significant portion of the variability in the data. The low residual mean squares also suggest that the experimental design and measurement precision were adequate for this study. The results showed strong genetic control for key traits such as DF, DM, PH, NCP, TW and SY, as evidenced by the highly significant genotype effects. These traits are crucial for plant development and yield and the presence of significant variation among genotypes indicates the potential for selecting superior genotypes for these traits in a breeding programme.

Similar results were reported for DF, PH, NPB, NSB, number of capsule per branch, lodging percentage, NSC, DM, harvest index and SY, which revealed highly significant differences among the studied genotypes (20). Similar findings were also reported in previous studies for PH, NPB, NSB and NCP (17, 36). However, traits such as NPB and NSC showed lower genetic variability, which may limit selection gains for these traits. The significant replication effect observed for SY suggests that environmental variation had a considerable impact on yield, highlighting the importance of managing experimental conditions and ensuring adequate replication to obtain reliable yield data. For most other traits, the non-significant replication effects indicate good consistency across experimental replicates. Overall, this study suggests that breeding efforts focusing on highly variable traits, especially those related to SY, could lead to significant genetic improvement in the population.

Estimates of variability, heritability and genetic advance

The evaluation of variability, heritability and GA for yield components of advanced breeding lines of linseed provides critical insights into the potential for genetic improvement through selection. The traits under study exhibited a range of variability, heritability and GA, indicating differing levels of genetic and environmental influence (Table 2). Days to flowering ranged from 56 to 68 days, with a mean of 61 days. The PCV and GCV were 5.06 % and 4.05 % respectively, indicating a low degree of variation. The environmental coefficient of variation (ECV) was relatively lower (3.03 %), suggesting a significant genetic component influencing this trait, as reflected by moderate heritability of 64 %. The GA was 4.14 and the GA as a percentage of the mean (GAM) was 6.69 %. For DM, the PCV and GCV values were very close (4.37 % and 4.29 % respectively) and heritability was low (0.96 %), indicating minimal environmental influence and a limited scope for selection based on this trait. The GA was 9.72, with a GAM of 8.71 %. Plant height showed a considerable range from 63.7–82.4 cm, with a mean of 74.72 cm. The PCV and GCV were closely aligned (7.18 % and 7.11 % respectively), resulting in high heritability (0.97 %). The GA for plant height was 10.83 and the GAM was 14.49 %, indicating substantial potential for improvement through selection. The number of basal branches (NBB) exhibited high variability, with a PCV of 29.87 % and a GCV of 14.66 %. Heritability was low (0.24 %), reflecting a strong environmental influence on this trait. Consequently, the GA and GAM were 0.40 and 14.83 % respectively, suggesting limited potential for selection. The number of top branches had a PCV of 17.67 % and a GCV of 13.82 %, with moderate heritability (0.61 %). The GA was 2.67 and the GAM was 22.27 %, indicating that moderate genetic improvement could be achieved through selection. The GA as a percentage of the mean varied from 5.40–58.84 % with the maximum recorded for capsules per plant (CP), followed by capsule weight per plant (CWP) and seed weight per plant (SWP) and the minimum for seed yield per capsule (SC) . The traits CP, CWP and SWP showed high heritability along with high GA. Higher LSD and standard error values were recorded for CP (8.85, 3.18), followed by PH and DF among all traits. A comprehensive compilation of 25 potential accessions

Table 1. Analysis of variance (ANOVA) (mean sum of squares) of different yield attributing traits of advanced breeding lines of linseed

Sources of Variation	df	DF	DM	PH	NPB	NSB	NCP	NSC	TW	SY
Genotype	10	22.41***	69.85***	85.34***	1.006	10.00***	1175.22***	0.33^{NS}	0.98***	195620***
Replication	2	1.48	0.03	0.04	0.84	2.54	40.94	0.21	0.002	104037**
Error	20	3.5182	0.764	0.604	0.515	1.7455	24.91	0.47879	0.02979	14387

df: degrees of freedom; DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSP: number of secondary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha); significance codes: ‘***’ (0.001); ‘**’ (0.01); ‘*’ (0.05); NS: non-significant

Table 2. Estimate of variability, heritability and genetic advance for yield components of advanced breeding lines of linseed

Sl. No.	Variables	Range		Mean	PCV (%)	GCV (%)	ECV (%)	h^2 (bs) (%)	GA	GAM (%)	SEm	CD (5 %)	CD (1 %)
		Max.	Min.										
1	DF	68	56	61	5.06	4.05	3.03	0.64	4.14	6.69	1.08	3.19	4.35
2	DM	123	107	111	4.37	4.29	0.78	0.96	9.72	8.71	0.50	1.48	2.03
3	PH	82.4	63.7	74.72	7.18	7.11	1.03	0.97	10.83	14.49	0.44	1.32	1.80
4	NPB	4	2	2.75	29.87	14.66	26.02	0.24	0.40	14.83	0.41	1.22 NS	1.66 NS
5	NSB	18	8	12	17.67	13.82	11.00	0.61	2.67	22.27	0.76	2.25	3.06
6	NCP	120	55	84	23.91	23.16	5.90	0.93	39.08	46.25	2.88	8.49	11.59
7	NSC	10	8	9.3	7.02	-	7.41	– 0.11	– 0.15	– 1.63	0.39	1.17 NS	1.60 NS
8	TW	7.9	6.1	6.87	8.56	8.18	2.50	0.91	1.10	16.12	0.09	0.29	0.40
9	SY	1866.66	850	1365.59	20.02	17.99	8.78	0.80	455.02	33.32	69.25	204.28	278.65

DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSP: number of secondary branches; NCP: number of capsules/plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha); PCV: phenotypic coefficient of variation; GCV: genotypic coefficient of variation; ECV: environmental coefficient of variation; h^2(bs): heritability (broad sense); GA: genetic advance; GAM: genetic advance as percentage of mean.

exhibiting highly desirable traits has been reported earlier (19). In the present study, moderate GA (> 17 %) was observed for lodging and DM, whereas other traits exhibited low GA (< 15 %) (20). These findings are in line with earlier investigations reported on linseed genotypes (37–39).

The NCP showed significant variability, with a PCV of 23.91 % and a GCV of 23.16 %. Heritability was high (0.93 %) and the GA was 39.08, with a GAM of 46.25 %, suggesting that this trait is highly heritable and could respond well to selection. The NSC showed a PCV of 7.02 % but no corresponding GCV value, suggesting issues with the estimation. The negative heritability value (- 0.11) and negative GAM (- 1.63 %) indicate unreliable estimates, possibly due to measurement errors or environmental effects overwhelming genetic influence. The 1000-seed weight had a PCV of 8.56 % and a GCV of 8.18 %, with high heritability (0.91 %). The GA was 1.10 and the GAM was 16.12 %, suggesting good potential for improvement through selection. Seed yield ranged from 850–1866.66 kg/ha, with a mean of 1365.59 kg/ha. The PCV (20.02 %) and GCV (17.99 %) were moderately high, with heritability of 0.80, indicating a strong genetic component. The GA was 455.02 and the GAM was 33.32 %, showing substantial scope for genetic improvement.

