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Trait-Based Genetic Variability of Linseed Genotypes for Seed Yield and Yield Components in West Shewa, Ethiopia

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Abstract

Linseed (*Linum usitatissimum* L.) is a significant oilseed crop in the central highlands of Ethiopia, where breeding efforts primarily focus on enhancing seed yield through the exploitation of genotypic diversity. However, progress has been hindered by the limited availability of superior varieties. This study aimed to assess the genetic diversity and trait associations among 35 linseed genotypes for key agronomic traits. The experiment was conducted during the 2023 main cropping season using an alpha lattice design. Analysis of variance (ANOVA) revealed highly significant differences ($P \leq 0.01$) among genotypes for all 14 agronomic and yield-related traits, indicating substantial genetic diversity. The results showed wide ranges in traits such as days to maturity, number of capsules per plant, seed yield, and oil content. Estimates of genetic parameters showed high phenotypic and genotypic coefficients of variation (PCV and GCV) for traits such as tiller number, harvest index, seed yield, oil yield, and oil content, indicating potential for effective selection. Broad-sense heritability was high (>90%) for most traits, indicating strong genetic control and high expected genetic gain. Principal Component Analysis (PCA) revealed that the first five components explained 77% of the total variation, with oil yield, seed yield, biomass, and plant height being major contributors. Cluster analysis grouped genotypes into five distinct clusters, highlighting significant inter-cluster genetic distances, especially between clusters III and V, which could be valuable for hybridization. Correlation analysis indicated significant positive associations among seed yield, oil content, and harvest index, while lodging was strongly correlated with plant height and maturity. The overall results underscore the presence of exploitable genetic variability among the tested linseed genotypes, providing a solid foundation for future breeding efforts to improve yield and adaptability.

Keywords: Genotypic coefficient of variation, genetic diversity, heritability, Linseed, Phenotypic traits.

1 Introduction

Linseed (*Linum usitatissimum* L.) is an important oilseed and fiber crop

belonging to the family *Linaceae* and genus *Linum* [16]. The crop species was thought to have originated from the Mediterranean-native Linum angustifolium Huds [47,11]. The world's leading producers of linseed are the Russian Federation, Kazakhstan, Canada, China, India, and Ethiopia [19].

In Africa, Ethiopia, Egypt, Tunisia, Kenya, Eritrea, and Morocco produce linseed in significant quantities [19]. The main production regions in Ethiopia were Tigray, Amhara, Oromia, and Beneshangul–Gumuz [7]. Smallholder farmers in Ethiopia cultivated linseed for many years. For domestic consumption, the linseed crop was primarily grown for its edible oil. However, the byproduct of linseed after oil extraction was used for animal feed [50]. Typically, the seed was roasted, crushed, and combined with spices and water before being eaten with the native bread. It was also eaten with baked potatoes or cereal, as well as in soups and soft drinks. Until 2019, more than 17 improved linseed varieties were released at the national level in Ethiopia [5,41]. Despite the vast area and varied utility of the linseed crop, in Ethiopia, it was commonly produced under marginal lands by smallholder farmers without the application of any input [49].

Currently, Ethiopia has very low total production (88,209.65 tons) compared to other important linseed-producing countries like Russia (672,691tons), Canada (579,000 tons), and Kazakhstan (561,771 tons). The yield difference was mainly due to the low yield potential of varieties, lack of suitable agro-technological practices, or a combination of both [20].

Studying genetic variability for economically important traits and the extent to which the desirable characters were heritable was an essential prerequisite for successful breeding [18]. According to [6], in any crop improvement program, variability in terms of genetic, highly heritable traits and high genetic advance for a trait of interest makes crop improvement effective and economical. Thus, for a crop to be further improved, it was necessary to understand the pattern and amount of variability, especially genetic variability, that exists in a population of that crop. Thus, details regarding the degree and kind of

relationships between characters aid in creating a successful multiple-trait selection scheme.

In Ethiopia, there was a shortage of edible oil and poor yield productivity related problems; farmers were not interested in growing linseed and shifted to produce cereal crops. Besides, different Authors reported that the low productivity of linseed in Ethiopia was due to late-maturing varieties, poor response to chemical fertilizers, susceptibility to pests, cultivation of the crop under poor agronomic management on marginal lands, and susceptibility to frost [16]. Therefore, the breeding program needs information on genetic variability and trait association among existing genotypes, and also wants to depict information on variance components as well as relationships of yield and yield-related traits in linseed genotypes. However, different works have been done so far, but there is little information available in Ethiopia about some characteristics of linseed. Thus, data on genotype and phenotype, and phenotype-specific variability, heritability, and relationships between yield and traits associated with yield in linseed genotypes were highly needed. Realizing the importance of the crop and the existing information gap, the present study was carried out to evaluate the genetic diversity, yield, and improvement potential of Linseed genotypes.

2 MATERIALS AND METHODS

2.1 Description of the Study Area

The experiment was conducted at the Holeta Agricultural Research Center (HARC) during the main cropping season of 2023. HARC is situated in the Oromia Regional State, Welmera district, that about 29 km west of Addis Ababa. The site was representative of central Oromia's highland agroecology, which was ideal for highland oil crops. Its average elevation was 2400 meters above sea level (masl), and its latitude and longitude were 9^0 5' 0"N and 44^o 29' 0" E, respectively. During the growing seasons (June to November), its temperature ranged between 20 °C and 220 °C, while the annual total rainfall varied between 900 and 1000 millimeters.

