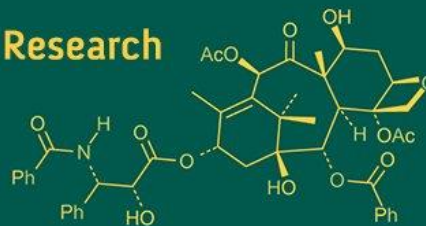


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Harnessing double cross populations to generate genetic variability for yield improvement in linseed

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Abstract

This study assessed genetic variability, heritability and genetic advance in a double cross-derived F_6 population of linseed developed from twenty diverse parents, experiment was conducted during rabi 2025-26 at Main Agricultural Research Station, UAS, Raichur in a randomized complete block design with three replications. Significant variation was observed for all seven quantitative traits, indicating substantial genetic diversity in the population. In all cases, PCV values were higher than GCV values, suggesting a moderate influence of the environment on trait expression. Among the traits studied, capsules per plant showed the highest variability and relatively high genetic advance, indicating good potential for effective selection. High heritability was recorded for days to 50% flowering and days to maturity, while capsules per plant combined moderate heritability with high genetic advance, suggesting the predominance of additive gene action.

Keywords: *Linum usitatissimum*, double cross breeding, genetic variability, heritability, genetic advance

1. Introduction

Linseed (*Linum usitatissimum* L.) is an important industrial oilseed crop cultivated worldwide for its high-quality oil rich in Alpha-Linolenic Acid (ALA) and its diverse applications in food, pharmaceutical, cosmetic and fiber industries (Kumar *et al.*, 2018) [11]. Despite its economic significance, genetic improvement for seed yield and related agronomic traits has been relatively slow due to the narrow genetic base of cultivated germplasm and the complex inheritance of quantitative traits (Dhirhi *et al.*, 2018; Mahto & Mishra, 2025) [3, 14].

Genetic variability provides the fundamental basis for crop improvement by enabling effective selection of superior genotypes with desirable combinations of agronomic traits (Kaur *et al.*, 2024; Mohammad *et al.*, 2022) [10, 18]. Conventional biparental crosses, although widely employed in linseed breeding, involve only two parental genomes and often produce limited allelic recombination, thereby restricting the probability of recovering transgressive segregants for complex traits like seed yield, capsule number and seed weight (Kumar *et al.*, 2017; Markandey *et al.*, 2022) [13, 17].

Double cross breeding offers an effective approach to expand the genetic base by combining favourable alleles from four genetically diverse parents into a single segregating population (Mahto *et al.*, 2019; Mahto *et al.*, 2020) [15, 16]. This multi-parent mating design increases opportunities for genetic recombination, enhances allelic diversity and facilitates the accumulation of favourable gene combinations governing quantitative traits (Chaudhari *et al.*, 2025) [2]. The greater recombination achieved through double crosses promotes transgressive segregation and increases the likelihood of identifying elite recombinants with improved yield potential and desirable agronomic performance (Mohammad *et al.*, 2022; Sahu *et al.*, 2022) [18, 23]. Furthermore, the use of genetically divergent parents minimizes the limitations associated with narrow genetic diversity and enhances breeding efficiency by generating populations with wider phenotypic and genotypic variations (Hoque *et al.*, 2020; Kumar *et al.*, 2021) [7, 12].

The effectiveness of selection largely depends on the magnitude of genetic variability, heritability and expected genetic advance present within breeding populations. Traits

exhibiting high genetic variability coupled with high heritability and substantial genetic advance are generally governed by additive gene action and respond efficiently to selection (Abtahi *et al.*, 2022; Kaur *et al.*, 2024; Paul *et al.*, 2017) [1, 10, 20]. Therefore, assessment of variability parameters in double cross-derived populations is essential for identifying promising recombinants and formulating effective breeding strategies for yield improvement. Although double cross breeding has been recognized as a valuable approach for enhancing recombination, limited information is available regarding the extent of genetic variability generated in such populations of linseed. Therefore, the present investigation was undertaken to evaluate the genetic variability, heritability and genetic advance in double cross-derived populations of linseed.