Overall, traits such as PH, NCP, 1000-seed weight and SY showed high heritability coupled with high GA, suggesting that these traits could be effectively improved through selection. Conversely, traits such as NBB and DM, with low heritability and GA, may require different breeding strategies or focus on improving environmental conditions to enhance their performance. The results indicated that PCV values were slightly greater than the corresponding GCV values for most traits, indicating that the traits under study were less influenced by environment (20). Similar results in linseed were also reported by earlier studies (37, 40). The highest GCV and PVC values were found particularly for lodging percentage (76.65 % and 90.63 %), harvest index (42.26 % and 47.92 %), SY (41.23 % and 48.19 %) and number of capsules per branch (30.81 % and 37.25 %) respectively. Similarly, earlier researchers reported the highest GCV and PCV values for SY per plant and for NCP (17, 18). The highest values of GCV and PVC show the presence of high variability in these traits. Additionally, breeding and selection strategies also depend on the type of gene action involved in the inheritance of quantitative traits. High heritability and GA indicate predominantly additive gene action, whereas high heritability along with moderate to low GA suggests non-additive gene action. Thus, traits controlled by additive gene action can be improved through simple selection during the breeding cycle. On the other hand, traits that are highly affected by environmental factors and governed by non-additive gene action may not give that much response to genetic improvement. Similar findings have also been reported earlier in linseed crops (20, 21, 23). Estimates of heritability help plant breeders in the selection of genotypes from diverse genetic populations. Therefore, high heritability helps in effective selection for a particular character.

Descriptive statistics to study the behaviour of yield components

The descriptive statistics of yield components for advanced breeding lines of linseed provide a comprehensive overview of the distribution and variability of the traits under study. These statistics, including measures of central tendency (mean), dispersion (sum of squares deviation and variance) and shape (skewness and kurtosis), are essential for understanding the behaviour of each trait in the breeding population. Days to flowering ranged from 56–68 days, with a mean of 61.87 days. The skewness value of –0.45 indicates a slight left skew, meaning that more values are concentrated above the mean. The kurtosis value (–0.23) suggests a relatively flat distribution. The sum of squares deviation (297.51) and variance (9.29 for the sample and 9.01 for the population) indicate moderate variability in this trait among the breeding lines (Table 3). Days to maturity exhibited a range from 107–123 days, with a mean of 111.60 days.

The skewness is positive (1.43), indicating a right-skewed distribution with a tail extending towards higher values. The kurtosis is 0.94, suggesting a distribution with slightly more pronounced peaks than a normal distribution. The sum of squares deviation (713.87) and the variance (22.30 for the sample and 21.63 for the population) reflect considerable variability, which could be valuable for selection. Plant height shows a relatively narrow range, with a minimum of 2 and a maximum of 4 and a mean of 2.75 cm. The skewness is positive (0.49), indicating a slight right skew, while the kurtosis of –1.37 suggests a distribution that is flatter than normal. The sum of squares deviation (22.06) and the variance (0.68 for the sample and 0.66 for the population) indicate low variability, which may limit selection effectiveness for this trait. An earlier study emphasized the significance of genetic variability and reported substantial variation for traits such as NCP, SY and branches, reinforcing the importance of variability assessment through descriptive statistics (41). The NBB shows a wide range, from 55–120,

Table 3. Descriptive statistics of yield components of advanced breeding lines of linseed

Sl. No.	Variable	Max.	Mean	Min.	Skew	Kurt	Sum.sq.dev	Var.amo	Var.pop
1	DF	68	61.87	56	– 0.45	– 0.23	297.51	9.29	9.01
2	DM	123	111.60	107	1.43	0.94	713.87	22.30	21.63
3	PH	4	2.75	2	0.49	– 1.37	22.06	0.68	0.66
4	NPB	120	84.51	55	0.23	– 1.15	12332.24	385.38	373.70
5	NSB	10	9.33	8	– 0.43	– 0.60	13.33	0.41	0.40
6	NCP	18	12	8	0.82	1.65	140	4.37	4.24
7	NSC	82.4	74.72	63.7	– 0.38	– 0.50	865.58	27.04	26.22
8	TW	1866.66	1365.59	850	0.10	– 0.95	2452011.13	76625.34	74303.36
9	SY	7.9	6.87	6.1	0.52	– 1.12	10.41	0.32	0.31

DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSP: number of secondary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha).

with a mean of 84.51. The skewness is 0.23, indicating a nearly symmetric distribution and the kurtosis of –1.15 suggests a flatter-than-normal distribution. The sum of squares deviation (12332.24) and the high variance (385.38 for the sample and 373.70 for the population) indicate substantial variability, providing ample opportunity for selection. The considerable variability in yield-related traits, such as SY, NCP and basal branches, demonstrates potential for selection, consistent with earlier findings and supporting the relevance of using descriptive statistics for identifying selection targets in linseed breeding programmes (42, 43).

The number of top branches ranges from 8–10, with a mean of 9.33. The skewness is -0.43, indicating a slight left skew, while the kurtosis of -0.60 indicates a flatter distribution. The sum of squares deviation (13.33) and low variance (0.41 for the sample and 0.40 for the population) suggest limited variability, which could constrain selection efforts. The NCP ranges from 8–18, with a mean of 12. The skewness is 0.82, indicating a right-skewed distribution and the kurtosis of 1.65 suggests a distribution with more pronounced peaks. The sum of squares deviation (140) and moderate variance (4.37 for the sample and 4.24 for the population) indicate a reasonable level of variability, which could be exploited in selection.

The NSC varies from 63.7–82.4, with a mean of 74.72. The skewness is - 0.38, indicating a slight left skew and the kurtosis of -0.50, indicates a flatter distribution. The sum of squares deviation (865.58) and variance (27.04 for the sample and 26.22 for the population) suggest moderate variability, which could support selection. The 1000-seed weight ranges from 6.1–7.9 g, with a mean of 6.87 g. The skewness is 0.10, indicating a nearly symmetrical distribution, while the kurtosis of –0.95 suggests a flatter distribution. The sum of squares deviation (10.41) and low variance (0.32 for the sample and 0.31 for the population) indicate limited variability, which might restrict selection potential for this trait. Seed yield per hectare ranges widely from 850–1866.66 kg/ha, with a mean of 1365.59 kg/ha.

The skewness of 0.52 indicates a slight right skew and the kurtosis of –1.12 suggests a flatter distribution. The large sum of squares deviation (2452011.13) and high variance (76625.34 for the sample and 74303.36 for the population) reflect considerable variability, making this trait a strong candidate for selection. The present findings are aligned with the results of the previous workers and state that traits with considerable variation, as revealed by descriptive statistics, serve as crucial indicators for effective selection in linseed breeding (43–45). The descriptive statistics indicate that traits such as SY, NBB and NCP exhibit substantial variability and are thus promising targets for selection in breeding programmes. On the other hand, traits such as PH, number of top branches and 1000-seed weight display limited variability, which may require the introduction of new genetic material or alternative breeding strategies to achieve significant improvements. The presence of skewness and kurtosis in some traits suggests that the distribution of these traits is not normal, which should be considered when selecting breeding lines.

BLUP based genetic parameter study

The estimation of genetic parameters using BLUP provides a comprehensive understanding of the genetic architecture and selection potential of key agronomic traits in linseed. The present study revealed substantial variability in both genetic and residual components across the evaluated traits, providing valuable insights for linseed improvement programmes (Table 4; Fig. 1 and 2). The genetic variance (Gen_var) was notably high for traits such as SY and NCP, recorded at 60410.98 and 383.44 respectively, underscoring the strong genetic contribution to these yield components. This aligns with findings of earlier researchers, who reported significant genetic variance for SY and NCP, indicating their amenability to

Table 4. Best linear unbiased prediction (BLUP) based genetic parameter study

Sl. No.	Parameters	DF	DM	PH	NPB	NSP	NCP	NSC	TW	SY
1	Gen_var	6.30	23.03	28.25	0.16	2.75	383.44	0.00	0.32	60410.98
2	Gen (%)	64.17	96.79	97.91	24.11	61.19	93.90	0.00	91.42	80.77
3	Res_var	3.52	0.76	0.60	0.52	1.75	24.91	0.43	0.03	14386.92
4	Res (%)	35.83	3.21	2.09	75.89	38.81	6.10	100.00	8.58	19.23
5	Phen_var	9.82	23.79	28.85	0.68	4.50	408.35	0.43	0.35	74797.90
6	H^2	0.64	0.97	0.98	0.24	0.61	0.94	0.00	0.91	0.81
7	h^2mg	0.84	0.99	0.99	0.49	0.83	0.98	0.00	0.97	0.93
8	Accuracy	0.92	0.99	1.00	0.70	0.91	0.99	0.00	0.98	0.96
9	CVg	4.06	4.30	7.11	14.67	13.82	23.17	0.00	8.19	18.00
10	CVr	3.03	0.78	1.04	26.03	11.01	5.90	7.03	2.51	8.78
11	CV ratio	1.34	5.49	6.84	0.56	1.26	3.92	0.00	3.26	2.05

DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSP: number of secondary branches; NCP: Number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha); Gen_var: genetic variance; Gen (%): genetic percentage; Res_var: residual variance; Res (%): residual percentage; Phen_var: phenotypic variance; H^2: heritability; h^2mg: CVg: genotypic coefficient of variation; CVr: residual coefficient of variation.