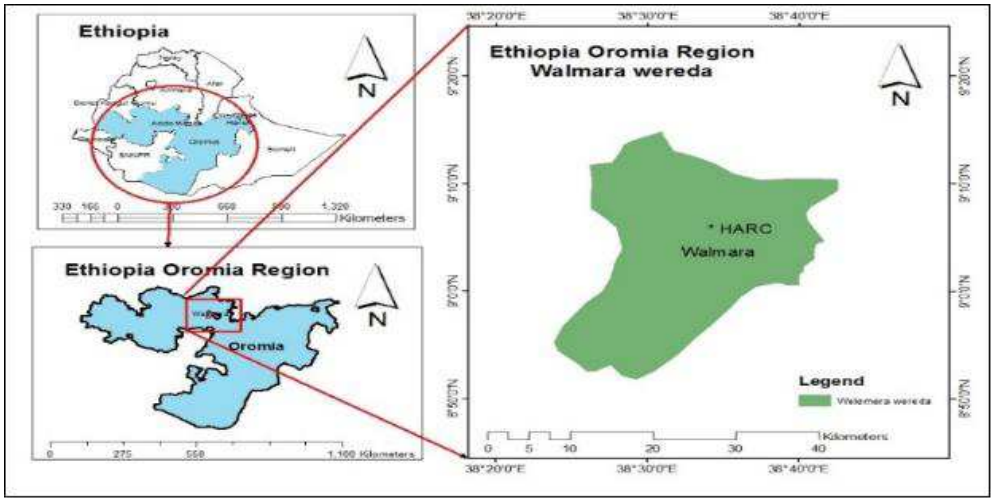


Figure 1. Map of the study area

2.2 Experimental Material

This study incorporated thirty-five (35) linseed genotypes, including checks, obtained from the National Mid and Highland Oilseeds Research Program at Holeta Agricultural Research Center, the Coordinating Center. The materials were first found from the Ethiopian Biodiversity Institute (EBI), and then purification work was done by the Holeta breeding program up to S-3, selecting the best materials as a single plant from the purified population at Holeta as a pre-breeding activity.

Table 1. List of genotypes

No	Genotypes/ materials	Origin	Sources	No	Genotypes/ materials	Origin	Sources
1	Acc34663/2	EBI	HR-PVT-19	19	Acc34586/9	EBI	HR-PVT-19
2	Acc89577/4	EBI	HR-PVT-19	20	Acc35146/1	EBI	HR-PVT-19
3	Acc34514/3	EBI	HR-PVT-19	21	Acc35137/2	EBI	HR-PVT-19
4	Acc35151/4	EBI	HR-PVT-19	22	Acc35150/8	EBI	HR-PVT-19
5	Acc35282/1	EBI	HR-PVT-19	23	Acc35149/1	EBI	HR-PVT-19
6	Acc35121/1	EBI	HR-PVT-19	24	Acc35140/4	EBI	HR-PVT-19
7	Acc35312/9	EBI	HR-PVT-19	25	Acc35139/7	EBI	HR-PVT-19
8	Acc83030/2	EBI	HR-PVT-19	26	Acc35148/3	EBI	HR-PVT-19
9	Acc35245/7	EBI	HR-PVT-19	27	Acc35328/5	EBI	HR-PVT-19
10	Acc35153/5	EBI	HR-PVT-19	28	Acc35277/6	EBI	HR-PVT-19
11	Acc35326/6	EBI	HR-PVT-19	29	Acc35141/9	EBI	HR-PVT-19
12	Acc34454/9	EBI	HR-PVT-19	30	Acc88722/2	EBI	HR-PVT-19
13	Acc35287/2	EBI	HR-PVT-19	31	Acc35279/7	EBI	HR-PVT-19
14	Acc35293/1	EBI	HR-PVT-19	32	Belay-96/11	PVT	HR-PVT-19
15	Acc35307/2	EBI	HR-PVT-19	33	Bekoji/12/6	PVT	HR-PVT-19
16	Acc35288/3	EBI	HR-PVT-19	34	Jeldu/16/1	PVT	HR-PVT-19

17	Acc35889/5	EBI	HR-PVT-19	35	Berene	BS	BS
18	Acc92373/6	EBI	HR-PVT-19				

Keys: BS- Breeder seed, EBI- Ethiopian Biodiversity Institute, HR-PVT-Holeta Research Preliminary Variety Trial-2019.

2.3 Experimental Design and Trial Management

The experiment was arranged in a 5x7 Alpha Lattice Design with two replications. Each genotype was planted in a plot with four rows spaced 20 cm apart and measuring 3 meters long. The entire experimental area was 11 m x 22.7 m = 249.7 m2, with the area of each experimental plot being 3 m x 0.8 m = 2.4 m2. At the time of planting, fertilizer was applied at the recommended rate of 25/60.5 kg/ha N/NPS, whereas a 25 kg/ha seed rate was used. According to the crop's recommendations, all additional agronomic management was applied uniformly for all plots.

The model for alpha lattice design.

as:

$$Y_{ijk} = \mu + R_i + B_{ij} + T_k + e_{ijk}$$

Where: μ=General mean, R_i=(fixed) effect of Replicate i, B_{ij}=(random) effect of Block j within Replicate i, T_k=Effect of treatment k and e_{ijk}= effects of error

Table 2. Skeleton of ANOVA and Expected mean square for Alpha Lattice Design

Source of variation	DF	Ms	Expected Mean
Replication	r-1	Msr	$\sigma^2_e + k\sigma^2_b + g\sigma^2_r$
Block with Replication	r(b-1)	Msb	$\sigma^2_e + \sigma^2_g + k\sigma^2_b$
Genotype	g-1	Msg	$\sigma^2_e + \frac{k}{k+1} \times r\sigma^2_g$
Error	rg-(g+rb)+1	Mse	σ^2_e
Total	gr-1		

2.4 Data Collected

The following data were collected both on plant bases and/or plot bases for quantitative and qualitative traits by using Descriptors of the International Board for Plant Genetic Resources [24] for Linseed. Plot-based data were collected from central rows of each plot, while plant-based data were obtained from ten randomly selected and tagged plants [15].