2. Materials and Methods

2.1 Plant material and development of double cross population

The experimental material comprised a double cross-derived population (Supplementary Table 1) of linseed (*Linum usitatissimum* L.) developed at Main Agricultural Research Station (MARS), University of Agricultural Sciences (UAS), Raichur. Twenty genetically diverse parental genotypes were selected based on their contrasting performance for seed yield and its component traits. Initially, two independent single crosses were made between the selected parents to produce F_1 hybrids. Subsequently, the two F_1 hybrids were intercrossed to generate the double cross population, thereby facilitating greater genetic recombination and broader allelic diversity. The resulting population was advanced through the pedigree method to the F_6 generation by selecting superior plants in each segregating generation.

2.2 Experimental design and crop management

The F_6 double cross-derived population, along with the parental lines was evaluated during *rabi* 2025-26 at Main Agricultural Research Station, Raichur. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was grown in a single row of 3.0 m length with 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 genotype in each replication for days to 50% flowering, days to maturity, plant height (cm), number of capsules, seeds per capsule, 1000-seed weight (g) and seed yield (kg ha^{-1}). The mean values of these observations were used for statistical analysis.

2.3 Statistical analysis

Analysis of Variance (ANOVA) was performed following the procedure described by Panse and Sukhatme (1985) [19] to determine the significance of differences among genotypes. Phenotypic variance and genotypic variance (σ^2) were estimated according to Burton (1952) [4]. The Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were calculated following Burton and DeVane (1953) [5]. Broad-sense heritability (H^2) was estimated as suggested by Hanson *et al.* (1956) [6], while expected genetic advance (GA) and genetic advance as

percent of mean (GAM) was computed using method of Johnson *et al.* (1955) [9].

3. Results and discussion

The highly significant differences (Table 1) among the double cross-derived linseed genotypes for all the studied characters demonstrate the successful generation of genetic variability through integration of genetically diverse parental lines. The substantial variation was observed for seed yield, capsules per plant, plant height, days to flowering, days to maturity; seeds per capsule and thousand-seed weight confirms that double cross breeding effectively broadened the genetic base compared with conventional biparental breeding populations. The incorporation of four parental genomes enhances meiotic recombination and facilitates the accumulation of favourable alleles, thereby increasing the probability of recovering superior recombinants in segregating generations (Priya *et al.*, 2018; Kumar *et al.*, 2017; Mahto *et al.*, 2020) [13, 15, 21]. Similar observations on the usefulness of broad-based breeding populations for generating exploitable genetic variability have been reported in linseed by Mohammad *et al.* (2022) [18], Kaur *et al.* (2024) [10] and Rathva *et al.* (2023) [22].

The estimates of genetic variability (Table 2, Figure 1) clearly demonstrated that the double cross population possessed sufficient phenotypic and genotypic diversity for effective selection. The consistently higher Phenotypic Coefficient of Variation (PCV) than the corresponding Genotypic Coefficient of Variation (GCV) for all characters indicates that environmental factors contributed to phenotypic expression. Nevertheless, the relatively narrow differences between GCV and PCV for days to maturity and days to 50% flowering suggest that these traits were less influenced by environmental conditions and were predominantly governed by genetic factors. Similar trends have been reported in linseed by Abdelaty *et al.* (2023), Ibrar *et al.* (2024) [8] and Paul *et al.* (2017) [20] who also observed relatively small differences between GCV and PCV for maturity-related traits.

Among all the characters, capsules per plant exhibited the highest GCV and PCV indicating the presence of substantial exploitable variability. Capsule number is one of the major yield-determining components in linseed because it directly influences the sink capacity of the plant. The high variability observed for this character suggests that recombination resulting from double cross breeding effectively disrupted unfavourable linkage blocks and generated novel gene combinations controlling reproductive development. Similar observations have been reported by Hosseini *et al.* (2025), Shah *et al.* (2025) [25] and Markandey *et al.* (2022) [17] who identified capsule number as one of the most variable and economically important characters in linseed improvement programmes.