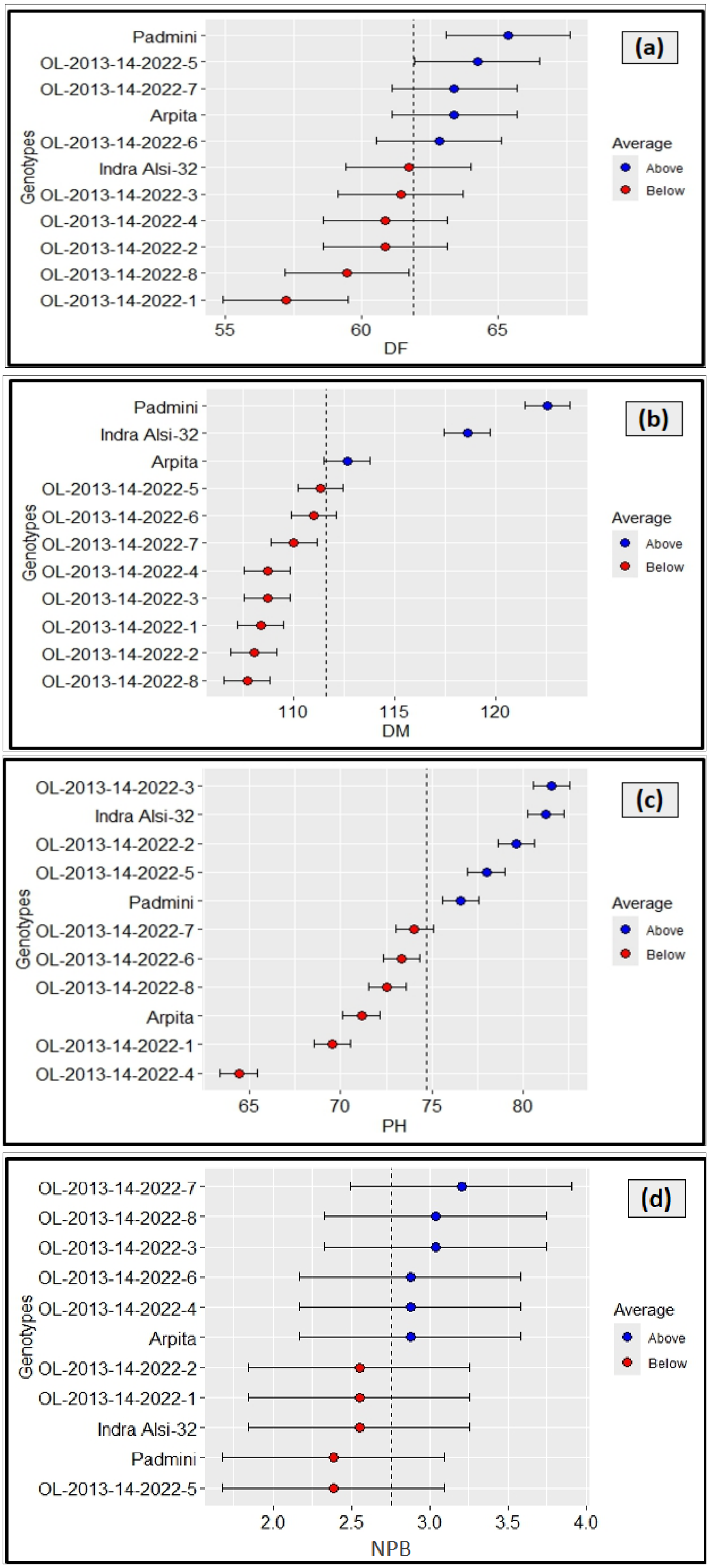

Fig. 1. Best linear unbiased prediction (BLUP) for (a) DF: days to flowering; (b) DM: days to maturity; (c) PH: plant height (cm); (d) NPB: number of primary branches.

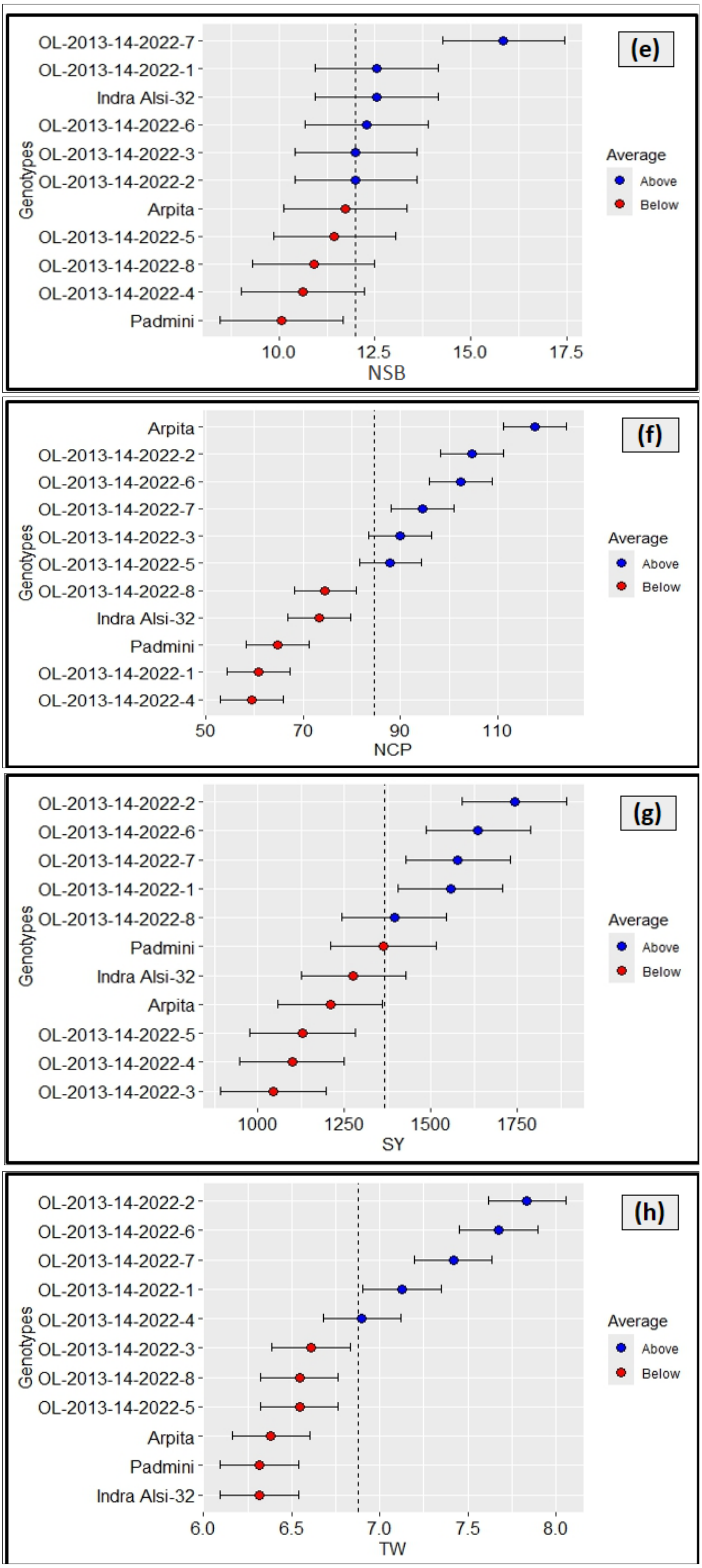

Fig. 2. Best linear unbiased prediction (BLUP) for (e) NSB: number of secondary branches; (f) NCP: number of capsules per plant; (g) TW: test weight (g); (h) SY: seed yield (kg/ha).