2.4.1 Plant-based Data

- Primary branches per plant (PBPP): Ten randomly chosen plants were used to count and calculate the average number of branches on each plant's main stem.
- Secondary branches per plant (SBPP): Ten randomly selected plants were used to count and calculate the average number of branches that emerge from each primary branch.
- Number of capsules per plant (NCPP): From 10 randomly selected plants, the average number of capsules was counted and calculated.
- Plant height (PH, cm): The average height of ten randomly taken plants was measured from the plant's ground level to the tip at harvesting time.
- Number of Tillers per Plant (TPP): Ten randomly selected plants were used to count and calculate the average tiller number per plant.

2.4.2 Plot-Based Data

- Days to 50% flowering (DF, days): Days from sowing to the point at which 50% of the plants begin to bloom.
- Biomass Yield per plot (B, kg): The above-ground plants' total dry matter weight in kilograms and transformed to tons.
- Lodging (log, %): The proportion of lodged plants was estimated in percentage
- Days to 90% Maturity (DM, days): Days between sowing to 90% of the overall plot reached physiological maturity. At this point, 90% of the

capsules turn brown in hue.

- One thousand seed weight (TSW, g): Using a delicate balance, the weight (g) of one thousand seeds was counted, and the weight was taken from each plot.
- Harvest index (HI, %): is the percentage representation of the seed yield divided by the total biomass of the plot.
- Oil content (OC, %): A nuclear magnetic resonance spectrometer was used to measure the oil content of seed samples.
- Seed yield per plot (SYPha, qt): Following a 7% moisture adjustment, the amount of seed per plot was weighted in grams. By converting the 1.2 m^2 area to a hectare basis, it was transformed to seed yield per hectare.
- Oil yield (OYH, ton/ha): The calculation of oil yield in kilograms per hectare involves multiplying the seed yield by the corresponding oil percentage derived from the oil analysis and converted to tons: $OY = OC \times SYH$

2.5 Statistical Analysis

2.5.1 Analysis of Variance

SAS software (Version 9.3) was used to compute analysis of variance (ANOVA) for seed yield and other traits using the techniques outlined by [23] for basic lattice design. Microsoft Excel was used to compute descriptive statistics, including the mean, range, and standard deviation, for quantitative features of the genotypes. Minitab V-17 [30] was used to cluster the average linkage approach with Euclidean distance.

2.5.2 Estimate of Heritability in Broad Sense

Heritability (H^2) in a broad sense for all characters was computed according to [4,13].

$$H^2 = (\sigma^2_g/\sigma^2_P) *100$$

$$\sigma^2P = \sigma^2g + \sigma^2e$$

Where, σ^2g = genotypic variance, σ^2P = phenotypic variance and σ^2e = error variance

The heritability was classified as indicated by [25]: low (< 40%), medium (60-80%), and very high (> 80%).

2.5.3 Estimation of Expected Genetic Advance

The genetic advance at selection intensity (k) of 5% was estimated by the following formula [4,25].

$$EGA = k * \sigma ph * H^2$$

Where the genetic advance expected (EGA) under selection was represented; σph was the phenotypic standard deviation; H^2 was heritability in a broad sense, and K was the selection differential (k=2.063 at 5% selection intensity). The genetic advance as a percentage of the population mean was estimated by the procedure suggested by [25]. Therefore, EGA was classified as low (< 10%), moderate (10-20%), and high (> 20%).

2.5.4 Character Association Analysis

SAS software was used to ascertain the relevance and correlation of features [36]. Using the approach outlined by [43], phenotypic and genotypic correlations between yield and yield-related traits linked to yield were computed from the corresponding variance and covariance components as follows:

$$rp_{xy} = \frac{\sigma_{pxy}}{\sqrt{\sigma^2{}_{px} \times \sigma^2{}_{py}}}$$

$$rg_{xy} = \frac{\sigma_{gxy}}{\sqrt{\sigma^2{}_{gx} \times \sigma^2{}_{gy}}}$$

Where, rp_{xy} = phenotypic correlation coefficient between characters X and Y,

rg_{xy}= genotypic correlation coefficients between X and Y

, σ^2_p = phenotypic variance between characters X and Y,

σ^2_g = Genotypic variance between characters X and Y.

The significance of the computed phenotypic correlation value was assessed using the t-test.

$$t = rp/SE_{rp}$$

where SE_{rp} was the standard error of the phenotypic correlation calculated using the formula technique, and rp was the phenotypic correlation (Sharma, 2006)

$$SE_{rp} = \sqrt{(1—r^2p)/ (n— 2)}$$

Where n was the number of genotypes tested, SE was the genotypic correlation at the genotypic levels, which were tested for their significance by using the formula described by [35] as indicated below:

$$t= rg_{xy}/ SE_{rgxy}$$

The calculated t-value was compared with the tabulated “t” value at (n-2) degrees of freedom at 5 % and 1% level of significance, where n is the number of genotypes.

$$SErgxy = (1—r\ ^2gry)/ (H^2x.H^2_y)$$

Where H^2_x= Heritability of trait x, H^2_y = Heritability of trait y.

2.5.5 Principal Component Analysis

Using Minitab V-14 Software, a principal components analysis was performed on 14 standardized quantitative traits to identify the most important trait in explaining the variation observed between the genotypes. We had taken into account primary components having eigenvalues greater than one, following the recommendation of [14].