Heritability (Figure 2) estimates provide valuable information regarding the relative contribution of genetic and environmental factors to phenotypic variation. In the present investigation, high heritability was recorded for days to maturity and days to 50% flowering, indicating that these traits were predominantly controlled by genetic factors and could be selected with greater reliability. However, their comparatively lower genetic advance as a percentage of the mean suggests that improvement through direct phenotypic selection may be gradual because both additive and non-additive genetic effects may contribute to their inheritance.

Similar conclusions have been drawn by Kaur *et al.* (2024)^[10], who emphasized that heritability should always be interpreted together with genetic advance to understand the underlying gene action.

Moderate heritability coupled with relatively high genetic advance for capsules per plant indicates the predominance of additive gene action, suggesting that selection for this character would be effective in early segregating generations. Traits governed largely by additive genetic effects respond efficiently to phenotypic selection because favourable alleles can be accumulated over successive generations. Comparable findings have been reported by Upadhyay *et al.* (2019), Rathva *et al.* (2023)^[22] and Mohammad *et al.* (2022)^[18], who highlighted capsule number as an important criterion for improving seed yield in linseed. In contrast, the relatively low heritability estimates observed for plant height and seed yield indicate that these traits were influenced considerably by environmental factors.

Seed yield is a complex quantitative trait resulting from the cumulative interaction of several component characters and environmental conditions consequently, direct selection for seed yield alone is generally less efficient than indirect selection through highly heritable yield components. Similar observations have been reported by Dhirhi *et al.* (2018)^[3], Mahto and Mishra (2025)^[14] and Sandhya *et al.* (2026)^[24]

who concluded that yield improvement in linseed should be achieved through simultaneous selection for major yield-contributing traits rather than seed yield alone.

The results clearly demonstrate that double cross breeding substantially enhanced the genetic variability available within the segregating population. Unlike conventional biparental populations, which recombine alleles from only two parents, double cross populations integrate favourable alleles from four genetically diverse parents, thereby increasing the frequency of recombination events and generating a wider spectrum of phenotypic variation (Priya *et al.*, 2018; Mahto *et al.*, 2020)^[15, 21]. Such broad-based populations increase the probability of recovering transgressive segregants possessing superior combinations of favourable alleles for yield and its component traits (Chaudhari *et al.*, 2025; Mohammad *et al.*, 2022)^[2, 18].

The observed variability parameters indicate that the present double cross population represents a valuable breeding resource for future linseed improvement. Among the evaluated traits, number of capsules emerged as the most reliable selection criterion because of its comparatively high genetic variability, moderate heritability and higher genetic advance. Therefore, selection based on this character is expected to accelerate genetic gain and facilitate the identification of elite recombinants with improved seed yield.

Table1: Analysis of variance for morphological and yield parameters

Source of variation	df	DFF	DTM	PH	NCP	NSC	TSW	SY
Genotype	10	14.87**	36.20**	66.27**	231.05**	1.01**	0.73**	18634.49**
Replication	2	1.82	1.31	194.49	5.25	0.14	0.14	10277.22
Error	20	2.68	2.90	33.39	81.59	0.30	0.22	8733.37

*P = 0.05; **P = 0.01

DFF=Days to 50 per cent Flowering, DM=Days to Maturity, PH= Plant Height (cm), NCP=Number of Capsules per

Plant, SY=Seed Yield (kg/ha), NSC= 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	56.78	59.33	51.00	3.59	4.63	60.29	3.22	5.75
2	Days to maturity	107.10	117.33	102.00	3.11	3.49	79.30	6.11	5.71
3	Plant height (cm)	48.25	56.67	40.67	6.86	13.80	24.72	3.39	7.03
4	Number of capsules per plant	63.39	80.67	48.00	11.13	18.08	37.91	8.95	14.12
5	Number of seeds per capsule	7.73	8.67	6.67	6.28	9.51	43.64	0.66	8.54
6	Thousand seed weight (g)	7.78	8.73	6.93	5.27	8.06	42.80	0.55	7.11
9	Seed yield (kg/ha)	998.18	1172.07	818.29	5.76	10.99	27.43	61.98	6.21