improvement through selection (41, 43). Likewise, PH exhibited considerable genetic variance (28.25), highlighting its substantial heritable component. In contrast, NSC displayed minimal genetic variance, suggesting that environmental factors or non-additive genetic effects may dominate its phenotypic expression, consistent with the observations from previous research (43).

The genetic percentage (Gen %), representing the proportion of phenotypic variance attributed to genetic factors, was remarkably high for DM (96.79 %), PH (97.91 %) and NCP (93.90 %). Such high genetic percentages indicate that these traits are predominantly governed by genetic factors, making them ideal candidates for direct selection. Conversely, traits such as NBB recorded a lower Gen % (24.11 %), implying greater environmental influence, corroborating previous studies that emphasize environmental sensitivity in branching traits (43). The residual variance (Res_var) remained lower than the genetic variance for most traits, except for NBB, where Res_var was relatively high (0.52) and Res % peaked at 75.89 %, indicating pronounced environmental control. Traits such as DM and PH, with minimal Res % (3.21 % and 2.09 % respectively), suggest stability across environments. Heritability estimates (H^2) were exceptionally high for key traits, including DM, PH, NCP, TW and SY, with values exceeding 0.90, demonstrating strong genetic control and high selection efficiency potential. These findings are consistent with previous reports, which highlighted high heritability for these traits, suggesting that they respond well to phenotypic selection (43).

In contrast, NBB presented a lower H^2 of 0.24, indicating limited efficiency of conventional selection and emphasizing the need for alternative approaches such as marker-assisted selection or environmental management to improve this trait. The genotypic coefficient of variation (CVg) and residual coefficient of variation (CVr) provided further clarity on trait variability. High CVg values for NCP (23.17) and SY (18.00) reflect substantial genetic diversity, enhancing selection prospects. Conversely, traits such as DM and PH exhibited lower CVg values, indicating more genetic uniformity. Notably, CVr was generally low across traits, except for NBB, which displayed a high CVr (26.03), reinforcing its environmental sensitivity. The prediction accuracy derived from BLUP exceeded 0.90 for most traits, including DM, PH, NCP, TW and SY, confirming the reliability of BLUP in estimating genetic parameters and guiding selection. The relatively lower accuracy for NBB (0.70) aligns with its low heritability and high residual variance, signaling caution in its direct selection. The traits such as DM, PH, NCP, TW and SY demonstrate high genetic variance, heritability and prediction accuracy, making them prime targets for genetic improvement through selection based on BLUP estimates. Conversely, traits with low genetic control, such as NBB, may require the integration of molecular tools or targeted environmental interventions to enhance breeding efficiency. Overall, the application of BLUP in linseed breeding offers a powerful framework for accurately dissecting genetic variability, optimising selection and accelerating genetic gain, as emphasized by previous researchers in quantitative genetic studies (46, 47). This study provides a robust foundation for breeding programmes aimed at improving key agronomic traits. The results further suggest that genetic factors play a significant role in the variation of most traits and that selection based on BLUP would be effective in improving them. However, the influence of environmental factors should not be ignored and further research is needed to understand their impact on the traits studied.

BLUP based genotype study

The use of BLUP analysis provides a robust framework for the unbiased assessment of genotype performance, facilitating the identification of superior lines for genetic improvement in linseed. In this study, 11 genotypes were evaluated across critical agronomic traits to identify candidates with high yield potential and favourable trait combinations (Table 5). Phenological traits, including DF and DM, exhibited considerable variability across the genotypes. OL-2013-14-2022-5 recorded the longest flowering duration (64.23 days), while Padmini (check) had the longest maturity period (122.55 days). Conversely, OL-2013-14-2022-8 flowered earliest (59.45 days), highlighting its potential suitability for short-duration environments or late sowing conditions.

Early maturity and flowering have been reported as critical factors for yield stability in linseed, especially under rainfed or terminal stress conditions (48, 43). Plant height ranged from 64.41 cm (OL-2013-14-2022-4) to 81.55 cm (OL-2013-14-2022-3), indicating variation in plant stature. Taller genotypes, such as OL-2013-14-2022-3 and Indra Alsi-32, may contribute to greater biomass and yield potential, while shorter genotypes may be advantageous in regions prone to lodging or where mechanical harvesting is implemented (44, 49). The NBB varied moderately among genotypes, ranging from 2.39 to 3.20, with OL-2013-14-2022-7 exhibiting the highest branching. Branching patterns directly influence canopy architecture and can enhance photosynthetic efficiency and yield potential (50). However, genotypes with fewer branches, such as

Table 5. Best linear unbiased prediction (BLUP) based genotype study

Sl. No.	Genotype	DF	DM	PH	NPB	NSP	NCP	NSC	TW	SY
1	OL-2013-14-2022-1	57.20	108.37	69.54	2.55	12.55	60.85	9.33	7.13	1556.34
2	OL-2013-14-2022-2	60.86	108.04	79.60	2.55	12.00	104.57	9.33	7.84	1740.77
3	OL-2013-14-2022-3	61.42	108.70	81.55	3.04	12.00	89.88	9.33	6.61	1044.18
4	OL-2013-14-2022-4	60.86	108.70	64.41	2.88	10.62	59.54	9.33	6.90	1097.92
5	OL-2013-14-2022-5	64.23	111.34	77.98	2.39	11.45	87.93	9.33	6.54	1128.80
6	OL-2013-14-2022-6	62.82	111.01	73.34	2.88	12.28	102.28	9.33	7.68	1635.95
7	OL-2013-14-2022-7	63.39	110.02	74.04	3.20	15.85	94.45	9.33	7.42	1577.27
8	OL-2013-14-2022-8	59.45	107.71	72.55	3.04	10.90	74.55	9.33	6.54	1393.70
9	Padmini (Check)	65.35	122.55	76.59	2.39	10.07	64.76	9.33	6.32	1362.47
10	Arpita (Check)	63.39	112.66	71.13	2.88	11.72	117.62	9.33	6.38	1208.16
11	Indra Alsi-32 (Check)	61.70	118.59	81.25	2.55	12.55	73.24	9.33	6.32	1276.00

DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSP: number of secondary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha).

Padmini and OL-2013-14-2022-5, may be more suitable for high-density planting systems. The NCP, a key yield component, demonstrated significant variability, ranging from 59.54 (OL-2013-14-2022-4) to 117.62 (Arpita). High NCP, as observed in Arpita, OL-2013-14-2022-2 (104.57) and OL-2013-14-2022-6 (102.28), is a desirable trait contributing to greater seed yield. Similar observations of high NCP variability and its positive association with yield have been reported earlier (42).