2.5.6 Cluster Analysis

Using the Minitab V-17 [30] software, hierarchical clustering of the average linkage method with Euclidean distance was carried out. Before clustering, data about quantitative qualities were normalized to a mean of zero and a variation of one to prevent any potential bias resulting from varying measurement scales. Euclidean distances and the average approach were used to compute the distances between clusters to determine whether the genotype was closest to or farthest away from others. The following formula was used to determine the genetic distance between clusters [29].

$$D^2_{ij}= (x_i-x_j)\ S^{-1}(x_i-x_j)$$

Where D^2_{ij} = the distance between any two groups i and j, x_i and x_j are the vector means of the traits for groups i and j, and S^{-1} is the pooled within-groups variance-covariance matrix.

3 RESULT AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance for 14 important traits of the 35 linseed genotypes studied is presented in Table 3. The results revealed highly significant differences ($P \leq 0.01$) among genotypes for 14 quantitative traits. It indicated that the studied genotypes had remarkably significant genetic variability in agreement with previous results [45,32,21], who found that all of the traits in linseed genotypes had extremely significant differences for seed yield and its related traits. The observed genetic variability provides an encouraging foundation for developing improved linseed varieties tailored to the unique conditions of the research site.

Breeding programs could make good use of this genetic variability to improve agronomic features and increase yield potential. The current study was comparable to the [45] study, which found that linseed genotypes varied greatly in terms of days to maturity, number of capsules per plant, seed yield per plant, 1000 seed weight, harvest index, and oil content. A study done by [27] showed that there was a great deal of variance in India's linseed genotypes for practically all of these traits.

Table 3. Mean square from analysis of variance for different sources of variation and the corresponding CV for quantitative traits

SN	Trait	Rep.(df=1)	Bl/Rep (df=8)	Gen. (df=34)	Error (df=26)	CV (%)
1	DF	1.16	1.41	36.5 **	1.00	5.54
2	DM	0.36	0.97	82.06 **	1.02	4.45
3	PH	0.01	0.18	0.36 **	0.08	9.50
4	Lod	0.28	0.18	3.46 **	0.65	18.34
5	TSW	0.1	0.03	0.8 **	0.02	14.95

SN	Trait	Rep.(df=1)	Bl/Rep (df=8)	Gen. (df=34)	Error (df=26)	CV (%)
6	TPP	0.01	0.05	1.7 **	0.05	50.54
7	PBPP	0.28	0.24	3.31 **	0.12	26.45
8	SBPP	0.4	2.9	8.08 **	2.13	21.25
9	NCPP	0.15	0.38	24 **	0.54	25.33
10	HI	0.04	0.12	55.26 **	0.31	34.70
11	BM	0.03	0.02	9.18 **	0.08	26.21
12	OC	0.86	0.05	116.07**	0.05	22.59
13	OYH	0.93	0.06	124.81**	0.06	46.89
14	SYPha	0.99	0.06	134.2 **	0.06	22.63

3.2 Mean Performance of Genotypes

Table 4 shows the estimated values for descriptive statistics of the 14 quantitative traits for the linseed genotypes. According to descriptive statistical analysis and Duncan's Multiple Range Test (DMRT) at the 5% level of significance, there was a wide range of variability among the 35 genotypes for the majority of the traits studied, indicating the possibility of improving genotypes for traits of interest. For Ethiopian linseed genotypes, these notable variations for every trait under investigation suggested enough room for development in the desired direction. Days to maturity ranged from 124 to 156 days, with an average of 144.67 days, whereas days to 50% flowering ranged from 70.00 to 87.00 days, with a mean of 77.42 days.

Table 4. Descriptive statistics for the studied quantitative traits

Traits	Mean	Standard Deviation	Range	Minimum	Maximum
DF	77.42	4.29	17.00	70.00	87.00
DM	144.67	6.44	32.00	124.00	156.00
PH	103.20	9.80	40.00	83.50	123.50
Lod	7.69	1.41	6.00	3.60	9.60
TSW	4.28	0.64	2.60	3.20	5.80
TPP	1.84	0.93	3.19	0.71	3.89
PBPP	4.99	1.32	5.90	2.00	7.90
SBPP	10.73	2.28	9.30	6.40	15.70
NCPP	13.82	3.50	16.40	6.70	23.10
HI	15.13	5.25	23.16	8.10	31.26

Traits	Mean	Standard Deviation	Range	Minimum	Maximum
BM	255.78	67.03	256.33	125.00	381.33
OC	33.69	7.61	37.29	18.77	56.06
OYH	1282.11	601.15	3000.44	378.83	3379.27
SYPha	36.19	8.19	40.10	20.40	60.10

Plant height and the number of capsules per plant varied from 83.5-123.5 and 6.7-23.1, with mean values of 103.2 and 13.82, respectively, whereas the number of secondary branches per plant ranged from 6.4-15.7, with a mean of 10.73 (Table 4). The average seed yield per hectare was 36.19, with a range of 40.1. The investigated genotypes for oil yield ha-^{1} showed significant variation, with a mean value of 1282.11 and a range of 3000.44. The maximum and minimum values of the oil and biomass were 56.06–18.77 and 381.33–125, respectively, with mean values of 33.69 and 255.78. The lodging ranged from 3.6 to 9.6, with mean values of 7.69, while the tiller number per plant and primary branches ranged from 0.71 to 3.89 and 2.0 to 7.9, with mean values of 1.84 and 4.99, respectively. The harvest index and 1000-seed weight ranged from 8.10-31.26 and 3.20-5.80, with mean values of 15.13 and 4.28, respectively. In general, based on mean performance, almost all tested genotypes showed higher mean values for most of the measured traits, as indicated in Table 4.

The results indicated that the evaluated linseed genotypes had genetic potential and gave an indication for improving yield and yield-related traits. Therefore, based on traits of interest, those genotypes could be used for further breeding programs to develop linseed varieties.