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

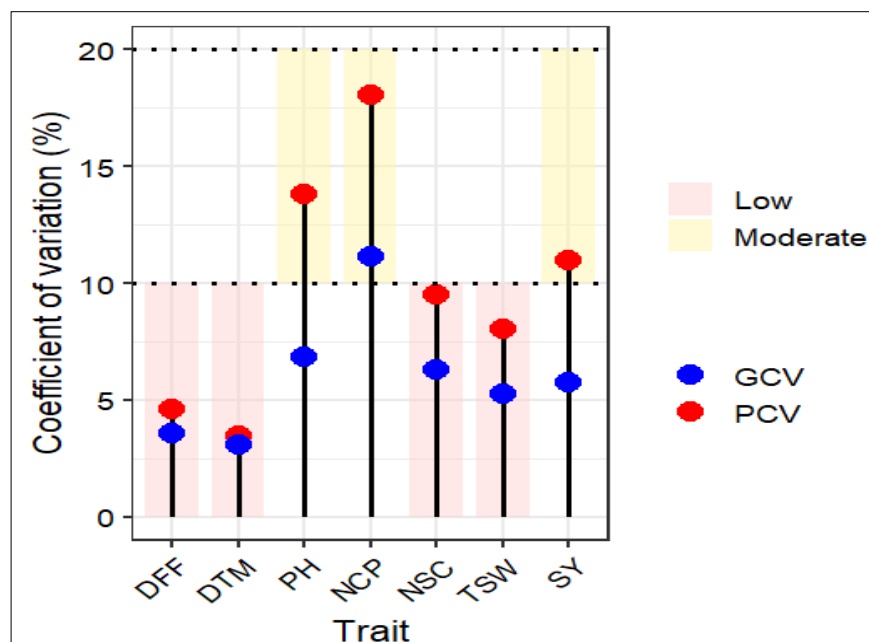


Fig 1: Genotypic (GCV) and phenotypic (PCV) coefficients of variation for seven quantitative traits in linseed. Blue and red circles represent GCV and PCV respectively. Shaded regions indicate low (<10%) and moderate (10-20%) variability

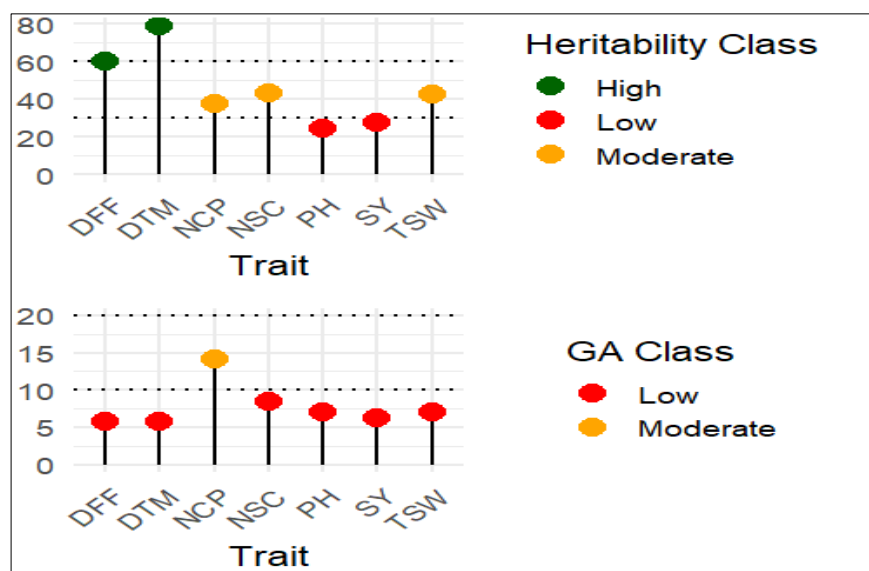


Figure 2; Heritability (%) and Genetic advance as percent of mean (GAM) for different quantitative traits, colors indicate the classification of heritability (low, moderate and high) and genetic advance (low and moderate)

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