Despite the significant variation in NCP, the NSC remained constant (9.33) across all genotypes, suggesting limited genetic variability for this trait within the evaluated population. This aligns with earlier reports indicating that NSC tends to be relatively stable compared to other yield components Test weight, reflecting seed size and quality, ranged from 6.32–7.84 g, with OL-2013-14-2022-2 exhibiting the highest TW. Seed weight contributes not only to market acceptability but also to overall yield; however, in this study, TW variability was relatively low, suggesting a more uniform seed size among genotypes. Comparable trends were reported in flax, where SW exhibited moderate variability (51). Seed yield, the most critical agronomic trait, showed substantial variation ranging from 1044.18 kg/ha (OL-2013-14-2022-3) to 1740.77 kg/ha (OL-2013-14-2022-2). High-yielding genotypes such as OL-2013-14-2022-2, OL-2013-14-2022-6 (1635.95 kg/ha) and OL-2013-14-2022-7 (1577.27 kg/ha) significantly outperformed the check variety Padmini (1362.47 kg/ha). These results suggest substantial genetic gain over existing cultivars and align with findings by earlier researchers, who emphasised the potential of BLUP and genomic prediction for yield enhancement in linseed (52). In summary, the BLUP-based evaluation revealed considerable variability across key agronomic traits, highlighting OL-2013-14-2022-2, OL-2013-14-2022-6 and OL-2013-14-2022-7 as superior genotypes for yield improvement programmes. Additionally, variations in phenological traits, PH, branching and seed characteristics provide further criteria for genotype selection tailored to specific agro-ecological zones. These findings reinforce the value of BLUP for accurate performance prediction and efficient genetic improvement, as demonstrated in previous studies on linseed (43, 51, 52).

Principal component analysis (PCA) for trait association

The PCA based on eigenvalues offers a detailed exploration of variability across several key agronomic traits in linseed. The eigenvalues and corresponding percentages of variance provide crucial insights into the contribution of each trait to the overall genetic variation observed in the population (Table 6 and Fig. 3). The first principal component (PC1), driven by DF, exhibited an

Table 6. Principal component analysis (PCA) based on eigenvalue

Sl. No.	Variables	Eigenvalue	Percentage of variance	Cumulative percentage of variance
1	DF	2.867	31.857	31.857
2	DM	2.117	23.521	55.378
3	PH	1.310	14.558	69.936
4	NPB	1.104	12.271	82.207
5	NSB	0.731	8.126	90.333
6	NCP	0.500	5.561	95.894
7	NSC	0.241	2.673	98.566
8	TW	0.099	1.101	99.668
9	SY	0.030	0.332	100.000

DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSB: number of secondary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha).

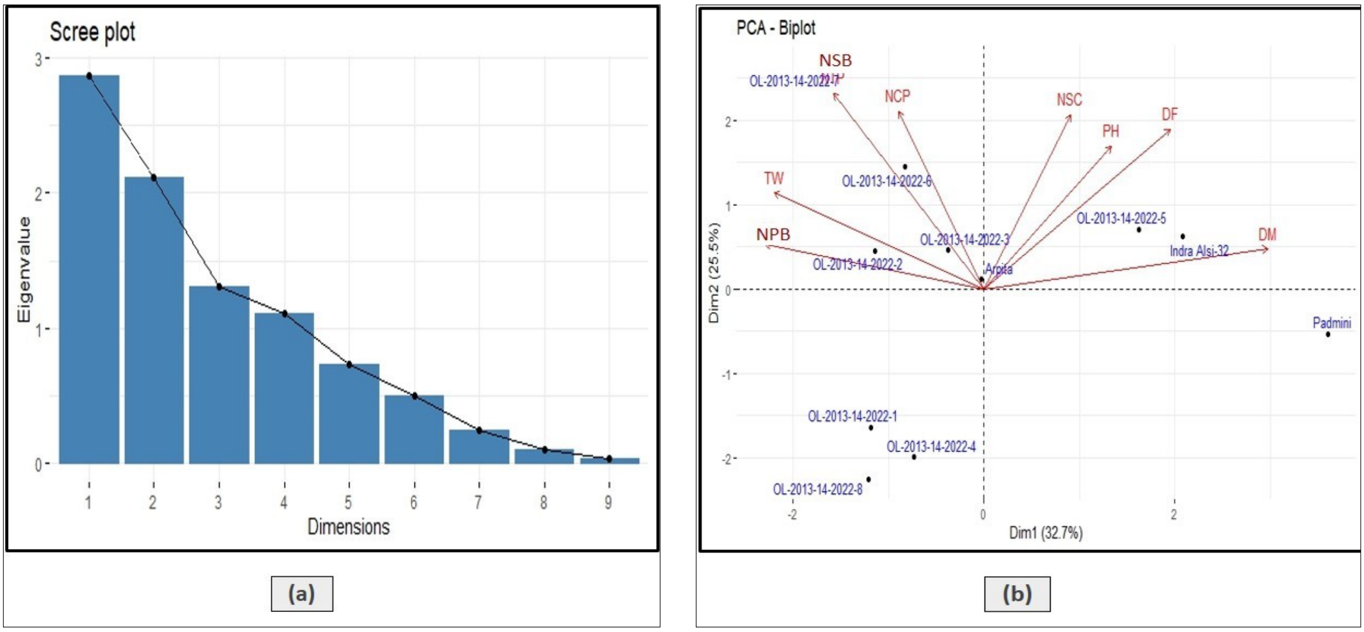

Fig. 3. (a) The scree plot represents the eigenvalues corresponding to each principal component (dimension) derived from the multivariate dataset of linseed genotypes. The x-axis indicates the principal components (Dimensions 1–9), each capturing a progressively smaller portion of total data variance, while the y-axis shows the eigenvalue, denoting the amount of variation explained by each component. (b) The PCA biplot displays the spatial distribution of linseed genotypes and trait vectors based on the first two principal components (Dim1 and Dim2), which together explain 32.7 % and 25.5 % of the total variance respectively.

Trait vectors (arrows)—DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSB: number of secondary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha)—indicates the direction and strength of their contribution to genotype differentiation.

eigenvalue of 2.867, accounting for 31.857 % of the total variance. This highlights the pivotal role of flowering time in differentiating the genotypes. The significance of this trait in PC1 suggests its critical influence on the genetic architecture of linseed, potentially serving as an early indicator of reproductive success and adaptation to diverse growing environments. The second principal component (PC2) was predominantly influenced by DM, with an eigenvalue of 2.117, contributing an additional 23.521 % to the total variance and raising the cumulative variance explained to 55.378 %, as also reported in previous studies (49, 50). This indicates that maturity timing, alongside flowering, exerts a substantial effect on variation among genotypes. The synchronisation between flowering and maturity is often crucial for yield stability, particularly in environments with variable growing seasons. Together, DF and DM account for over half of the observed variance, underscoring the importance of reproductive timing traits in linseed breeding programmes.

Plant height emerged as the dominant trait in the third principal component (PC3), with an eigenvalue of 1.310 and explaining 14.558 % of the variance, bringing the cumulative variance explained to 69.94 %. Plant height is a vital trait often linked to biomass production and mechanical harvesting efficiency and its significant contribution suggests that height variation is another key factor driving genetic differentiation among the studied genotypes. The fourth principal component (PC4) was characterized by NPB, which explained 12.271 % of the variance with an eigenvalue of 1.104. With the cumulative variance reaching 82.207 %, the contribution of branching to genetic variability highlights the role of plant architecture in influencing yield potential. Primary branches are often associated with greater capsule production, making this trait essential for breeding high-yielding lines. Traits contributing less to genetic variation include NSB (8.126 % variance, PC5) and NCP (5.561 % variance, PC6). While these traits explain a smaller portion of the variance individually, their combined influence, as reflected in their cumulative variance contribution, suggests that they are still integral to overall plant productivity, particularly in environments where plant architecture and reproductive efficiency are critical for yield optimization. Finally, traits such as NSC, 1000-seed weight and SY showed relatively low eigenvalues (0.241, 0.099 and 0.030 respectively) and contributed minimally to the total variance (2.673 %, 1.101 % and 0.332 %). Similar patterns were observed by earlier researchers, where yield traits often exhibited indirect genetic variability mediated through physiological and morphological components (52). Despite their smaller direct influence in this analysis, these traits are nonetheless crucial for determining overall crop performance and marketability. Seed yield, in particular, remains the ultimate measure of productivity, even if its genetic variation is influenced indirectly by other traits such as flowering time, PH and branching. This PCA demonstrates that the major contributors to genetic variation in linseed are reproductive timing (DF and DM), plant stature (height) and plant architecture (branching). These traits should be prioritized in breeding programmes aimed at enhancing adaptation and yield potential. The cumulative variance explained by the first four components suggests that these traits encapsulate the majority of genetic diversity, providing a clear focus for targeted genetic improvement.

