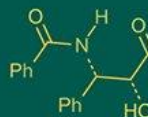


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Evaluation of Advanced Breeding Lines for Seed Yield and Yield Contributing Traits in Linseed (*Linum usitatissimum* L.)

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Abstract

The present study assessed genetic variability, heritability, genetic advance, and trait associations in 19 advanced breeding lines of linseed evaluated during *rabi* 2024/25 at Main Agricultural Research Station, AICRP on Linseed, UAS, Raichur. The experiment was laid out in a randomized block design with three replications. Analysis of variance revealed significant differences among genotypes for all traits, indicating substantial genetic variability. PCV values were higher than GCV values for all traits, suggesting environmental influence on trait expression, although the narrow differences for days to 50% flowering, days to maturity, and seed yield indicated greater genetic control. High GCV and PCV were observed for seeds per capsule, capsules per plant, and seed yield. Heritability was moderate to high for most traits, with seed yield showing the highest estimate, while seeds per capsule recorded the highest genetic advance as percent of mean, followed by seed yield and capsules per plant. Correlation and path analyses indicated a significant negative association of seed yields with 1000-seed weight, whereas capsules per plant and days to maturity showed favorable relationships with yield-related traits.

Keywords: Linseed, genetic variability, heritability, genetic advance, correlation, path analysis, seed yield

Introduction

Linseed (*Linum usitatissimum* L.) is an important oilseed crop cultivated worldwide because of its high α -linolenic acid content and its wide applications in the food, pharmaceutical, nutraceutical and industrial sectors (Mohammad *et al.*, 2022; Sandhya *et al.*, 2026) [11, 18]. In recent years, increasing demand for healthy edible oils and climate-resilient cultivars has intensified efforts to improve seed yield and other economically important traits through genetic enhancement (Kaur *et al.*, 2024) [6].

Genetic variability forms the foundation of any crop improvement programme, as the effectiveness of selection depends on the availability of sufficient variation within breeding populations. Several studies have reported considerable variability among linseed germplasm for flowering time, maturity, plant height, branching pattern, capsule number, seed weight and seed yield, indicating substantial scope for genetic improvement (Markandey *et al.*, 2022; Toor *et al.*, 2024; Singh *et al.*, 2025) [8, 20, 24].

Genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance are widely used to assess the nature and magnitude of genetic variability. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and suggests that direct phenotypic selection would be effective (Prameela *et al.*, 2022; Sahu *et al.*, 2024) [16, 17]. Several researchers have reported high heritability for yield-contributing traits such as capsules per plant, biological yield, and thousand-seed weight, emphasizing their importance as reliable selection criteria in linseed improvement programmes (Toor *et al.*, 2023; Patel *et al.*, 2025) [24].

Seed yield in linseed is a complex quantitative trait influenced by several interrelated characters. Correlation and path coefficient analyses have been extensively employed to partition the direct and indirect effects of yield-contributing traits, thereby identifying characters with the greatest influence on seed yield. capsules per plant, primary branches,

biological yield, harvest index and thousand-seed weight have consistently exhibited strong positive associations with seed yield, making them useful targets for indirect selection (Abeje & Zewodu, 2024; Washimkar *et al.*, 2025; Karla *et al.*, 2024) [1, 26].

Beside to above, recent investigations have also highlighted the importance of evaluating elite breeding materials for developing climate-resilient and high-yielding cultivars. Assessment of advanced breeding lines facilitates the identification of promising genotypes with superior performance and provides valuable information for their utilization in future breeding programmes (Dabalo *et al.*, 2020; Negash *et al.*, 2026) [11]. Furthermore, the integration of variability parameters, heritability estimates and association analyses enhances the efficiency of selection and accelerates genetic gain in linseed breeding (Kol *et al.*, 2024; Thakur *et al.*, 2020; Meena *et al.*, 2020; Terfa & Gurmu, 2020; Paul *et al.*, 2020) [7, 10, 15, 21, 22].

Despite considerable progress in linseed improvement, information on the performance and genetic variability of advanced breeding lines under diverse agro-climatic conditions remains limited. Therefore, the present study is undertaken to evaluate advanced breeding lines is essential for identifying superior genotypes with enhanced yield potential and other desirable characteristics that can be exploited in future varietal development programme.

Materials and Methods

The experimental material comprised 19 advanced breeding lines of linseed which were evaluated during Rabi 2024-25 at Main agriculture research station, AICRP on Linseed, UAS, Raichur. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in a single row of 5 length maintaining a spacing of 30 cm between rows and 10 cm between plants. All recommended agronomic and plant protection practices were followed uniformly throughout the crop growth period. Observations were recorded on five randomly selected competitive plants from each plot for days to 50% flowering, days to maturity, plant height (cm), capsules per plant, seeds per capsule, 1000-seed weight (g) and seed yield per ha (kg). The mean values of these observations were subjected to statistical analysis.