3.3 Estimates of Genetic Parameters

Estimates of genetic parameters, including predicted genetic advancement, heritability in the broadest sense, phenotypic and genotypic variances, and phenotypic coefficient variations (PCV) and genotypic coefficients of variation (GCV), are depicted in Table 5. The PCV and GCV values >20% were

classified as high, <10% as low, and 10% to 20% as medium, as suggested by [17].

3.4 Phenotypic and Genotypic Coefficients of Variation

For any crop advancement through selection and other breeding techniques, the species' level of genotypic and phenotypic variability was crucial. Understanding the PCV and GCV aids in forecasting the variation seen in the specified genotypes. According to [44], GCV and PCV values below 10%, 10%–20%, and beyond 20% were deemed low, intermediate, and high, respectively. Phenotypic coefficients of variation varied from 50.70 percent for tiller per plant to 4.45 percent for maturity dates. Harvest index, Tiller per plant, seed yield per ha^{-1}, capsules per plant, primary branch, oil content and yield, biomass, and secondary branches/plant were shown to have the highest PCV estimates.

For every trait that was measured, the GCV was less than the PCV (Table 5). These suggested that the apparent variance resulted from interactions in addition to environmental influences and genotypes. Because environmental variation was unexpected, selection for those features based solely on phenotype might not be effective. To obtain a stable phenotype, these genotypes should be examined throughout time and across locations. Several researchers have already shown similar results in linseed, including [28,40].

The estimates of GCV and PCV for the following characters showed a close correspondence: Days to flowering (5.43%-5.60%), days to maturity (4.4%-4.45%), thousand seed weight (14.54%-14.96%), seed yield per ha (22.63%-22.64%), harvest index (34.78%-34.95%), biomass (13.46%-13.55%), oil content (22.63%-22.64%), and oil yield per ha (22.63%-22.64%). This suggests that the characters were less affected by environmental factors, as evidenced by the smaller differences in the magnitude of GCV and PCV values. However, as evidenced by the significant discrepancies between the estimates of GCV and PCV, environmental factors had a significant impact on the following characters: primary branch (25.19%–26.37%), plant height (3.5%–4.45%),

lodging (15.68%–18.34%), secondary branch per plant (15.86%–21.28%), tiller number (49.25%–50.75%), and capsule per plant (24.82%–25.35%). The variability in soil fertility status and other unpredictability in the environment may be the cause of this [34].

The outcome of this study was similar to that of [38], who noted that the phenotypic coefficients of variation for oil yield and seed yield per plant were of large magnitude. While [45] observed the same for the number of seeds per capsule, seed yield per plant, and number of secondary branches, [31,28] found high PCV values for the number of secondary branches and seed yield per plant. Similar findings for biological yield, number of seeds per plant, and seed yield per plant were also noted by [40]. Nevertheless, low PCV values were noted for the number of days to flowering and maturity, and plant height. In contrast, the lodging and thousand-seed weight were all at a medium level. Plant height had a genotypic coefficient of variation of 3.5%, whereas tiller per plant had a value of 49.25%. Tiller per plant, harvest index, primary branch, capsules per plant, seed yield per hectare, oil content, biomass, and oil yield all showed high-magnitude GCV values.

In contrast, the 1000 seed weight, lodging per plant, and secondary branch were medium, and plant height, days to maturity, and days to flowering were low. The high GCV values in the genotypes under study indicated that these qualities might be improved by selection. In terms of seed yield per plant, number of secondary branches per plant, and number of seeds per capsule, the current result was comparable to that of [26], who found a large genotypic coefficient of variation in linseed. High GCV was also demonstrated by [45] for both the number of secondary branches per plant and seed output per plant. Similarly, significant GCV for seed yield per plant was noted by [33,9]. Nonetheless, the low GCV for plant height, number of days to flowering, and maturity was shown, indicating less variability in these characteristics. This was consistent with the findings of [11,37,10] who also noted low GCV for days to maturity.

According to this delineation, characters such as TPP, PBPP, SBPP, NCPP, HI%, BM, OC%, OYH, and SYPha showed high PCV (>20%), while the traits under study showed high GCV values (Table 5), demonstrating the extremely high potential for genetic improvement of the genotypes being studied. The results were consistent with earlier research [38,33], which found that linseed had significant genotypic and phenotypic coefficients of variation.

3.5 Heritability

In this study, the estimate of heritability in a broad sense ranged from 52.98 % for Plant height to 99.93 % for Oil yield ha-1 (Table 5). [42] considers that a heritability value of a trait ≥80% is considered very high, and selection for such characters could be relatively easy because there is a close correspondence between genotype and phenotype due to the relatively small environmental contribution. However, for characters having a heritability value (≤ 40%), selection may be considerably difficult or virtually impractical due to environmental masking. Heritability values of 40-80% are considered to be moderate. Considering the above benchmark in the present study, high heritability values were recorded for Oil yield ha-1, Seed yield ha-1, Oil content%, Harvest index, Biomass, Days to maturity, Capsule per plant, thousand seed weight, Tiller per plant, Days to flowering, and Primary branches per plant. The finding indicated that these characters are expected to be highly heritable and governed by additive gene effects, and phenotypic values could give a fairly good idea 35 of their genetic potential. Hence, good progress can be made if these traits are considered as selection criteria.

Table 5. Heritability, genetic advance, and coefficients of variation in Linseed genotypes evaluated at Holeta in 2024.

