Received: 09 Jul 2025 | Accepted: 24 Oct 2025 | Online: 14 Nov 2025

Electronic Journal of Plant Breeding

Research Article

Characterization of linseed (*Linum usitatissimum* L.) germplasm for genetic diversity and G x E interaction

Alka[1], A K. Toor[2*], C. Attri[1], S. Sharma[1], N. Sandhu[1] and R. Kapoor[1]

[1]Punjab Agricultural University (PAU), Ludhiana
[2]Punjab Agricultural University (PAU), Regional Research Station (RRS), RRS Gurdaspur
***E-Mail**: arvinderktoor2@gmail.com

Abstract

A comprehensive evaluation of 60 linseed (*Linum usitatissimum* L.) genotypes was conducted across two contrasting agro-ecological locations—Ludhiana and Gurdaspur—using 10 key agro-morphological traits to assess genetic variability, heritability, genetic advance, and genotype × environment (G × E) interaction. Analysis of variance (ANOVA) revealed significant differences among the genotypes for all traits, confirming the presence of substantial genetic variability. High estimates of phenotypic and genotypic coefficients of variation (PCV and GCV), heritability (H^2), and genetic advance as percent of mean (GAM) were recorded for traits such as number of secondary branches, capsules per plant, and seed yield, indicating strong additive gene action and their suitability for selection in breeding programs. In contrast, traits like days to 75% maturity and 1000-seed weight exhibited low variability and heritability, suggesting stronger environmental influence. Combined ANOVA and GGE biplot analysis identified significant G × E interactions, with genotype BAU-2019-13 showing superior performance in Ludhiana and LCK-2134 in Gurdaspur. Dendrogram-based clustering using Ward's method grouped the genotypes into six distinct clusters at each of the locations, revealing considerable genetic divergence. Smaller, isolated clusters contained highly divergent genotypes suitable for hybridization, while larger clusters suggested potential for intra-population selection. The study highlights the importance of multi-environment testing and advanced multivariate tools such as GGE biplot and cluster analysis in identifying stable, high-yielding genotypes and guiding targeted breeding strategies for linseed improvement.

Keywords: Linseed, PCV, GCV, heritability, G x E interaction, Diversity

INTRODUCTION

Linseed (*Linum usitatissimum* L.), commonly known as "Alsi" in Punjabi and "Tisi" or "Avishi" in other languages, is a self-pollinating crop with a diploid chromosome number (2n=2X=30). After rapeseed-mustard it is the second most important oilseed crop, grown for its oil, seed, and fibre. Cultivated since ancient times, linseed has held significant value due to its diverse applications. The genus name Linum is derived from the Celtic word "lin," meaning thread, while the species name *usitatissimum*, given by Carl Linnaeus, means "very useful," emphasizing its multifunctional importance in ancient civilizations (Dash *et al.,* 2017). India ranks 5th globally in linseed cultivation and 6th in production. Linseed covers 3.22 million hectares, producing 3.07 million tonnes, with an average yield of 952 kg/ha worldwide. In India, it is grown on 0.17 million hectares, producing 0.1 million tonnes, with an average productivity of 574 kg/ha (FAO Stat, 2019).

Linseed (*Linum usitatissimum* L.) is a unique and versatile oilseed crop valued for its multifaceted applications in human nutrition, industry, and livestock feeding. The seed possesses a mucilaginous outer layer that enhances its functional food properties, making it a rich source of dietary fibre (35–45%), of which approximately one-third is soluble, and two-thirds is insoluble (Morris, 2008). Linseed oil, extracted from the seed, is highly prized for its high α-linolenic acid (omega-3) content, which contributes to cardiovascular health and has significant industrial utility in paints, varnishes, and linoleum production (Oomah, 2001; Hall *et al.,* 2011).

Following oil extraction, the residual linseed meal or cake serves as a nutritious by-product rich in protein and minerals, making it a valuable ingredient in livestock feed formulations (Singh *et al.,* 2011). It contains all eight essential amino acids— isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine—thus offering high-quality plant-based protein for both human and animal consumption (Morris, 2008). For vegetarians, linseed provides an important source of minerals such as calcium, magnesium, and phosphorus. Overall, the dual utility of linseed oil and meal underscores its importance as both a health-promoting food and an industrially significant crop.

The global population continues to rise, making the need for a balanced and nutrient-rich diet more critical than ever. However, the agricultural sector faces challenges in meeting this demand, particularly in crops like linseed, due to climate change and the lack of improved varieties. To address this, the evaluation and characterization of existing germplasm, including varieties, landraces, and wild relatives, is essential. A comprehensive assessment of genetic variability is key to identifying promising genotypes. This can be achieved through the analysis of phenotypic, genotypic, and environmental coefficients of variation, heritability (h^2), and genetic advance as a percentage of the mean. Such studies provide valuable insights into the variability present within the germplasm. In recent years, due to the lack of improved varieties. linseed production has declined, largely. Therefore, it is crucial to develop new, high-yielding linseed varieties that can meet growing production demands. This study aims to assess genetic variability, heritability, genetic advance, and trait associations, along with genotype × environment interactions across two contrasting agro-ecological zones of Punjab (Ludhiana – plains and Gurdaspur – sub-mountainous). Analysis of parameters such as PCV, GCV, ECV, heritability, and GAM will help understand the genetic potential of traits. Cluster analysis through dendrograms will provide insights into genetic divergence and relatedness among genotypes. The results will facilitate identification of environment-specific, high-yielding, and stable genotypes suitable for direct cultivation or as parents in breeding. This will ultimately aid in developing improved linseed cultivars adapted to diverse environments, thereby enhancing productivity and profitability

MATERIALS AND METHODS

The experimental material comprised of 60 linseed (*Linum usitatissimum* L.) genotypes (**Table 1**) collected from diverse agro-ecological zones across India. The field experiments were conducted during the *Rabi* season of 2022–23 at two locations in Punjab: (1) the Oilseed Section fields, Punjab Agricultural University (PAU), Ludhiana, and (2) the PAU Regional Research Station, Gurdaspur. The experiments were laid out in a randomized block design (RBD) with three replications in both locations. Each genotype was sown in three-meter-long rows with a spacing of 23 cm between rows and 10 cm between plants. All recommended agronomic practices were followed throughout the crop's growth period to ensure uniform crop stand and optimal performance. Observations were recorded on Agro-morphological traits, namely days to 50% flowering (DTF), days to 75% maturity (DTM), number of primary branches (PB), number of secondary branches (SB), capsules per plant (CPP), seeds per capsule (SPC), plant height up to the highest capsule (PH, cm), 1000-seed weight (TSW, g), seed yield per plant (SYPP, g), and seed yield per plot (SYP, kg/ha).The mean values were utilized for statistical analysis to assess the magnitude of genetic variation and other genetic parameters. Analysis of variance (ANOVA) was carried out for all recorded traits to determine the significance of genotypic differences. Mean separation was conducted at the 5% and 1% levels of probability.

Estimates for genetic variability, namely, genotypic and phenotypic coefficients of variation (GCV and PCV), was calculated as per the formula proposed by Falconer (1964) and were categorised as low (<10%), moderate (10-20%) and high (>20%) as per Siva Subramanian and Madhava Menon (1973). The broad-sense heritability (h^2) was estimated following the formula proposed by Allard (1960) and categorized according to the classification of Johnson *et al.* (1955) as low (0–30%), moderate (30–60%), and high (above 60%). This classification serves as a valuable guide for assessing the proportion of phenotypic variance attributable to genetic factors and predicting the expected response to selection. The heritability estimates helped to estimate the genetic advance were according to Burton (1952) and traits were classified as high (>20%), moderate (10-20%), and low (<10%). All the statistical analyses were performed using R Studio software 4.3.1 (Kurt Hornik and R core team 2023)

To analyze genotype × environment interaction (GEI), the GGE biplot method was used, which is based on principal component analysis (PCA) of environment-centered yield data. Genotype means were adjusted for environment main effect. Singular value decomposition (SVD) was applied to the GEI matrix. The first two principal components (PC1 and PC2) were extracted to construct biplots. The analysis was conducted using R software (version 4.3.1) with the packages 'GGEBiplotGUI' and 'GGEBiplotR'.