Analysis of variance (ANOVA) was performed according to the procedure described by Panse and Sukhatme (1985) [13]. Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated following Burton and DeVane (1953) [3]. Broad-sense heritability was computed according to Hanson *et al.* (1956) [4] while genetic advance and genetic advance as a percentage of the mean were calculated using the method proposed by Johnson *et al.* (1955) [5]. Genotypic and phenotypic correlation coefficients were estimated to determine the association among different traits, and path coefficient analysis was performed to partition the correlation coefficients into direct and indirect effects on seed yield.

Results and Discussion

The analysis of variance (ANOVA) revealed highly significant ($P \leq 0.01$) differences among the advanced breeding lines for all the studied traits, indicating substantial

genetic variability (Table 1). Such significant variability among linseed genotypes has also been reported by Paul *et al.* (2017) [14] and Mohammad *et al.* (2022) [11], suggesting that these breeding lines possess adequate genetic diversity for effective selection. The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits (Table 2), indicating environmental influence on trait expression, as also reported by Toor *et al.* (2024) [24]. However, the narrow differences between GCV and PCV for days to maturity, days to 50% flowering and seed yield indicate that these traits were less influenced by environmental factors and could be improved through direct selection, which agrees with the findings of Markandey *et al.* (2022) [8].

The high GCV and PCV recorded for number of seeds per capsule, number of capsules per plant and seed yield indicate considerable genetic variability for these yield-related traits. The close correspondence between GCV and PCV suggests limited environmental influence and a major role of genetic factors in their expression. Similar results were reported by Mohammad *et al.* (2022) [11], confirming the potential of these traits for improvement through selection.

Heritability was moderate to high for most traits, with seed yield showing the highest estimate (65.16%), indicating that phenotypic expression was largely genetically controlled number of seeds per capsule recorded the highest genetic advance as percent of mean (15.32%), followed by seed yield (13.29%) and number of capsules per plant (11.22%). As suggested by Johnson *et al.* (1955) [5], the combination of high heritability and high genetic advance points to additive gene action and the effectiveness of direct phenotypic selection. These findings are in agreement with Paul *et al.* (2017) and Toor *et al.* (2024) [24].

Phenotypic correlation analysis (Table 3) revealed a significant negative association between seed yield and 1000-seed weight ($r = -0.482$), indicating that selection for heavier seeds alone may not improve yield in the present material. A similar negative relationship between these traits was also observed by Siddique *et al.* (2023) [19]. In contrast, capsules per plant showed a significant positive correlation with 1000-seed weight ($r = 0.475$), while days to maturity was positively associated with 1000-seed weight ($r = 0.383$) suggesting favourable interactions among these traits. The negative association of days to 50% flowering with number of capsules per plant and 1000-seed weight indicates that earlier flowering genotypes tended to produce more capsules and heavier seeds, a trend also reported by Mathur *et al.* (2024) [9].

Path coefficient analysis (Table 4) revealed that days to 50% flowering (0.080) and plant height (0.063) exerted positive direct effects on seed yield, whereas 1000-seed weight (-0.427) had the highest negative direct effect. This indicates that the observed negative correlation between seed yield and thousand-seed weight was mainly due to its strong negative direct effect rather than indirect influences through other traits. Paul *et al.* (2017) [14] and Markandey *et al.* (2022) [8] similarly demonstrated that path coefficient analysis provides a more reliable basis for identifying effective selection criteria than simple correlation analysis

Table 1: Analysis of variance for morphological and yield parameters

Source of variation	df	DFF	DM	PH	CP	SC	TSW	SY
Genotype	10	3.76**	18.48**	47.35**	101.05**	1.48**	0.81**	21204.08**
Replication	2	1.48	9.30	15.48	28.76	0.03	0.05	646.20
Error	20	1.42	4.10	19.55	31.09	0.33	0.24	3207.89

*P = 0.05; **P = 0.01 Where, DFF=Days to 50 per cent flowering, DTM=Days to maturity, PH= Plant height (cm), NCP=Number of capsules per plant, SY=Seed yield, NSC=Number of seeds per capsule, TSW=1000-seed weight (g).

Table 2: Mean, Range and variability parameters for yield and yield attributing traits

Sl.No	Character	Mean	Range		GCV	PCV	h ² (%)	GA	GAM
			Max	Min					
1	Days to 50% flowering	57.30	59.33	56.00	1.54	2.59	35.54	1.09	1.89
2	Days to maturity	114.88	118.33	111.67	1.91	2.60	53.88	3.31	2.88
3	Plant height (cm)	54.12	59.33	48.67	5.62	9.92	32.16	3.56	6.57
4	Number of capsules per plant	58.06	65.67	49.67	8.32	12.70	42.86	6.51	11.22
5	Number of seeds per capsule	6.12	7.33	5.00	10.13	13.82	53.81	0.94	15.32
6	Thousand seed weight (g)	6.77	7.52	6.07	6.42	9.67	44.07	0.59	8.78
7	Seed yield (kg/ha)	968.93	1107.64	798.90	7.99	9.90	65.16	128.79	13.29

GCV= Genotypic Co-Efficient of Variation, PCV= Phenotypic Co-Efficient of variation, h² = Heritability, GA= Genetic Advance, GAM= Genetic Advance as per cent of Mean

Table 3: Phenotypic correlation co-efficient between yield and yield attributing traits

	DFF	DTM	PH	NCP	NSC	TSW	SY
DFF	1	-0.244	0.216	-0.356 *	0.010	-0.410 *	0.270
DTM		1	0.018	-0.083	0.007	0.383 *	-0.232
PH			1	-0.146	0.313	0.059	0.029
NCP				1	0.200	0.475 **	-0.223
NSC					1	0.302	-0.173
TSW						1	-0.4821 **
SY							1

*: Significant @ 5%, **: @1% level of significance, respectively

Where, DFF=Days to 50 per cent flowering, DTM=Days to maturity, PH= Plant height (cm), NCP=Number of capsules per plant, SY=Seed yield, NSC=Number of seeds per capsule, TSW=1000-seed weight (g).