Traits	Mean	σ2g	σ2p	σ2e	PCV (%)	GCV (%)	H2 (%)	GA	GAM (%)
DF	77.50	14.74	15.55	0.81	5.60	5.43	94.16	8.41	10.85
DM	144.70	33.99	35.14	1.15	4.45	4.40	97.58	12.96	8.95
PH	103.15	58.34	83.04	24.70	9.51	6.92	52.98	10.70	10.38

Traits	Mean	σ2g	σ2p	σ2e	PCV (%)	GCV (%)	H2 (%)	GA	GAM (%)
Lod	7.71	0.88	1.48	0.60	18.34	15.68	73.08	2.13	27.61
TSW	4.28	0.30	0.32	0.02	14.96	14.54	94.47	1.25	29.12
TN	1.84	0.77	0.82	0.05	50.70	49.21	94.22	1.81	98.41
PB	4.99	1.42	1.52	0.10	26.37	25.19	91.26	2.47	49.56
SB	10.71	2.80	4.79	1.98	21.28	15.86	55.58	2.61	24.36
CP	13.81	9.16	9.78	0.62	25.35	24.82	95.90	6.92	50.08
HI	15.08	21.42	21.70	0.28	34.95	34.78	99.04	10.75	71.30
BM (ton)	256.17	3493.82	3571.95	78.13	26.19	25.99	98.44	136.07	53.12
OC%	33.66	44.56	44.61	0.05	22.64	22.63	99.91	15.68	46.60
SY/Ha(ton)	36.19	51.52	51.57	0.05	22.64	22.63	99.91	16.86	46.60
OY (ton)	1278.57	275742.06	275956.35	214.29	47.07	47.06	99.93	1238.96	96.90

NB: GA=genetic advance, GAM=genetic advance as a percent of the mean, GCV=genotypic coefficient of variation, H^2= heritability (%), PCV=phenotypic coefficient of variation, σ^2e =environmental variance, σ^2g =genotypic variance, σ^2p=phenotypic variance

3.6 Principal Component Analysis (PCA)

The contribution of various variables to each principal component, as shown by the eigenvector (Table 6), could be used to quantify principal component analysis (PCA). Additionally, PCA was utilized to help evaluate diversity and identify the independent principal components that impacted plant attributes and the interactions between traits [48,22]. For about 77.02% of the population, significant genetic variability was observed from the first five principal components (PC), all of which had greater than or equal to one eigenvalue.

This suggested that the 14 studied traits showed differences among the examined populations. About 26.52% came from the PC1. The first Principal component was heavily influenced by traits including harvest index, oil yield, seed yield, plant height, lodging, oil content, and maturity date. The second principal component contributed to oil content, secondary branch, thousand seed weight, biomass, seed yield, and oil yield, which contributed 19.8% of the total variation. Biomass, plant height, lodging, and primary branches all contributed more to the third principal component, which accounted for about 12.2% of the variation.

About 10% of the total variation was elucidated by the fourth principal component, which was mostly caused by the secondary and primary branches, lodging, plant height, and days to maturity. The primary branch, tiller per plant, harvest index, and thousand seed weight were the main contributors to the fifth principal component, which contributed about 8.5% for the total variation. The present findings were similar to earlier research findings by [32].

Table 6. Eigenvalues of the correlation matrix and related statistics

PC	Eigenvalue	Proportion%	Total variance %	Cumulative Eigenvalue	Cumulative %
PC1	3.71	26.52	38.75	3.71	26.52
PC2	2.77	19.80	35.04	6.48	46.32
PC3	1.71	12.2	28.56	8.19	58.52
PC4	1.39	10.0	20.36	9.59	68.52
PC5	1.19	8.5	10.78	10.78	77.02

Table 7. Contributions of traits for the first five components

Traits	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
DF	0.032	-0.039	-0.096	-0.728	0.044
DM	0.233	-0.29	0.006	0.173	-0.178
PH	0.288	-0.212	0.219	0.187	-0.214
Lod	0.257	-0.296	0.176	0.227	-0.148
TSW	-0.07	0.443	0.029	-0.105	0.158
TN	0.146	-0.241	0.094	-0.088	0.497
PB	-0.116	0.104	0.19	0.351	0.654
SB	-0.163	0.324	-0.17	0.432	-0.068
CP	-0.202	0.125	-0.496	0.115	-0.287
HI	0.303	-0.08	-0.561	0.097	0.199
BM (ton)	-0.032	0.353	0.522	-0.043	-0.266
OC%	0.445	0.302	-0.042	-0.007	0.002
SY/Ha(ton)	0.445	0.302	-0.042	-0.007	0.002

Traits	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
OY (ton)	0.447	0.288	-0.001	-0.03	0.032
Eigenvalue	**3.713**	**2.770**	**1.708**	**1.394**	**1.194**
Proportion (%)	**26.5**	**19.8**	**12.2**	**10**	**8.5**
Cumulative	**26.52**	**46.3**	**58.5**	**68.5**	**77.02**

3.7 Cluster Analysis

Clustering is the assignment of gathering a set of objects in such a way that objects within the same bunch (called a cluster) are more comparable (in some sense) to each other than to those in other bunches (clusters). Based on quantitative information, genotypes were assembled by cluster analysis on the basis of Euclidean distance from their particular groups.

Thirty-five genotypes were categorized into five clusters based on 14 traits of interest. The first cluster had 18 genotypes, the largest cluster. Cluster II was 6 sunflower genotypes, followed by cluster III with 5 genotypes and cluster IV with 5 genotypes, and the last cluster was solo (Table 8).

Each cluster had its unique trait; cluster-1 had genotypes with higher mean values for days to flowering, and late maturing, having medium height, susceptible to lodging, fewer branches, both primary and secondary branches, less oil content, and seed-yielding genotypes were grouped under this cluster. Cluster 1 genotypes were important to improve the above-mentioned traits for future crossing programs. Cluster-2 also includes genotypes characterized by early flowering and maturing short height, medium primary and secondary branches, low number of capsules per plant, high seed yield and biomass, low values for oil content, and average values for the other traits.