The "which-won-where" view of the GGE biplot was employed to identify specifically adapted and widely adapted genotypes. In this method, a polygon is drawn by connecting the outermost genotypes in the biplot, and

Table 1. List of 60 linseed genotypes collected from different regions

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	LCK-2001	21	LMS-2018-1-10	41	LSL-93
2	LSL-93	22	RLC-153	42	RLC195
3	RLC-184	23	RL-18101	43	RLC187
4	NL-367	24	SLS135	44	Priyam
5	LCK-2030	25	Himani	45	Divya
6	SABOUR TISI-1	26	LCK2037	46	LMS-2017-1-12
7	KL-263	27	LCK2018-R-6	47	SHEKHAR
8	RLC-143	28	T-397	48	BRLS-120
9	LMS-2018-R-4	29	RL18106	49	SLS129
10	RL18107	30	LMS-2018-1-14	50	LCK-1611
11	SLS138	31	BAU-2019-13	51	SLS-136
12	BRL-103-1	32	BRLS-110-7	52	SurbhixLC2023
13	RLC181	33	RLC-185	53	19620x19617
14	SLS137	34	RLC196	54	19620x19621
45	DLV-17	35	LCK2117	55	LC2023xBAU-06-03
16	JLS-95	36	RUCHI	56	LC2063XBAU-06-03
17	AZAD ALSI-1(LMS-9-2K)	37	JRF2	57	LC54xBAU-06-03
18	RLC-183	38	LCK2134	58	LC-2063
19	SL-3	39	LCK2024	59	LC-2023
20	SLS-134	40	BAU-2021-08	60	LC-54

perpendicular rays are drawn from the biplot origin to each side of the polygon, dividing the plot into sectors. Each environment falls into one of these sectors, and the genotype located at the vertex of that sector is considered the best performer (winner) in those environments, identified as specifically adapted genotypes (those winning in one or few environments) and highlight widely adapted genotypes (those close to the origin performing consistently across environments).

RESULTS AND DISCUSSION

The crop was evaluated under two distinct agro-climatic zones of Punjab namely, the central plains zone represented by Ludhiana and the sub-mountainous zone represented by Gurdaspur. These locations differ notably in their climatic conditions, including temperature regimes and rainfall.

The primary objective of the study was to assess how environmental variability between these two regions affects the expression of key growth parameters and agronomic traits in linseed. By evaluating the same set of genotypes across these contrasting environments, the study aimed to quantify genotype × environment interactions and identify traits and genotypes that are either stable or highly responsive to specific environmental conditions. Such analysis is crucial for understanding the adaptability and performance of genotypes under variable climatic scenarios and for selecting suitable varieties for specific agro-ecological zones. The observed differences in trait expression between the two locations underscore the influence of environment on plant growth and yield-related characteristics.

Analysis of Variance (ANOVA): The pooled ANOVA revealed highly significant ($p < 0.001$) differences among genotypes for all traits studied, namely days to 50% flowering , days to maturity, primary branches, secondary branches , capsules per plant , seeds per capsule , plant height , 1000-seed weight , seed yield per plant , and seed yield per plot in **Table 2**. Mean sum of squares for genotypes was consistently higher than that of replications, highlighting the predominance of genetic variation over environmental influence. The largest variation was recorded for seed yield per plot, followed by capsules per plant and days to maturity, indicating their major contribution to total variability. Replication effects were non-significant across traits, confirming uniform experimental conditions. These findings are consistent with earlier reports by Kaur *et al.* (2017), Verma *et al.* (2019), and Singh *et al.* (2021), who also documented considerable genetic variability for yield and its component traits in linseed. Such variability provides ample opportunities for effective selection and genetic improvement of high-yielding, stable cultivars.

*Estimates of descriptive statistics at Ludhiana and Gurdaspur for agro- morphological traits:*The mean values

Table 2. Analysis of variance for pooled Agro-morphological traits for both locations

Pooled Data

Source of variation	df	G	DTF	DTM	PB	SB	CPP	SPC	PH	TSW	SYPP	SYP
Genotype	59	91.75***	564.2***	95.42***	2.50***	178.50***	226.91***	6.41**	386.51**	1.24 4**	4.75**	710773**
Replication	2	0.57ns	142.67^{ns}	5.95^{ns}	0.27^{ns}	8.04^{ns}	8.8^{ns}	0.54^{ns}	3.57^{s}	0.38^{ns}	0.10^{ns}	216.0^{ns}

G-Germination ,DTF- Days to 50% flowering, DTM- days to 75% maturity, PB- number of primary branches, SB- number of secondary branches, CPP- number of capsules per plant, SPC- number of seeds per capsules, PH- plant height till highest capsule, TSW- 1000-seed weight, SYPP- seed yield per plant, SYP- seed yield per plot

for 10 key morphological traits of linseed genotypes were recorded at two locations—Ludhiana and Gurdaspur—and are summarized in **Table 3**. At Ludhiana, the mean values were: days to 50% flowering (DTF) 81.6 days, days to maturity 155.5 days, primary branches 5.5, secondary branches 51.0, capsules per plant 75.2, seeds per capsule 7.9, plant height 88.4 cm, 1000-seed weight 7.1 g, seed yield per plant 6.5 g, and seed yield per hectare 2598 kg. At Gurdaspur, the corresponding values were slightly lower or comparable: DTF 80.0 days, DTM 159.1 days, PB 4.0, SB 41.1, CPP 38.5, SPC 7.8, PH 74.7 cm, TSW 7.5 g, SYPP 4.8 g, and SYP 1460 kg/ha.

Substantial variability among the genotypes was observed at both locations. In Ludhiana, DTF ranged from 53.6 days (LSL-93) to 112.0 days (Divya), and DTM from 147.3 days (Sabour Tisi-1) to 166.3 days (LC2063 × BAU-06-03). The genotype RLC-143 recorded the highest PB (9.7) and SB (84.3), while Shekhar and LCK-2134 had the lowest (3.6 and 24.1, respectively). CPP ranged from 48.0 (Shekhar) to 125.6 (KL-263), SPC from 3.6 (JLS-95) to 10.3 (Ruchi), and PH from 66.3 cm (Him Alsi-2) to 114.5 cm (LC2023 × BAU-06-03). TSW ranged between 5.1 g (RLC-143) and 9.1 g (BRLS-110-7), SYPP from 1.3 g (Him Alsi-2) to 8.6 g (RLC-183), and SYP from 981.8 kg/ha (RLC-143) to 3325.0 kg/ha (BAU-2019-13).

At Gurdaspur, DTF ranged from 45 days (Him Alsi-2) to 116 days (Priyam), and DTM from 108.0 days (SLS-136) to 170.0 days (LC2023). RLC-143 had the highest PB (6.0) and BRL-103-1 recorded the highest SB (38.3). CPP ranged from 19.5 (LSL-93) to 57.5 (19620 × 19617), and SPC from 3.2 (JLS-95) to 10.0 (Ruchi). PH ranged from 42.5 cm (Him Alsi-2) to 99.4 cm (LC2063 × BAU-06-03), while TSW ranged from 5.8 g (Him Alsi-2) to 9.1 g (T-397). SYPP varied from 1.3 g (Him Alsi-2) to 8.6 g (RLC-183), and SYP from 628.2 kg/ha (RL-18101) to 5652.0 kg/ha (LCK-2134).

The overall mean performance of linseed genotypes for key morphological and yield traits was consistent with earlier reports. Days to 50% flowering (≈81 days) and days to maturity (≈157 days) were within the ranges (70–85 and 145–165 days, respectively) observed by Meena *et al*. (2019)**,** Kaur *et al.* (2017)**,** and Verma *et al.* (2023) under similar agro-ecological conditions. The mean plant height (≈82 cm) and 1000-seed weight (≈7.3 g) correspond closely with values reported by Kumar *et al.* (2020) and Meena *et al.* (2019)**.** Similarly, the average number of capsules per plant (≈57), seeds per capsule (≈8), and seed yield per plant (≈5.6 g) were comparable to the findings of Verma *et al.* (2018) and Kaur *et al.* (2017)**.** The mean seed yield per hectare (≈2000 kg/ha) was also within the range (1400–2800 kg/ha) reported across multi-location evaluations in India (Kaur *et al.,* 2017; Verma *et al.,* 2023), confirming that the present values reflect typical performance of linseed genotypes under North Indian conditions.