Table 4: Phenotypic path co-efficient of yield attributing traits

Characters	DFF	DTM	PH	NCP	NSC	TSW	SY
DFF	0.080	0.012	0.014	-0.010	-0.001	0.175	0.270
DTM	-0.019	-0.048	0.001	-0.002	-0.001	-0.163	-0.232
PH	0.017	-0.001	0.063	-0.004	-0.022	-0.025	0.029
NCP	-0.028	0.004	-0.009	0.028	-0.014	-0.203	-0.223
NSC	0.001	0.000	0.020	0.006	-0.070	-0.129	-0.173
TSW	-0.033	-0.018	0.004	0.013	-0.021	-0.427	-0.482

*, ** indicates significant at 5 per cent and 1 per cent level of probability, respectively.

Residual: 0.585

Where, DFF=Days to 50 per cent flowering, DTM=Days to maturity, PH= Plant height (cm), NCP=Number of capsules

per plant, SY=Seed yield, NSC=Number of seeds per capsule, TSW=1000-seed weight (g).

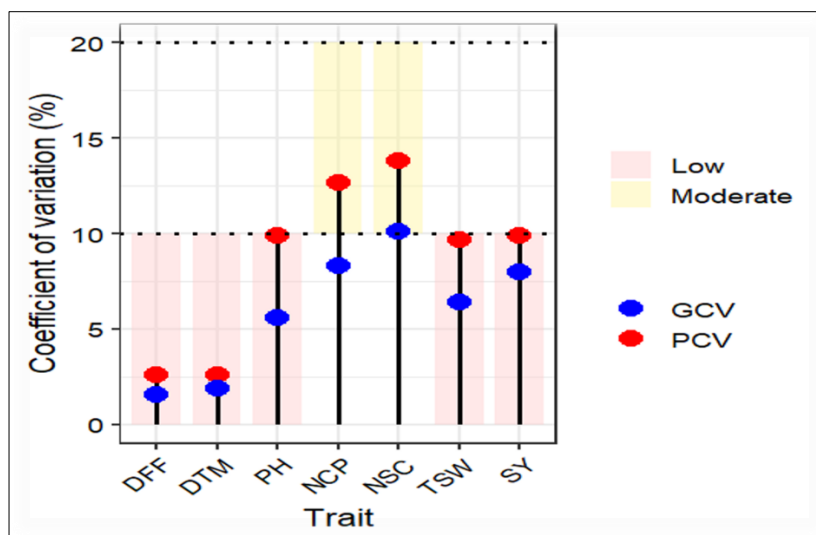


Fig 1: Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for quantitative traits in advanced breeding lines of linseed. Blue and red circles represent GCV and PCV respectively. Shaded regions indicate low (<10%) and moderate (10-20%) variability

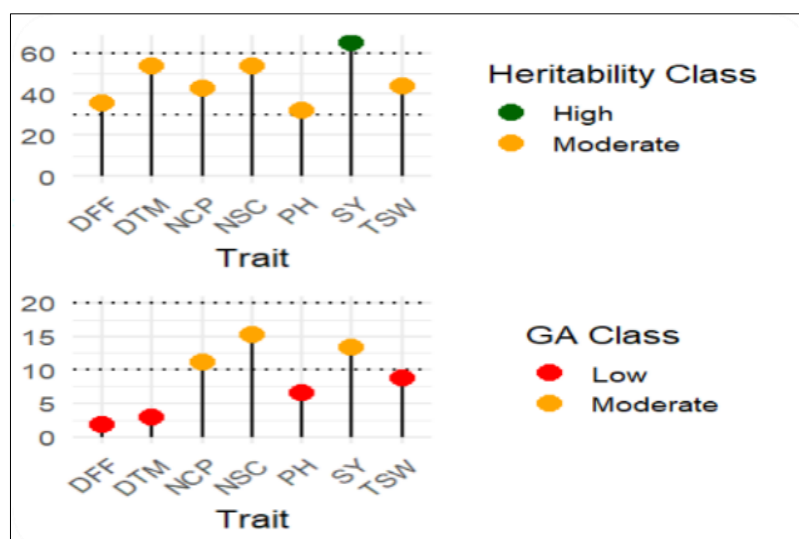


Fig 2: Broad-sense heritability (%) and genetic advance as percent of mean (GAM) for quantitative traits in advanced breeding lines of linseed. Green and orange circles represent high and moderate heritability classes, while red and orange circles indicate low and moderate genetic advance classes respectively

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