Principal components with an eigenvalue greater than or equal to 1.0 were considered for determining the number of primary PCs (53). The accessions from these clusters may serve as potential genetic material for genetic improvement programmes, as unrelated accessions would contribute novel alleles at different loci and thereby generate a wider spectrum of transgressive segregants (54). Earlier findings also reported results similar to the present investigation, using PCA to simultaneously examine all attributes (23, 55–57). PCA proved beneficial in identifying associations among traits, determining the dominant PCs that significantly influence plant characteristics and evaluating genetic diversity.

Correlation studies to understand the trait relationships

The correlation matrix presented in Fig. 4 visually depicts the relationships among various yield-attributing traits in linseed. The matrix includes scatter plots, correlation coefficients and histograms, providing a comprehensive view of how these traits are interrelated. The following key points can be drawn from this correlation analysis: the strongest positive correlation was observed between SY and NCP, with a correlation coefficient of 0.67 ($p < 0.001$). This suggests that NCP is a major contributor to SY and selection for this trait could significantly enhance yield. A notable positive correlation (0.45) was observed between 1000-seed weight and SY, indicating that heavier seeds are generally associated with higher yield, making 1000-seed weight a valuable selection criterion in breeding programmes. Additionally, a positive correlation of 0.52 between DM and DF indicates that genotypes that flower later also tend to mature later. This relationship suggests a developmental link between these two traits. A significant negative correlation (-0.51, $p < 0.01$) was observed between 1000-seed weight and DM, indicating that lines that mature earlier tend to have heavier seeds. This trade-off could be important when selecting for both early maturity and high seed weight. A moderate negative correlation (-0.36) was observed between DM and NBB, suggesting that lines with more basal branches tend to mature earlier. This relationship may be useful for selecting branching patterns that favour early maturity. The correlation between NSC and SY was weak (0.20) and non-significant, suggesting that this trait may not be a strong determinant of yield in this population. Consequently, selection for yield may not be effectively achieved through this trait alone. The weak negative correlation (-0.13) between DF and SY suggests that early flowering does not strongly influence yield, indicating that flowering time may be less critical for direct selection aimed at yield improvement.

The histograms along the diagonal of the matrix show the distribution of each trait, while the scatter plots illustrate the relationships among traits (Fig. 4). The scatter plots reveal trends, with some traits showing linear relationships and others displaying more variability. The correlations also highlight potential trade-offs between traits, such as the inverse relationship between seed weight and DM. Understanding these trade-offs is crucial for balancing different breeding objectives, such as selecting for both early maturity and high yield. The correlation analysis provides valuable insights into the relationships among yield components in linseed. The strong positive correlations between SY and traits such as NCP and 1000-seed weight suggest that these traits are critical targets for selection. However, the observed negative correlations, such as between DM and 1000-seed weight, indicate the need to carefully balance selection for these traits to avoid unintended consequences. Overall, this analysis supports the identification of key traits that can be effectively used to improve SY in linseed breeding programmes.

An earlier study reported a negative association between PH and both SY and TW, suggesting that taller plants may not always translate to higher yield under certain conditions (21). Among other

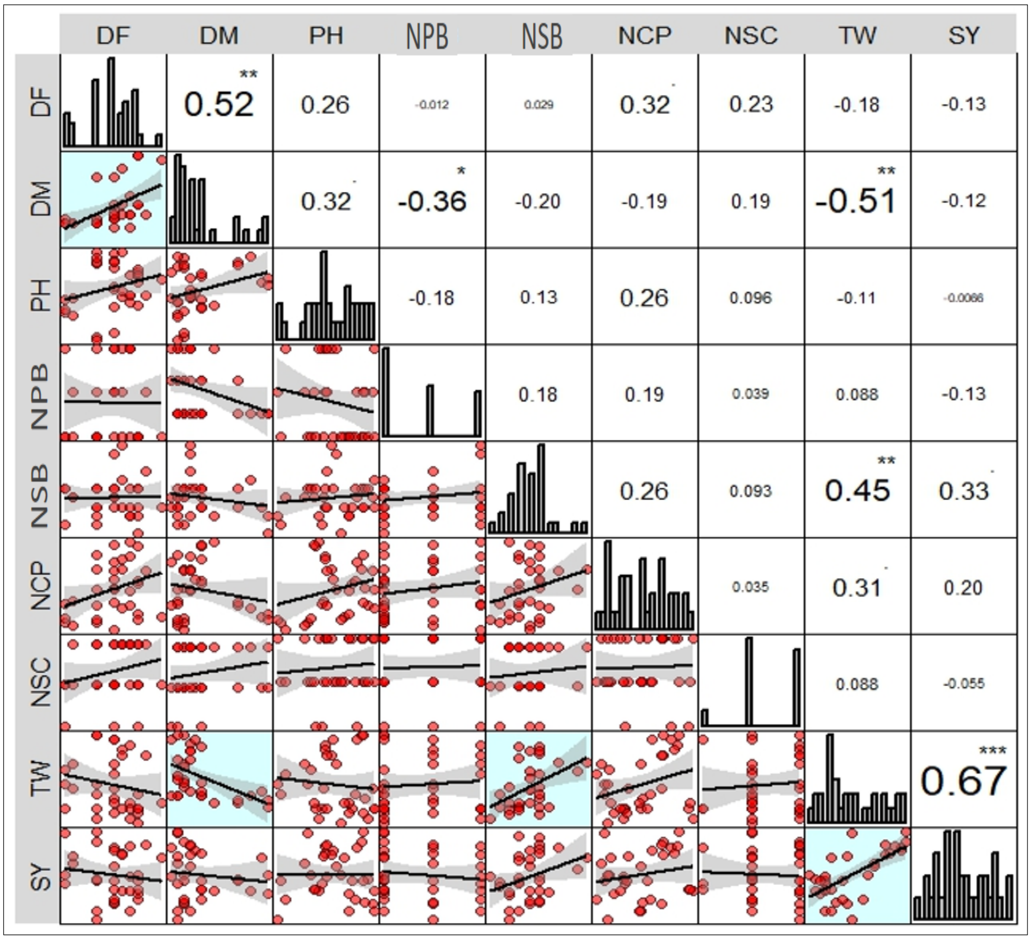

Fig. 4. The scatterplot matrix displays histograms of the variables along the diagonal and correlation coefficients in the upper part of the matrix. DF: days to flowering; DM: days to maturity; PH: plant height (cm); NPB: number of primary branches; NSB: number of secondary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; TW: test weight (g); SY: seed yield (kg/ha).

yield-related traits, the number of branches per plant exhibited a positive and significant correlation with CP (r = 0.23) and harvest weight (r = 0.15), but a negative and significant correlation with TW (r = – 0.22). Furthermore, CP showed a strong positive and significant association with capsule weight per plant (r = 0.74), reinforcing its role as a key component trait contributing to yield as reported earlier (19). Understanding the magnitude and direction of correlations among various quantitative traits provides crucial information for devising effective selection strategies aimed at genetic improvement of target traits. Correlation coefficient analysis serves as a vital statistical tool to assess the strength and direction of linear associations between traits, guiding breeders in identifying indirect selection pathways. The significant positive correlations of SY with number of branches per plant, CP and NCP suggest that indirect selection through these traits may be effective for enhancing SY potential in linseed. Similar trends of positive associations among these yield-contributing traits have been reported in earlier studies (21, 23, 58).