Phenotypic and Genotypic coefficients of variation (PCV and GCV): The estimates of PCV and GCV for agro-morphological traits are summarized in **Table 3** and revealed varying degrees of variability across traits, indicating their potential utility in selection and breeding. At Ludhiana, high PCV and GCV (>20%) were observed for primary branches (PCV: 28.2%, GCV: 26.3%), secondary branches (PCV: 31.0%, GCV: 30.2%), capsules per plant (PCV: 20.8%, GCV: 20.4%), and seed yield per plant (PCV: 27.6%, GCV: 25.5%). These indicate strong genetic influence and potential for improvement through selection. In Gurdaspur, high PCV and GCV were observed for econdary branches (PCV 32.9%, GCV 31.2%), seed yield per plant (PCV 32%, GCV29.8%) and seed yield per plot (PCV 28.6%, 23.6%). These indicate strong genetic influence and potential for improvement through selection.

Moderate PCV and GCV, ranging between 10–20%, were observed under Ludhiana conditions for several traits: days to 50% flowering (PCV: 17.0%, GCV: 16.9%), plant height to highest capsule (PCV: 14.1%, GCV: 13.8%), 1000-seed weight (PCV: 13.8%, GCV: 12.9%), and seed yield per plot (PCV: 20.4%, GCV: 19.7%). Similar trends under Gurdaspur were observed, for days to 50% flowering (PCV: 17.0%, GCV: 16.9%), primary branches per plant (PCV: 19.6%, GCV: 14.2%), number of capsules per plant (PCV: 21.6%, GCV: 19.5%), seeds per capsule (PCV: 18.8%, GCV: 15.9%), and plant height to highest capsule (PCV: 16.9%, GCV: 14.4%). The moderate estimates

Table 3. Genetic variability parameters of morphological traits for both locations

Measure of variability	Mean		Range		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Broad sense heritability (%)		Genetic advance as mean percent (%)	
Location	**Ludhiana**	**Gurdaspur**	**Ludhiana**	**Gurdaspur**	**Ludhiana**	**Gurdaspur**	**Ludhiana**	**Gurdaspur**	**Ludhiana**	**Gurdaspur**	**Ludhiana**	**Gurdaspur**
Days to flowering	81.6	80.0	112.0-53.6	116.0-45.0	17.0	17.0	16.9	16.9	98.0	87.0	29.8	33.2
Days to maturity	155.5	159.1	166.3-147.3	170.0-108.0	4.2	7.2	3.2	3.0	56.0	17.0	7.7	2.6
Primary branches	5.5	4.0	9.3-3.6	6.0-1.2	28.2	19.6	26.3	14.2	86.0	13.0	2.7	21.2
Secondary branches	51.0	41.1	84.3-24.1	38.3-13.9	31.0	32.9	30.2	31.2	95.0	94.0	25.0	59.8
Number of capsules per plant	75.2	38.5	125.6-48.0	57.5-19.5	20.8	21.6	20.4	19.5	95.0	81.0	31.0	36.4
Number of seeds per capsules	7.9	7.8	10.0-3.6	10.0-3.2	19.8	18.8	17.9	15.9	81.0	71.0	2.6	27.8
Plant height till highest capsule (cm)	88.4	74.7	114.5-66.3	99.4-42.5	14.1	16.9	13.8	14.4	95.0	72.0	24	25.2
1000-seed weight (g),	7.1	7.5	9.1-5.1	9.1-5.8	13.8	8.9	12.9	8.6	87.0	92.0	1.7	17.1
Seed yield per plant (g)	6.5	4.8	8.6-1.3	8.6-1.3	27.6	32.1	25.5	29.8	85.0	84.0	3.2	55.9
Seed yield per plot (kg/ha)	2598.0	1460.0	3325.0-981.8	5652.0-628.2	20.4	28.6	19.7	23.6	93.0	68.0	20.9	32.7

of PCV and GCV suggest that both genetic factors and environmental conditions contribute to the expression of these traits; however, the narrow gap between PCV and GCV indicates that selection could be effective due to a relatively high genetic influence indicating the potential for effective selection (Kumar *et al.,* 2022; Kaur *et al.,* 2019). Low PCV and GCV (both less than 10%) was recorded for days to 75% maturity indicating limited genetic variability for this trait at Ludhiana. Similarly, at Gurdaspur, days to 75% maturity (PCV: 7.2%, GCV: 3.0%) and 1000-seed weight (PCV: 8.9%, GCV: 8.6%) also exhibited low variation. The narrow differences between PCV and GCV for 1000-seed weight suggest a relatively stable genetic expression with minimal environmental influence. However, for days to 75% maturity, the wider gap between PCV and GCV points toward a greater environmental effect.

Overall, traits with low PCV and GCV indicate limited scope for improvement through direct selection due to their low genetic variability and potentially high environmental dependency (Meena *et al.,* 2021; Sharma *et al.,* 2020). In such cases, genetic enhancement may require the incorporation of diverse germplasm or advanced breeding techniques like marker-assisted selection to identify and introgress favorable alleles. These findings agree with earlier studies by Tyagi *et al.* (2014), who reported high PCV and GCV for yield and yield-contributing traits in linseed, and Dabalo *et al.* (2020), who observed PCV values ranging from 3.78% to 39.29%, with the highest for number of tillers per plant and substantial values for seed yield and oil content. Pali and Mehta, 2017 reported the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for most of the traits, suggesting a minor influence of environment on their expression. The high heritability coupled with high genetic advance as percent of mean was observed for plant height, number of capsules per plant, and seed yield per plant, indicating the predominance of additive gene action and the possibility of improving these traits through selection.

Heritability: The broad-sense heritability (H^2) estimates represent the proportion of total phenotypic variance attributed to genetic variance. High heritability (>60%) suggests that a trait is largely controlled by genetic factors and can be reliably improved through selection. High heritability (>60%) at Ludhiana was observed for several traits, including DTF (98.0), PB (86.0), SB (95.0),CPP (95.0), PH(95.0), SPC (81), TSW (87.0), SYPP (85.0), and SYP (93.0) (**Table 3**). Moderate heritability (30-60%) was recorded for (DTM) (56.0). In Gurdaspur, high heritability values were observed for (DTF)87.0, (SB) 94.0, CPP (81.0), SPC 71.0, (PH) 72.0, TSW (92.0), SYP (84.0) and SYPP 84 while low heritability was noted for (DTM) 17.0 and (PB)13.0. The results from Ludhiana and Gurdaspur reveal that traits like DTF, SB, CPP, TSW, SYPP, and SYP consistently exhibit high heritability, suggesting strong genetic control and minimal environmental influence. These traits are ideal candidates for direct selection in breeding programs aimed at improving yield and adaptability. In contrast, traits like DTM and PB showed moderate to low heritability, especially at Gurdaspur. This indicates greater environmental influence, reducing the efficiency of selection. For such traits, multi-environment testing and use of G×E interaction models are recommended.