Table 8. Cluster number, Number and Lists of Genotypes, Proportion, Average distance from Centroids, and Maximum distance from Centroids.

Cluster	Number of genotypes	Proportions	Average distance from the Centroids	Maximum distance from the Centroids	Genotype Code

1	18	51.43	3.00	3.92	G1,12,22,23,3,5,2,9,25,12,24,26,6,8,17,13,27,18
2	6	17.14	3.03	3.34	G4,20,30,14,21,16
3	5	14.29	3.31	4.08	G19,31,32,33, 35
4	5	14.29	2.50	2.90	G7,28,29,10,11
5	1	2.86	0.01	0.01	G34

Genotypes grouped under cluster 3 had characters of late flowering and medium maturity, nearly medium height, high oil content, and seed yield. The fourth cluster was grouped with genotypes having late flowering and maturing, medium height, high lodging, high number of capsules per plant, medium oil content, and low seed yield. The last cluster includes one genotype, which was called solo, Jeldu/16/1, with a unique trait from the other cluster genotypes (Figure 2).

Table 9. Cluster and centroid means for fourteen quantitative characters

Traits	Cluster Mean					Centroid mean
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	
DF	78.3	75.6	79.4	79	69.3	76.32
DM	148	141.9	143.6	143.1	151.1	145.54
PH	106	98.9	106.5	103.5	110.1	105
Lod	8.1	6.9	8.9	7.8	2.1	6.76
TPP	2.4	1.3	2.3	1.3	0.75	1.61
PBPP	4.7	5.5	5.0	4.4	6.1	5.14
SBPP	9.5	11.7	11.0	11.6	13.6	11.48
NCPP	12.4	15.3	9.5	18.3	25.2	16.14
TSW	4.0	4.6	4.5	4.0	5.2	4.46
SYPha	32.9	34.5	51.3	38.2	60.1	43.4
HI	15.5	11.4	15.7	24.9	26.1	18.72
BM	217.3	306.4	329.2	156	351.2	272.02
OC	30.6	32	47.7	35.5	33.6	35.88
OYH	1036.7	1133.1	2468.9	1407.6	1894.8	1588.22

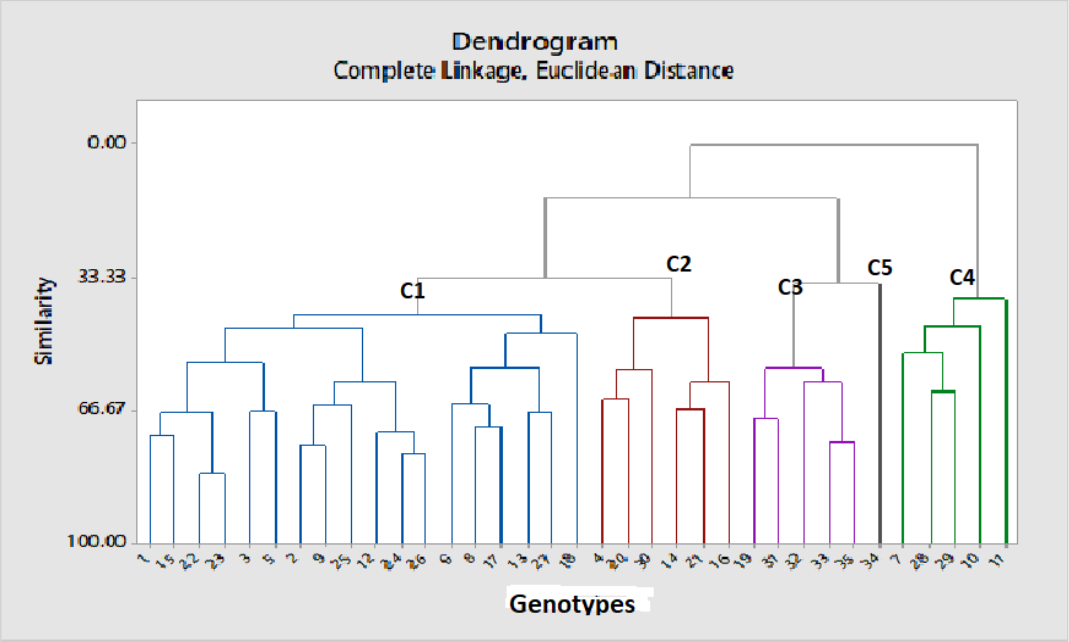


Fig. 2. Dendrogram of cluster analysis based on fourteen quantitative Traits

Genetic divergence among linseed genotypes has been documented by several investigators, suggesting that they are grouped into varying numbers of clusters. About 103 linseed accessions were examined for genetic diversity by [1], who categorized them into 12 distinct groups. Ten unique clusters were found by [46] after studying genetic diversity across 81 linseed genotypes. Cluster study of 60 linseed accessions revealed 11 distinct classes, with accessions in clusters V to XI being genetically more distant from one another [3].

Table 10. Inter-cluster (off-diagonal) and Intra-cluster (diagonal) distance analysis.

Cluster	I	II	III	IV	V
I	**1.031^{NS}**	2.717*	4.489**	3.731**	6.677**
II		**1.132^{NS}**	4.565**	3.905**	6.867**
III			**2.031^{NS}**	4.530**	8.517**

IV	**2.061^{NS}**	5.154**
V		**2.171^{NS}**

Where, NS=non-significant, *significant at p<0.05 for X^2 =2.25; ** significant at p<0.01 for X^2=3.08

The D^2 analysis for the five clusters is presented in Table 10. above. The analysis showed that all inter-cluster distances were highly significant, while there was a non-significant intra-cluster distance. The maximum genetic distance was observed between cluster III and cluster V (D^2=8.517), the most divergent clusters. These high values of inter-cluster distances may result from the different genetic backgrounds of the genotypes. The least genetic distance was found between cluster I and cluster II (D^2=2.717). So, clusters with the largest genetic distance indicate the real variability between genotypes within those clusters. A unique and maximum variation is expected from crosses of parents from clusters with high inter-cluster distance. Thus, crossing genotypes selected from cluster III and cluster V, cluster II and cluster V, cluster I and cluster V, cluster IV and cluster V, and those from cluster II and cluster III could be a source of desirable variation or hybrid development, as the inter-cluster distance between them was large, respectively.