Conclusion

The comprehensive assessment of variability, heritability, GA and trait interrelationships in advanced linseed breeding lines highlights substantial potential for accelerating genetic improvement through strategic selection. High heritability coupled with high GA for key yield-contributing traits such as PH, NCP, 1000-seed weight and SY indicates predominant additive gene action. This underscores the strong effectiveness of direct phenotypic selection for these traits and their importance in enhancing overall productivity. The slightly higher PCV values relative to GCV for most traits suggest moderate environmental influence; however, the dominance of genetic factors for major yield traits confirms the stability and reliability of these traits for selection across environments. BLUP-based genetic parameter estimation further strengthened these conclusions by revealing high heritability, substantial GA and strong prediction accuracy for SY, CP, TW, PH and DM. These findings demonstrate the robustness of mixed-model approaches in identifying stable, high-performing genotypes. In contrast, traits such as basal branches and seeds per capsule exhibited low heritability and strong environmental dependence, highlighting the limited potential for improving these traits through conventional selection. For such traits, molecular breeding tools, marker-assisted selection or refined environmental management strategies may be necessary to achieve meaningful gains. Principal component analysis explained over 82 % of the total variability through traits associated with reproductive timing, plant stature and branching behaviour, establishing these as pivotal contributors to overall genetic divergence among genotypes. Their prominence in the PCA underscores their utility as key targets for selection to enhance adaptability and yield potential under diverse agro-ecological conditions. Correlation analyses further emphasised the strong positive associations between SY and major yield components particularly CP and 1000-seed weight, validating their effectiveness as indirect selection criteria. Nonetheless, trade-offs, such as the negative correlation between TW and maturity duration, indicate that careful, balanced selection is necessary to optimise both early maturity and high productivity. Overall, the integrated use of variability metrics, BLUP-based estimates, multivariate analysis and trait correlations provides a powerful framework for identifying superior genotypes and refining breeding priorities. Genotypes such as OL-2013-14-2022-2, OL-2013-14-2022-6 and OL-2013-14-2022-7 emerged as promising candidates for yield enhancement. These findings significantly contribute to the design of efficient breeding strategies aimed at accelerating genetic gain and ensuring sustainable improvement of linseed under variable climatic conditions.

Acknowledgements

The authors express their sincere gratitude to the Linseed Project Coordination Unit, ICAR- Indian Institute of Oilseeds Research (IIOR), Hyderabad and the ICAR-All India Coordinated Research Project on Linseed, Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology (OUAT), Keonjhar, Odisha, for providing the necessary resources, facilities and support throughout the course of this research.

Authors' contributions

PKM, KCS and MR contributed to conceptualisation and methodology; PKM, ST and SD conducted the field experiments and data collection; PPB, SS and PKM performed the statistical analysis; PKM, SS, SD and AN were involved in manuscript writing, reviewing and editing. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors declare that there is no conflict of interest.

Ethical issues: None

References

1. Kajla P, Sharma A, Sood DR. Flaxseed - a potential functional food source. J Food Sci Technol. 2015;52(4):1857–71. https://doi.org/10.1007/s13197-014-1293-y
2. Majhi PK, Sahoo KC, Tudu S. Nutritional profile of functional food—flaxseed. Biotica Res Today. 2023;5(4):298–301.
3. Tadesse T, Parven A, Singh H, Weyessa B. Estimates of variability and heritability in linseed germplasm. Int J Sustain Crop Prod. 2010;5(3):8–16.
4. Kaur V, Gomashe SS, Yadav SK, Singh D, Sheela, Chauhan SS, et al. Leveraging genetic resource diversity and identification of trait-enriched superior genotypes for accelerated improvement in linseed (*Linum usitatissimum* L.). Sci Rep. 2024;14(1):20266. https://doi.org/10.1038/s41598-024-71044-8
5. Kurt O, Bozkurt D. Effect of temperature and photoperiod on seedling emergence of flax (*Linum usitatissimum* L.). J Agron. 2006;5(3):541–5. https://doi.org/10.3923/ja.2006.541.545
6. Mohanty GR, Majhi PK, Samantaray S, Ray M, Mallik SK, Swain A, et al. Flaxseed: the marvel of nature for humanity. Int J Adv Biochem Res. 2024;8(6):450–8. https://doi.org/10.33545/26174693.2024.v8.i6f.1348
7. Singh KK, Mridula D, Rehal J, Barnwal P. Flaxseed: a potential source of food, feed and fiber. Crit Rev Food Sci Nutr. 2011;51:210–22. https://doi.org/10.1080/10408390903537241
8. Manimurugan C, Lakshmi P, Anand Z, Sujatha M. Diversified uses of linseed. Hyderabad (India): ICAR-Indian Institute of Oilseeds Research; 2021.
9. Manimurugan C, Zanwar A, Sujatha M. Genetic enhancement of nutraceuticals in linseed: breeding and molecular strategies. In: Kole C, editor. Compendium of crop genome designing for nutraceuticals. Singapore: Springer Nature; 2023. p. 519–43. https://doi.org/10.1007/978-981-19-4169-6_19
10. Nair B, Anand Z, Nandan M, Payasi D, Mogali S, Rathnakumar AL, et al. Value added products of linseed. Hyderabad (India): ICAR-Indian Institute of Oilseeds Research; 2021.
11. Megan N. What is flaxseed oil? An oil that may reduce inflammation and promote heart and gut health. 2023. https://www.verywellhealth.com/flaxseed-oil-health-benefits-how-to-use-and-cautions-4178046
12. Rachael A. 6 benefits of flaxseed oil plus how to use it. 2017. https://www.healthline.com/nutrition/flaxseed-oil-benefits
13. Rabetafika HN, Remoortel VV, Danthine S, Paquot M, Blecker C. Flaxseed proteins: food uses and health benefits. Int J Food Sci Technol. 2011;46(2):221–8. https://doi.org/10.1111/j.1365-2621.2010.02477.x
14. Parikh M, Maddaford TG, Austria JA, Aliani M, Netticadan T, Pierce GN. Dietary flaxseed as a strategy for improving human health. Nutrients. 2019;11(5):1171. https://doi.org/10.3390/nu11051171
15. Majhi PK, Mohanty GR. Medicinal properties of flaxseed - a superfood. Biotica Res Today. 2023;5(8):563–5.
16. Kumar N, Paul S, Chaudhary HK, Sood VK, Mishra SK, Singh AD, et al. Combining ability, gene action and heterosis for seed yield and its attributes in linseed (*Linum usitatissimum* L.). Int J Curr Microbiol Appl Sci. 2016;5(5):434–44.
17. Kumar S, Ram S, Chakraborty M, Ahmad E, Verma N, Lal HC, et al. Role of genetic variability for seed yield and its attributes in linseed (*Linum usitatissimum* L.) improvement. J Pharmacogn Phytochem. 2019;2:266–8.
18. Upadhyay S, Mehta N, Tiwari AK. Assessment of variability among flax type linseed genotypes (*Linum usitatissimum* L.) of Chhattisgarh plains. Int J Curr Microbiol Appl Sci. 2019;8(6):2633–7. https://doi.org/10.20546/ijcmas.2019.806.316
19. Yadav SK, Singh N, Yadav HK. Genetic variability and trait association analysis in linseed (*Linum usitatissimum* L.) for yield and related traits. Oil Crop Sci. 2024;9(3):151–9. https://doi.org/10.1016/j.ocsci.2024.06.003
20. Terfa GN, Gurmu GN. Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) genotypes. Oil Crop Sci. 2020;5(3):156–60. https://doi.org/10.1016/j.ocsci.2020.08.002
21. Ataii E, Mirlohi A, Sabzalian MR, Goli SA, Sadri N, Sharif-Moghaddam N, et al. Genetic variability of seed yield and oil nutritional attributes in linseed dominated by biennial variation. Crop Pasture Sci. 2021;72(6):443–57. https://doi.org/10.1071/CP20275
22. Hussain ME, Goyal VK, Paul PJ, Yadav Y, Jha UC, Moitra PK. Assessment of genetic variability, diversity and identification of promising lines in linseed germplasm. J Plant Breed Crop Sci. 2022;14(1):12–20. https://doi.org/10.5897/JPBCS2021.0990
23. Dabalo DY, Singh BC, Weyessa B. Genetic variability and association of characters in linseed (*Linum usitatissimum* L.). Saudi J Biol Sci. 2020;27(8):2192–206. https://doi.org/10.1016/j.sjbs.2020.06.043
24. Posit Team. RStudio: integrated development environment for R. Boston (MA): Posit; 2022.
25. R Core Team. R: a language and environment for statistical computing. Vienna (Austria): R Foundation; 2021.
26. Raj Popat, Patel AJ, Patel JS, Patel RD, Patel DH. Genetic variability, heritability and genetic advance in linseed. Int J Curr Microbiol Appl Sci. 2020;9(8):1701–9.
27. Singh D, Choudhury BD. Biometrical methods in quantitative genetic analysis. New Delhi (India): Kalyani Publishers; 1977.