High and stable heritability across environments strengthens the reliability of selection for traits such as early flowering, secondary branching, seed size, and yield in linseed. Traits with low heritability require integrated strategies, including genotype-by-environment interaction analysis, marker-assisted selection, or improved agronomic practices to enhance breeding outcomes. These findings are consistent with earlier studies. Tewari, (1999) and Kumar *et al.* (2012) also reported high heritability for traits such as plant height, seed yield per plot, and seed yield per plant. Ahmad *et al.* (2014) reported a wide range of heritability values (0.51 to 0.99), with maximum heritability for days to flower initiation (99%), days to maturity (97%), and 1000-seed weight (96%). In contrast, traits such as oil percentage with lower heritability (0.51) were more influenced by environmental variation, thereby reducing selection efficiency

Genetic advance as mean percentage: In Ludhiana high GAM (>20%) was recorded for days to 50% flowering (29.8), secondary branches (25.0), capsules per plant (31.0), plant height to the highest capsule (24.0), and seed yield per plot (20.9) (**Table 3**). In contrast, low GAM (0-10%) was observed for primary branches (2.7), days to 75% maturity (7.7), seeds per capsule (2.6), 1000 seed weight (1.7), and seed yield per plant (3.2). At Gurdaspur, high GAM values (>20%) were noted for days to 50% flowering (33.2), primary branches (21.2), secondary branches (59.8), capsules per plant (36.4), seeds per capsule (27.8), plant height (25.2), seed yield per plant (55.9), and seed yield per plot (32.7). Moderate GAM (10-20%) was recorded for 1000 seed weight (17.1), while low GAM (0-10%) was noted for days to 75% maturity (2.6). The traits such as secondary branches, capsules per plant, seed yield per plot, and days to 50% flowering consistently showed high GAM and heritability across both locations, indicating strong additive gene action and high selection response. Traits like days to 75% maturity and 1000-seed weight had low GAM, reflecting greater environmental influence or non-additive gene action, making selection less efficient. The contrasting GAM values for primary branches and seeds per capsule between locations suggest a significant role of environment, highlighting the need for multi-environment trials before final trait selection. Thus, the traits with high heritability and high GAM, such as secondary branches (SB), capsules per plant (CPP), and seed yield SYP) helps in rapid genetic improvement in Linseed. Similarly, Terfa and Gurmu, (2020**)** studied high GAM for lodging percentage, number of capsules per branch, seed yield per hectare, and harvest index, indicating the predominance of additive gene action for these characters. Furthermore, Yadav *et al.* (2024) studied the GAM varied from 5.40% to 58.84%, with the maximum recorded for capsules per plant, followed by capsules per weight and seeds per weight, indicating the potential for selection in linseed breeding programs.

Heritability coupled with genetic advance mean percentage: The present study revealed considerable genetic variability among the evaluated linseed genotypes across two locations. Traits such as (DTF), (SB), (CPP), (PH), and (SYP) exhibited high heritability coupled with high genetic advance as a percentage of the mean (GAM) across both environments, indicated a prevalence of additive gene action and suggesting that these traits can be improved through simple phenotypic selection.

In contrast, traits like DTM, TSW, SPC, and PB exhibited low to moderate GAM which indicates either environmental influence or non-additive gene effects which further requires refined selection strategies, possibly involving marker-assisted selection or multi-location evaluations. For effective genetic improvement in linseed, traits combining high heritability and high GAM, such as days to 50% flowering, secondary branches, capsules per plant, plant height and seed yield per plot should be prioritized as they promise high selection gain due to additive gene action. On the other hand, traits with low GAM (e.g., days to 75% maturity, 1000-seed weight) may require long-term selection, multi-location evaluation, or molecular approaches to enhance their stability and gain.

Similarly, Pali and Mehata, (2017) reported the high heritability coupled with high genetic advance as percent of mean was observed for plant height, number of capsules per plant, and seed yield per plant, indicating the predominance of additive gene action and the possibility of improving these traits through selection. Furthermore, Terfa and Gurmu, (2020) found moderate to high heritability (30–77%) with coupled with high genetic advance mean traits, indicating the predominance of additive gene action for these traits. These findings are consistent with earlier reports by Kumar *et al.* (2012), who also observed high heritability for seed yield and plant height, indicating that yield-contributing traits are often governed by stable additive effects. Kumar *et al.* (2012) and Pali and Mehta (2013) reported similar results, indicating that traits like PB, PH, DTM, CPP, and SYP can be improved through direct phenotypic selection. Traits with high heritability significantly contribute to genetic variability in germplasm, while those with low and moderate heritability are influenced by non-additive gene effects, contributing less to genetic variability. Similarly Pali and Mehta (2017) reported high heritability coupled with high genetic advance observed for plant height, number of capsules per plant, and seed yield per plant, indicated additive gene action

Analysis of variance for genotype, environment, and G×E effects: The analysis of variance (ANOVA) revealed highly significant differences among genotypes for all studied traits, including DTF, DTM, PB, SB, CPP, SPC, PH, TSW, SYPP, and SYP due to the presence of sufficient genetic variability, a prerequisite for effective selection and crop improvement. Similar findings have been reported in linseed by Kaur *et al.* (2017), who highlighted wide genetic variability in yield and yield-attributing traits. The environmental effect was also found to be highly significant for all traits, suggesting that environmental conditions play a crucial role in the expression of these traits. Traits such as CPP, SYP, and SB exhibited particularly large environmental mean sum of squares, reflecting their strong dependence on growing conditions in **Table 4**. Earlier studies in oilseed crops, emphasized

Table 4. Genotype × Environment ANOVA for morphological traits in two locations

Character	Mean Sum of squares			
	Genotype	**Replication**	**Environment**	**G × E**
df	**59**	**2**	**1**	**59**
Days to 50% flowering	1094.9*	66.5^{ns}	2992.9**	151.6**
Days to 75% maturity	190.7**	0.5^{ns}	1166.4**	94.2**
Number of primary branches	5.0**	0.5^{ns}	179.0**	2.5**
Number of secondary branches	357.2**	10.8^{ns}	24306.8**	216.9**
Number of capsules per plant	457.0**	6.0^{ns}	120395.0**	25611.0**
Number of seeds per capsules	10.8**	0.1^{ns}	2.7**	1.0**
Plant height till highest capsule	774.0**	11.2^{ns}	16750.8**	72.9**
1000 seed weight	2.7**	0.3^{ns}	17.0**	2.2**
Seed yield per plant	9.6**	0.1^{ns}	79.2**	6.4**
Seed yield per plot	1423080.0**	398.0^{ns}	116604049.0**	73852340.0**

** Significant at 1% level of significance.

the strong environment influence on yield and related traits (Kumar *et al.,* 2019; Singh *et al.,* 2021). The genotype × environment (G × E) interaction was also significant for almost all traits, especially for CPP and SYP, suggesting differential responses of genotypes under varying environments. Such significant interactions highlight the importance of multi-environment trials to identify stable and high-performing genotypes. According to Yan and Kang (2003**)**, significant G × E interaction indicates that genotype performance is not consistent across environments, and hence biplot analyses such as GGE biplot or AMMI are effective tools to identify stable genotypes. Replication effects were mostly non-significant, indicating uniform experimental conditions and reliability of data record

GGE biplot and PCA analysis: The GGE biplot and principal component analysis (PCA) were performed to evaluate genotype performance, stability, and genotype × environment interaction (GEI) for seed yield per plot (SYP, kg/ha) across Ludhiana and Gurdaspur.

The GGE biplot simultaneously represents the genotype main effect (G) and G×E interaction, allowing identification of environment-specific winners, stable genotypes, and mega-environments. In this study, PC1 (86.82%) and PC2 (13.18%) cumulatively explained nearly 100% of the G + GE variation, providing a reliable visualization of genotype performance. Gurdaspur was positioned far along the negative side of PC1, indicating strong discriminating ability but low representativeness, whereas Ludhiana, located near the origin, was more representative of the average performance but less discriminating. The polygon view identified environment-specific winners: LCK-2037 performed best under Gurdaspur conditions, while SLS-134, LCK-2024, DLV-17, and SLS-93 were superior in Ludhiana. Genotypes near the origin, such as Priyam, BAU-2021-08, and RLC-195, exhibited moderate but consistent performance across both locations, indicating wide adaptability and stability. These results suggest at least two distinct mega-environments and emphasize the need for both environment-specific recommendations and broad-adaptation strategies.

The PCA further supported these findings by summarizing overall variation patterns. PC1 (86.82%) captured the mean yield differences among genotypes across environments, while PC2 (13.18%) represented stability and environment-specific adaptation. Most genotypes clustered around the origin, reflecting average performance and low G×E interaction, whereas genotypes such as SABOUR TISI-1, LCK-2024, NDL-367, DLV-17, LCK-1217, and LSL-93 were dispersed along PC1 and PC2, indicating variable performance. Genotypes near the origin (e.g., RLC-2037, RL-18107, LC-2023×BAU-06-03) demonstrated wider adaptability, while those with high PC1 and low PC2 values combined superior performance with stability, making them promising candidates for broad adaptation. Genotypes with high PC2 scores exhibited environment-specific responses, suggesting their suitability for targeted recommendations.

Overall, the GGE biplot emphasizes which genotypes “win” in specific environments, while PCA provides a general overview of performance patterns and stability. The results from both analyses were consistent, confirming the stability and adaptability of genotypes such as Priyam, RLC-2037, and BAU-2021-08, as well as the environment-specific superiority of LCK-2037 in Gurdaspur and SLS-134, LCK-2024, DLV-17, and SLS-93 in Ludhiana. Similar applications of GGE and PCA in multi-environment trials have been reported in linseed (Kaur *et al.,* 2017) and other crops, including maize (Samonte *et al.,* 2005) and sorghum (*Rakshit et al.,* 2012), demonstrating their robustness for genotype evaluation and selection.

The polygon view of the GGE biplot revealed distinct winners for each environment, thereby highlighting environment-specific adaptation. LCK-2037 was identified as the best-performing genotype under Gurdaspur conditions, whereas SLS-134, LCK-2024, DLV-17, and SLS-93 were superior in Ludhiana and similar environments. Genotypes clustered near the origin, such as Priyam, BAU-2021-08, and RLC-195, demonstrated moderate but consistent performance across both environments and can be regarded as stable performers with wide adaptation. These results emphasize the presence of at least two mega-environments in the study and underline the need for both environment-specific recommendations (LCK-2037 for Gurdaspur; SLS-134, LCK-2024, DLV-17, and SLS-93 for Ludhiana) and broad-adaptation strategies through stable genotypes. Similar findings on GGE biplot application in oilseed crops were reported by Yan and Tinker (2006) and Kaur *et al.* (2017), confirming its robustness for selecting both stable and specifically adapted cultivars.

The evaluation of 391 linseed accessions across multi-environment trials revealed significant genetic variability. Cluster analysis grouped 92 fiber accessions into three clusters and 299 linseed accessions into eight clusters, consistent with the findings of You *et al.* (2017). Similar studies have reported comparable clustering patterns, indicating the robustness of these groupings across different datasets (Singh *et al.,* 2018; *Yadav et al.,* 2024). These results underscore the substantial genetic diversity present in linseed germplasm, which is crucial for breeding programs aiming to enhance desirable traits. Average performance across environments. Also, Hoque (2020) assessed 350 worldwide accessions using SNP markers and generated neighbor-joining trees revealing seven distinct sub-populations based on global distribution

GGE biplot: Which- won- where: The “Which-Won-Where” view of the GGE biplot (Scaling = 0, Centering = 2, SVP = 2) explained 86.82% and 13.18% of the total variation through the first and second principal components, respectively in (**Fig. 2**) for seed yield per plot (SYP, kg/ha). This high cumulative variance indicates that the model effectively captured both genotype and genotype × environment (G×E) interaction effects.

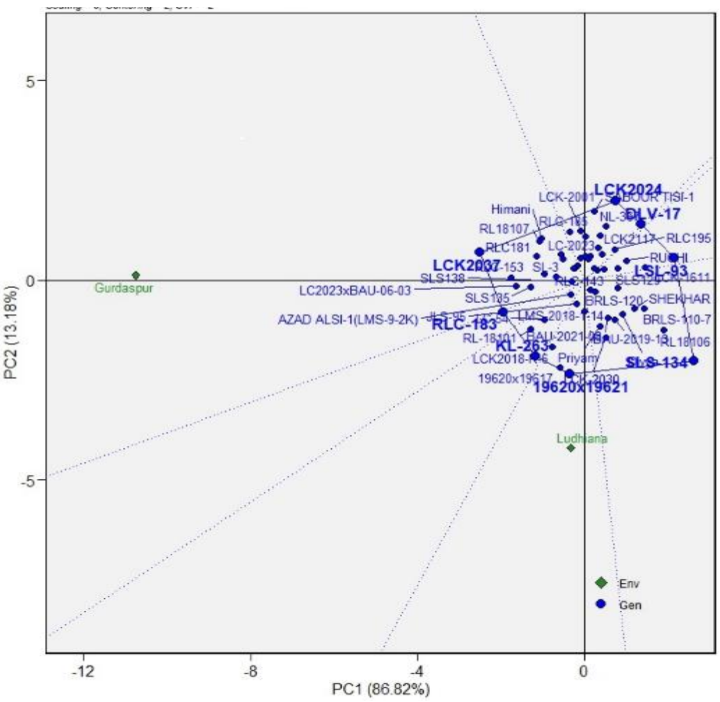

Fig.1. GGE biplot seed yield per plot

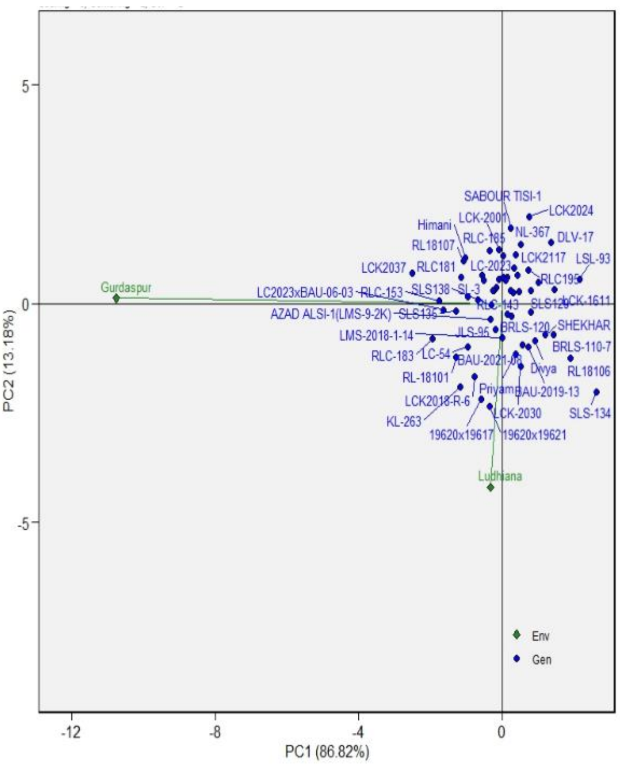

Fig.2. Which-Won-Where plot for seed yield per plot

The polygon view clearly divided the genotypes into sectors, with test environments falling into distinct sectors, thereby identifying environment-specific winners. Gurdaspur was grouped with genotypes such as LCK-2037, RLC-153, LC2023×BAU-06-03, and SLS-138, indicating superior performance under its specific growing conditions. Ludhiana was positioned near genotypes such as LCK-2024, SLS-134, DLV-17, and RLC-195, highlighting their adaptation to this location. Genotypes located close to the origin, including Priyam, RLC-196, and BAU-2021-08, exhibited moderate but consistent performance across both environments, reflecting broad adaptability.

The analysis also revealed that Gurdaspur had stronger discriminating ability, as indicated by its longer vector, making it suitable for identifying specifically adapted genotypes, while Ludhiana, being closer to the average environment axis, was more representative of the overall test environments, favoring selection of widely adaptable genotypes. Overall, the GGE biplot identified LCK-2037 as the winner for Gurdaspur, SLS-134. a LCK-2024 as winners for Ludhiana. Also, Priyam and RLC-196 as stable genotypes across both environments.

These results are consistent with previous studies, where PC1 typically represents genotypic main effects and PC2 reflects stability (Yan *et al.,* 2000; Gauch *et al.,* 2008). Similar findings using GGE biplots for identifying mega-environments and superior genotype-environment combinations have been reported in linseed (Kaur *et al.,* 2017; Chobe *et al*., 2018) and other crops such as maize (Samonte *et al.,* 2005) and sorghum (Rakshit *et al.,* 2012), demonstrating the robustness of this method in multi-environment trials.