28. Olivoto T, Lucio AD. metan: an R package for multi-environment trial analysis. Methods Ecol Evol. 2020;11(6):783–9. https://doi.org/10.1111/2041-210X.13384

29. Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*). Agron J. 1953;45(10):478–81. https://doi.org/10.2134/agronj1953.00021962004500100005x

30. Olivoto T, Lúcio AD, da Silva JA, Marchioro VS, de Souza VQ, Jost E. Mean performance and stability in multi-environment trials I. Agron J. 2019;111(6):2949–60. https://doi.org/10.2134/agronj2019.03.0220

31. Shivasubramanian S, Menon M. Genotypic and phenotypic variability in rice. Madras Agric J. 1973;60:1093–6.

32. Lush JL. Heritability of quantitative traits in farm animals. Hereditas. 1949;35(S1):356–75. https://doi.org/10.1111/j.1601-5223.1949.tb03347.x

33. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agron J. 1956;48(6):268–72. https://doi.org/10.2134/agronj1956.00021962004800060008x

34. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and dominance in corn. Agron J. 1949;41(8):353–9. https://doi.org/10.2134/agronj1949.00021962004100080005x

35. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314–8. https://doi.org/10.2134/agronj1955.00021962004700070009x

36. Patial R, Paul S, Sharma D, Sood VK, Kumar N. Morphological characterization and genetic diversity of linseed. J Oilseeds Res. 2019;36(1):8–16. https://doi.org/10.56739/jor.v36i1.126048

37. Paul S, Kumar N, Chopra P. Genetic variation and characterization of linseed genotypes. J Appl Nat Sci. 2017;9(2):754–62. https://doi.org/10.31018/jans.v9i2.1268

38. Singh A, Prashant KR, Arvind K, Shailesh M, Yadav PK. Study on variability, heritability and correlation in linseed. Adv Appl Sci Res. 2015;6(10):14–7.

39. Singh VK, Kerkhi SA, Singh SP, Tomar P. Genetic variability and genetic advance in linseed. J Pharmacogn Phytochem. 2019;8(2):761–5.

40. Kumar S, You FM, Duguid S, Booker H, Rowland G, Cloutier S. QTL for fatty acid composition and yield in linseed. Theor Appl Genet. 2015;128:965–84. https://doi.org/10.1007/s00122-015-2483-3

41. Kumar S, Yadav SK, Singh PK, Yadav RK. Genetic variability in linseed. J Pharmacogn Phytochem. 2020;9(3):1557–60. https://doi.org/10.22271/phyto.2020.v9.i5aq.12822

42. Sahu P, Patel AR, Mishra SB. Genetic variability and trait association in linseed. Int J Curr Microbiol Appl Sci. 2022;11(3):87–96.

43. Meena RK, Yadava DK, Kumar A. Evaluation of advanced breeding lines of linseed. Indian J Agric Sci. 2021;91(4):589–93.

44. Rahman MM, Akter N. Genetic variability and path analysis in linseed. Bangladesh J Agric Res. 2019;44(2):217–29. https://doi.org/10.3329/bjar.v44i1.40906

45. Singh A, Kumar S. Variability and heritability in linseed. Plant Arch. 2023;23(1):75–81.

46. Resende MDV, Duarte JB. Statistical methods in quantitative genetics. Crop Breed Appl Biotechnol. 2014;14(4):234–43.

47. Henderson CR. Best linear unbiased estimation and prediction. Biometrics. 1975;31(2):423–47. https://doi.org/10.2307/2529430

48. Thakur G, Paul S, Thakur R. Genetic variability in linseed. Himachal J Agric Res. 2022;48(2):151–6.

49. Kulhari S, Mukul, Kumar M, Kishan R. Assessment of principal component analysis and genetic diversity among linseed germplasm. Int J Environ Clim Change. 2023;13(12):537–44. https://doi.org/10.9734/ijecc/2023/v13i123711

50. Samantara K, Mohapatra SR, Pradhan BD. Assessment of genetic diversity in linseed (*Linum usitatissimum* L.). Int J Curr Microbiol Appl Sci. 2020;9(5):508–13. https://doi.org/10.20546/ijcmas.2020.905.057

51. Abtahi M, Mirlohi A, Sharif Moghaddam N, Ataii E. Seed color variation in flax. Front Plant Sci. 2022;13:1038079. https://doi.org/10.3389/fpls.2022.1038079

52. Mohammadi-Mirik A, Parsaeian M, Rohani A, Lawson S. Optimizing linseed seed yield through agronomic modeling. Agriculture. 2024;14(1):25. https://doi.org/10.3390/agriculture14010025

53. Sclove SL. Determining an adequate number of principal components. In: Pedro García Márquez F, editor. Advances in Principal Component Analysis; 2022. http://dx.doi.org/10.5772/intechopen.97992

54. Maurya R, Singh PK, Ranade SA, Yadav HK. Diversity analysis in Indian linseed genotypes. Gene. 2014;549(1):171–8. https://doi.org/10.1016/j.gene.2014.07.067

55. Abdel-Monaem MA, Abido WA, Hadházy Á, Ghoneima MH, El-Mansy YM, El-Shazly MW. Genetic divergence under water deficit. Acta Ecol Sin. 2022;42(2):11–8. https://doi.org/10.1016/j.chnaes.2020.11.007

56. Kumar N, Paul S. Selection criteria of linseed genotypes for seed yield traits through correlation, path coefficient and principal component analysis. J Anim Plant Sci. 2016;26(6):1688–95.

57. Sathish K, Parte D, Rohit MV, Roy S, Sahu J, Mehta N. Genetic-morphological characterization of linseed. Int J Plant Soil Sci. 2022;34(22):1655–63. https://doi.org/10.9734/ijpss/2022/v34i2231545

58. Chandrawati, Singh N, Kumar R, Kumar S, Singh PK, Yadav VK, et al. Genetic diversity and population structure in linseed. Physiol Mol Biol Plants. 2017;23:207–19. https://doi.org/10.1007/s12298-016-0408-5

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.