The dendrogram generated using R software with the Ward method (**Fig. 3 and 4**) categorized the 60 genotypes into six clusters based on performance and origin. In Ludhiana, Cluster V comprised of the fewest genotypes, while Cluster VI encompassed the most, with 24 genotypes. Similarly, in Gurdaspur, the genotypes were grouped into six clusters, with Cluster V containing a single genotype (SLS-136) and Cluster VI housing 21 genotypes, (**Table 5, Fig. 3 and 4**). This cluster analysis reveals significant genetic divergence, beneficial for future hybridization breeding programs. Similar findings were reported by You *et al.* (2017) and others who employed hierarchical clustering methods, demonstrating consistent results across different genotypes. This clustering underscores significant genetic divergence among the genotypes, which is advantageous for future hybridization and breeding programs. At Ludhiana, the cluster 1 contains genotypes like Divya, RLC-184, RLC-143, SLS-137, JLS-95, BAU-2021-08. These genotypes are closely related and form a tight sub-group. Cluster 2 includes NL-367, Sabour Tisi-1, KL-263, RLC-181, and RLC-183 genotypes which are moderately similar. Cluster III is a smaller and distinct group with

Table 5. Clustering based on agro-morphological data

Clusters	Colour	Genotypes
Ludhiana		
Custer 1	Orange	Divya, RLC-143, RLC-184, SLS-137, JLS-95, BAU-2021-08
Cluster 2	Green	NL-367, Sabour Tisi-1, KL-263, RLC-181, RLC-183
Cluster 3	Blue	DLV-17, 19620 **×** 19617, SLS-138, RL-18108
Cluster 4	Yellow	Himani, Priyam, LC2063 × BAU-06-03, LCK-2117, LC 2023, Surbhi × LC 2023, LC 2063, LC 54 × BAU-06-03, LC 54, BRL-103-1, BRLS-120, Ruchi, RLC-187, SLS-129, SL-3, RLC-196, JRF-2, LCK-2134, LC 2023 × BAU-06-03
Cluster 5	Cyan	LSL-93, Him alsi-2
Cluster 6	Pink	LCK-2037, RLC-195, RLC-185, LCK 2024, LCK-2001, LCK-2030, LMS-2017-1-12, LCK-2018-R-6, SLS-136, BRLS-110-7, RL-18101, SLS-135, LMS-2018-1-14, 19620 × 19621, LMS-2018-R-4, BAU-2019-13, RLC-153, T-397, RL-18107, SLS-134, Shekhar, Azad Alsi-1, LCK-1611
Gurdaspur		
Custer 1	Orange	RLC-143, RLC-184, RLC-181, Himani, 19620×19617
Cluster 2	Green	RLC-196, LCK-2134
Cluster 3	Blue	LCK-2037, Divya, RLC-195, Priyam, BAU-2021-08, LC2063 × BAU-06-03, LCK-2117, LC 2023, Surbhi × LC 2023, LC 2063, LC 54, BRL-103-1, RLC-187, JRF-2, LCK-2134, KL-263, Sabour Tisi-1, LC 54 × BAU-06-03, LCK-2001
Cluster 4	Yellow	Him alsi-2, LSL-93, SLS-137, 19620 × 19621, JLS-95, SLS-135, RL-18106, BRLS-110-7, LMS-2018-R-4, LMS-2018-1-14, DLV-17, LCK-2024.
Cluster 5	Cyan	SLS-136
Cluster 6	Pink	SLS-134, Shekhar, LCK-1611, T-397, BAU-2019-1, Ruchi, BRLS-120, SLS-129, RL-18101, LCK-2018-R-6, LCK-2030, LMS-2017-1-12, RLC-185, LC 2023 × BAU-06-03, LMS-2018-1-10, NL-367, SLS-138, Azad Alsi-1, RLC-183, RLS-153, RL-18101

moderately divergent genotypes DLV-17, 19620 × 19617, SLS-138, RL-18106. Cluster 4, a diverse cluster, includes more than 20 genotypes including Himani, Priyam, LCK-2117, LC 2023, Ruchi, JRF-2, etc which have high variability and can be used for intra cluster selection and recombination. Cluster 5 is a small but highly divergent group that includes promising hybridization candidates such as LSL-93 and Him Alsi-2. In contrast,

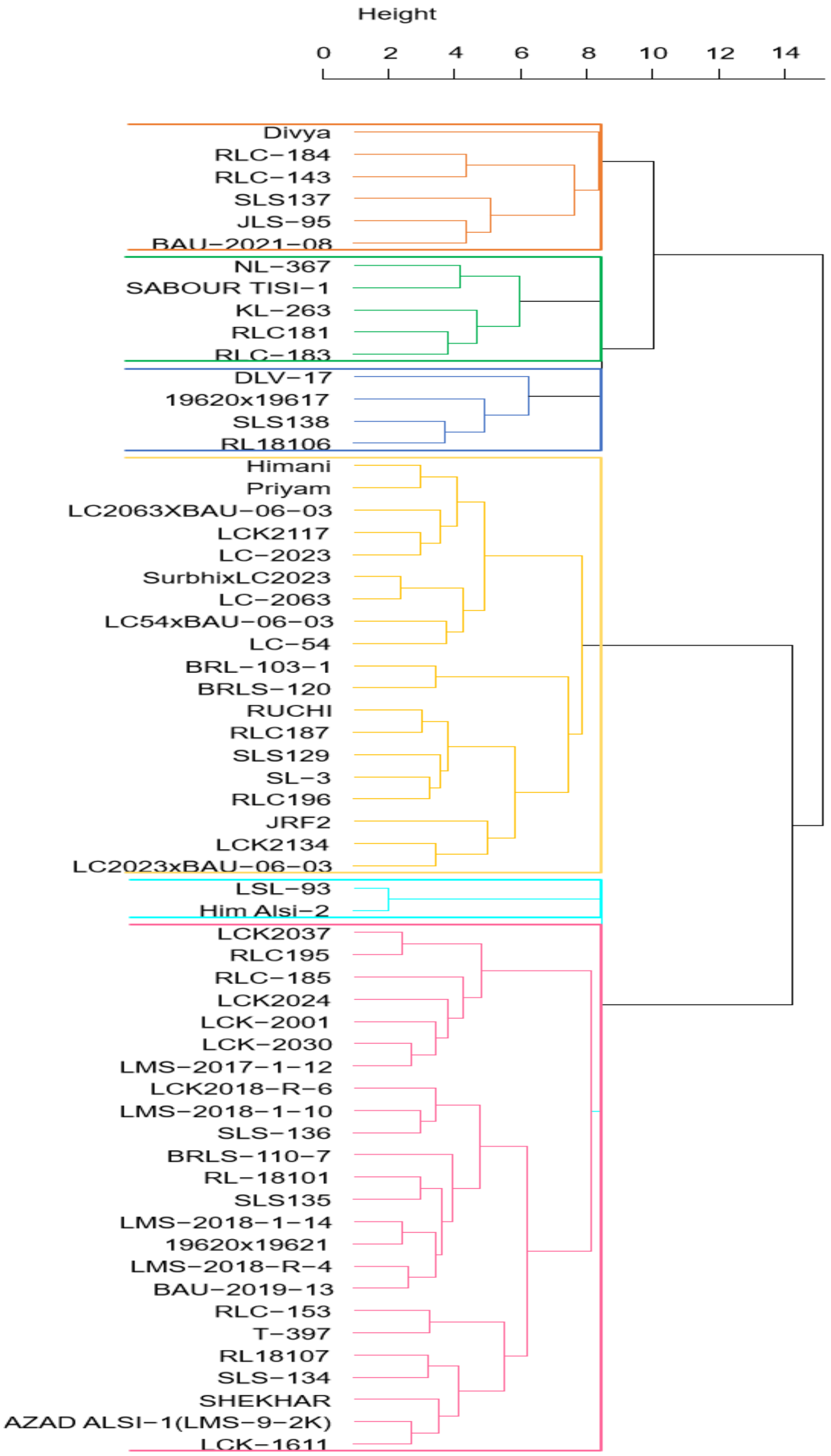

Fig. 3. Dendrogram of genotypes based on performance at Ludhiana

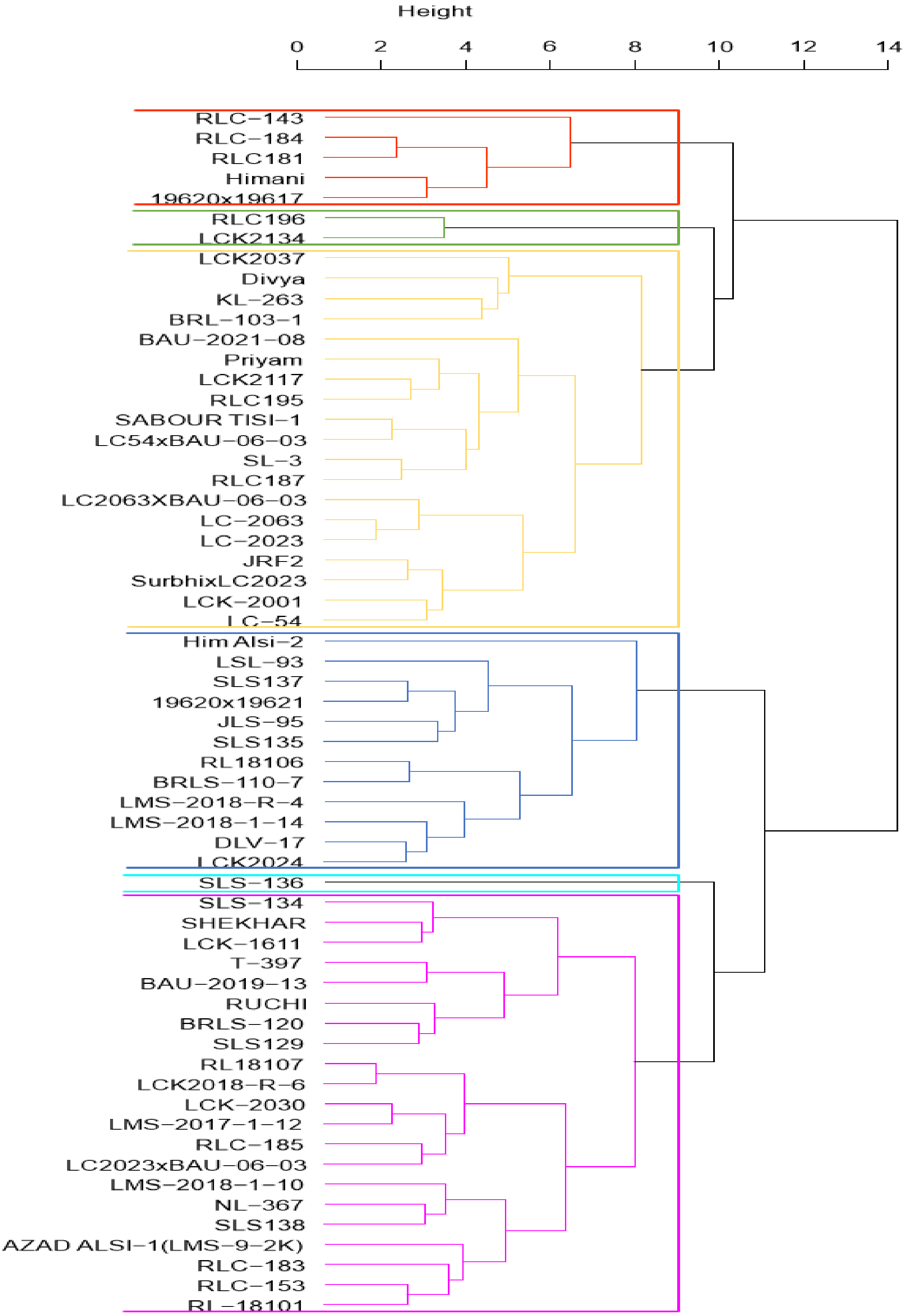

Fig. 4. Dendrogram of genotypes based on performance at Gurdaspur

the genetically broad Cluster 6, the largest cluster with 24 genotypes (including LCK-2037, RLC-195, various LMS lines, T-397, and Azad Alsi-1), shows strong potential for stable performance across diverse environments.

In Gurdaspur, the genetic diversity analysis using Ward's method grouped the linseed genotypes into six distinct clusters, consequently revealing considerable variation among the evaluated accessions. Cluster 1, specifically, represented a genetically compact group comprising RLC-143, RLC-184, RLC-181, Himani, and 19620×19617, reflecting close genetic relatedness. In contrast, Cluster 2 was the smallest, including only RLC-196 and LCK-2134, suggesting limited variability within that group. Likewise, Cluster 3, consisting of genotypes such as Divya, KL-263, Priyam, LC-2063, RLC-195, and JRF-2, exhibited moderate diversity, thereby indicating a balance between genetic similarity and distinctiveness. Moreover, Cluster 4 was highly diverse, encompassing Him Alsi-2, LSL-93, SLS-137, BRLS-110-7, RL-18106, and LMS-2018 lines, along with DLV-17; hence, it can serve as an important source of genetic variability for future breeding programs. Similarly, Cluster 5 was identified as the most divergent, containing a single genotype, SLS-136, which could be a valuable donor for introgression of unique alleles into breeding populations. Furthermore, Cluster 6, the largest cluster, comprised 21 genotypes, including SLS-134, Shekhar, T-397, Azad Alsi-1, LCK-2030, RLC-153, and RL-18101, and represented a genetically broad group with strong potential for stable and adaptable performance across diverse environments. Overall, the clustering pattern clearly revealed substantial genetic diversity among the evaluated genotypes, thereby highlighting the potential for exploiting divergent clusters—particularly Clusters 4, 5, and 6—for hybridization and the development of improved linseed varieties with enhanced adaptability and yield potential. Previous studies support these findings. Xiao *et al.* (2017) demonstrated that their comprehensively evaluated flax core collection is phenotypically rich and genetically structured, making it a valuable resource for targeted breeding of both linseed and fibre types, with promising prospects for dual-purpose cultivars, which aligns with our research. Similarly, You *et al.* (2017) grouped 92 fiber accessions into 3 clusters and 299 linseed accessions into 8 clusters, consistent with our results. In addition, Hoque (2020) assessed 350 worldwide accessions using SNP markers and generated neighbour-joining trees revealing seven distinct sub-populations based on global distribution. Overall, both dendrograms confirm substantial genetic diversity among the linseed genotypes. Genotypes in smaller, isolated clusters are ideal candidates for crossing to introduce novel alleles, while larger clusters with internal diversity are suitable for selection within populations.

This study revealed significant genetic variability among 60 linseed genotypes across two environments (Ludhiana and Gurdaspur). The traits such as secondary branches, capsules per plant, and seed yield showed high heritability and genetic advance, indicating their suitability for effective selection, whereas days to maturity and 1000-seed weight exhibited low heritability, reflecting strong environmental influence. Genotype × environment analysis confirmed variation in performance between locations. GGE biplot identified BAU-2019-13 as the best performer in Ludhiana and LCK-2134 in Gurdaspur, while stable genotypes such as LCK-2037, LC-54, and JLS-95 clustered near the origin, indicating broad adaptability. The which-won-where view revealed environment-specific winners (vertex genotypes), whereas stability analysis distinguished widely adaptable lines. Dendrogram clustering further supported genetic diversity and location-specific grouping. Overall, multivariate tools like GGE biplot and cluster analysis are valuable for identifying superior and stable genotypes, supporting targeted breeding strategies for yield and adaptability in linseed.

REFERENCES

Ahmad, M., Khan, M.A., Qureshi, A.S. and Khan, M. A. 2014. Genetic variability and heritability studies in linseed (*Linum usitatissimum* L.) for yield and its components. *Pakistan Journal of Agricultural Research,* **27**(1): 1–7.

Allard, R.W. 1960. *Principles of Plant Breeding*. John Willeyand Sons, Inc., New York USA. p. 484

Burton, G.W. and Devane, E.H. 1952. Estimating heritabilityin tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J*., **45:** 478-481. [Cross Ref]

Chobe, A. C. and Ararsa, A. D. 2018. AMMI and GGE biplot analysis of linseed (*Linum usitatissimum* L.) genotypes in central and south-eastern highlands of Ethiopia. *Journal of Plant Breeding and Genetics*, **6(3):** 117–127.[Cross Ref]

Dash, J., Naik, B. S. and Mohapatra U B .2017. Linseed: a valuable crop plant. *Int J Adv Res,* **5**(3): 1428-42. [Cross Ref]

Dabalo, D.Y., Singh, B.C.S. and Weyessa, B. 2020. Genetic variability and association of characters in linseed (*Linum usitatissimum* L.) plant grown in central Ethiopia region. *Saudi J Biol Sci,* **27**: 2192—2206. [Cross Ref]

FAO STAT .2019: FAO statistical data. http://faostat.fao.org

Falconer, D. S., 1964. *Introduction to Quantitative Genetics.* Oliver and Boyd, Edinburgh.

Gauch, H.G., Piepho, H.P. and Annicchiarico, P. 2008. Statistical analysis of yield trials by AMMI and

GGE: Further considerations. *Crop Science*, **48**(3): 866–889. [Cross Ref]

Hall, C., Tulbek, M.C. and Xu, Y. 2011. Flaxseed. In *Wiley Encyclopedia of Food Science and Technology* (pp. 1–9). [Cross Ref]

Hoque, A., Fiedler, J. D. and Rahman, M. 2020. **Genetic** diversity analysis of a flax **(***Linum usitatissimum* L.) global collection. *BMC Genomics*, **21**, 557: **1–17.** [Cross Ref]

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soya beans *Agron J.,***47** : 314—318. [Cross Ref]

Kaur, S., Sharma, R. and Verma, A. 2017. Yield potential and constraints in linseed production in India. *Journal of Oilseed Research,* **34**(2): 85–92.

Kaur, S., Sharma, R. and Verma, A. 2019. Genetic variability and correlation analysis in linseed (*Linum usitatissimum* L.). *International Journal of Current Microbiology and Applied Sciences*, **8**(3), 2801–2808.

Kurt, H. and R team core. 2023. An Introduction to R Notes on R: A Programming Environment for Data Analysis and Graphics Version 4.3.1

Kumar, S., Kerkhi, S. A., Gangwar, L. K., Chand, P. and Kumar, M. 2012. Improvement in the genetic architecture through study of variability, heritability and genetic advance in linseed crop (*Linum usitatissimum* L.). *Int Confer Agric Sci Eng (ICASE)*: 170-87.

Kumar, A., Singh, K. K. and Singh, M. 2019. Genetic variability and heritability studies in linseed (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry,* **8**(5): 354–358

Kumar, N. and Kumar V. 2021. Assessment of genetic diversity in linseed germplasm using morphological traits. *Elect. J. Plant Breed.*, **12**(1): 66-7[Cross Ref]

Kumar, S., Singh, B., Yadav, M. K. and Arya, R. K. 2022. Genetic variability, heritability and genetic advance for seed yield and its contributing traits in linseed (*Linum usitatissimum* L.). *Journal of Oilseeds Research*, **39**(2): 97–102.

Meena, H.P., Meena, R.S. and Meena, R.K. 2019. Genetic variability and heritability estimates for yield and yield components in linseed (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry*, **8**(4): 1872–1876

Meena, H. S., Verma, O. P., Maurya, K. N. and Singh, P. 2021. Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) under different agro-climatic conditions. *Journal of Pharmacognosy and Phytochemistry*, **10**(1): 1554–1558.

Morris, D.H. 2008. *Flax—A Health and Nutrition Primer.* Flax Council of Canada, Winnipeg.

Oomah, B.D. 2001. Flaxseed as a functional food source. *Journal of the Science of Food and Agriculture*, **81**(9): 889–894. [Cross Ref]

Pali, V. and Meheta N. 2013. Studies on genetic variability, correlation and path analysis for yield and its attributes in linseed (*Linum usitatissimum* L.). *Plant Archives*, **13(1)**:223-227.

Pali, V. and Mehta, N. 2017. Genetic diversity assessment of flax (*Linum usitatissimum* L.) germplasm usingmolecular and morphological markers. *Electron. J. Plant Breed.* **7**(4): 986-99 . [Cross Ref]

Rakshit, S., Ganapathy, K.N., Gomashe, S.S., Rathore, A., Gaur, A., Ganesamurthy, K., .. and Patil, J.V. 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica*, **185**(3): 465–479. [Cross Ref]

Samonte, S.O.P.B., Wilson, L.T., McClung, A.M. and Medley, J.C. 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analyses. *Crop Science*, **45**(6): 2414–2424. [Cross Ref]

Sharma, R., Kumar, S., Kaur, S. and Verma, A. 2020. Assessment of variability parameters and genetic divergence in linseed (*Linum usitatissimum* L.) genotypes. *Journal of Oilseeds Research*, **37**(Special Issue), 133–137. [Cross Ref]

Singh, K.K., Mridula, D., Rehal, J. and Barnwal, P. 2011. Flaxseed: A potential source of food, feed, and fiber. *Critical Reviews in Food Science and Nutrition*, **51**(3): 210–222. [Cross Ref]

Singh, R., Yadav, S. and Kumar, P. 2021. Genetic variability studies in linseed for yield and its attributing traits. *Journal of Pharmacognosy and Phytochemistry,* **10**(1): 1900–1904.

Singh J. *et al. 2018.* Stability analysis of linseed/flax genotypes by deployment of AMMI and GGE models under rain-fed environment. *Oil Crop Research.,* **41:**182-188. [Cross Ref]

Siva Subramanian, V. and Madhava, M.P. 1973. Path analysis for yield eld and yield components of rice. *Madras Agric J.,* **60**: 1217—1221.

Terfa, G. N. and Gurmu, G. N. 2020. Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L) genotypes for seed yield and other agronomic traits. *Oil Crop Sci,* **5**(3): 156-60. [Cross Ref]

Tewari, Nalini .1999. Genetic analysis of yield and quality parameters in linseed. *(Linum usitatissimum* L.). Ph.D. Thesis submitted to S.S.J.M.U., Kanpur.

Tyagi, A. K., Sharma, A. K., Mishra, S. K. Kerkhi, S. A. and Chan, P .2014. Estimates of genetic variability, heritability and genetic advance in Linseed (*Linum usittatissinum* L) gemplasm. *Prog Agric.,* **14**(1): 37-48.

Verma, A., Sharma, R. and Kaur, S. 2018. Evaluation of linseed genotypes for yield and stability under different agro-climatic conditions. *Indian Journal of Agricultural Sciences*, **88**(4): 566–57

Verma, A., Kaur, S. and Singh, B**.** 2023**.** Evaluation of linseed genotypes for yield and related traits under different agro-climatic zones. *Plant Archives*, **23**(1): 551–558.

Yadav, S. K., *et al*. 2024. *Genetic variability and trait association analysis in linseed (Linum usitatissimum L.) germplasm*. *Journal of Oilseed Brassica*, **15**(1): 1-10.\

Yan, W. and Kang, M. S. 2003. *GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists.* CRC Press. [Cross Ref]

Yan, W., Hunt, L.A., Sheng, Q. and Szlavnics, Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, **40**(3): 597–605. [Cross Ref]

Yan, W. and Tinker, N. A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science*, **86**(3): 623–645. [Cross Ref]

You, F.M., Jia, G., Xiao, J., Duguid, S.D., Rashid, K.Y., Booker, H.M. and Cloutier, S. 2017. Genetic variability of 27 traits in a core collection of flax (*Linum usitatissimum* L.). Front Plant Sci. Sep **21**;8:1636. [Cross Ref]

Xiao, S., Zhang, H., Xie, Y., Zhao, X., Liu, L. and Wang, R. 2017. A core collection and its evaluation for genetic diversity in flax (*Linum usitatissimum* L.). *Genetic Resources and Crop Evolution*, **64**, 171–181.