3.8 Correlation of Traits

3.8.1 Phenotypic Correlation Coefficient

Below, Table 11. provides an estimate of a phenotypic correlation coefficient. Plant height and days to maturity (r: 0.404), lodging with days to maturity (r: 0.32) and plant height (r: 0.377), capsules per plant with secondary branch (r: 0.344), thousand seed weight with biomass (r: 0.32), seed yield with harvest index (r: 0.462), oil content with harvest index (r: 0.462), and seed yield (r: 0.702) demonstrated positive and highly significant correlations at the phenotypic level. In contrast, there was a positive and substantial association between the harvest index and the days to maturity (r: 0.263) and the thousand seed weight with secondary branches (r: 282). In a different instance, the following variables were positively non-significant: Seed yield, oil content, and

oil yield with days to flowering, days to maturity, plant height, lodging, tiller number per plant, primary branch with tiller number per plant, secondary branch with the primary branch, harvest index with days to flowering, plant height, lodging, tiller number per plant, and capsules per plant; biomass with primary branch and secondary branch; and thousand seed weight with flowering date, primary branch, and capsules per plant. In contrast, there was a negative and highly significant correlation between the secondary branch, the days to maturity, the number of tillers, the capsules per plant, the plant height, the lodging, the biomass, the harvest index, and the thousand seed weight with the lodging.

On the other hand, there was a significant negative correlation between the number of capsules per plant and the days to flowering, as well as between the number of primary and secondary branches and the days to maturity, and the number of seeds. Additionally, there was a negative non-significant correlation between days to maturity, plant height, and lodging; primary branch and days to maturity; plant height and lodging; secondary branch and plant height and lodging; capsules per plant and flowering date; maturity date and primary branch; harvest index and primary and secondary branch; biomass and flowering date, maturity date, plant height, lodging, tiller number, and capsules per plant; thousands of seed weight with plant height and harvest index; and seed yield, oil yield and content.

Table 11. Phenotypic correlation

Traits	DF	DM	PH	Lod	TSW	TN	PB	SB	CP	HI	BM (ton)	OC%	SY/Ha (ton)	OY (ton)
DF														
DM	-0.171													
PH	-0.053	0.404**												
Lod	-0.057	0.320**	0.377**											
TSW	0.037	-0.236*	-0.205	-0.542**										
TN	0.047	0.220	0.071	0.215	-0.240*									
PB	-0.247*	-0.182	-0.110	-0.132	0.201	0.072								
SB	-0.250*	-0.371**	-0.178	-0.168	0.282*	-0.318**	0.183							
CP	-0.098	-0.104	-0.339**	-0.330**	0.067	-0.249*	-0.155	0.344**						
HI	0.049	0.263*	0.145	0.165	-0.169	0.141	-0.117	-0.059	0.098					
BM (ton)	-0.121	-0.232	-0.061	-0.129	0.320**	-0.189	0.055	0.135	-0.090	-0.709**				
OC%	0.022	0.136	0.212	0.153	0.208	0.057	-0.118	-0.001	-0.174	0.462**	0.224			
SY/Ha(ton)	0.022	0.136	0.212	0.153	0.208	0.057	-0.119	-0.001	-0.174	0.462**	0.224	0.702**		
OY (ton)	0.048	0.100	0.218	0.183	0.172	0.082	-0.087	-0.040	-0.223	0.431**	0.239*	0.988**	0.988**	

Key: BM= biomass, NCPP=capsule per plant, DF =Days to flowering, DM= Days to maturity, HI= harvest index, Lod=lodging (%), OC=oil content, OYH= oil yield, PBPP=primary branch, PH=plant height, SBPP =secondary branch, SYPha=seed yield, TPP= Number of tillers per plant, and TSW= thousand seed weight.

3.8.2 Genotypic Correlation Coefficient

Below, Table 12. displays the genotypic correlation coefficients between yield and its contributing traits. Lodging had a highly significant and positive association with plant height (r: 0.683) and plant height and days to maturity (r: 0.571), as well as a positive and significant correlation with days to maturity (r: 0.372). Oil content was very significant and positively correlated with the harvest index (r: 464), seed yield (r: 0.667), and the number of capsules per plant, which was highly significant and positively correlated with a secondary branch (r: 466).

Additionally, there were positive and highly significant correlations between oil yield and the harvest index (r:433), seed yield (r:0.988), and oil content (r:0.988), respectively. The findings of [2,6], who found a positive association between seed yield per plot, oil yield per plot, and seed yield per plant, were consistent with this outcome. In the same manner, lodging demonstrated a positive significant connection with days to maturity (r: 0.372) and tiller number (r: 0.266); whereas with seed per capsule (r: -0.418), and thousand seed weight (r: -0.585). Additionally, there was a positive but non-significant correlation between other important traits of interest. Similarly, the harvest index was positively and significantly correlated with the days of maturity, oil content, seed yield, and oil yield, but negatively correlated with biomass both genotypically and phenotypically.

On the other hand, there was both phenotypically and genotypically significant negative correlation between the secondary branch and the days to maturity and flowering, tiller number, plant height, and also the biomass with the harvest index, and the thousand seed weight with lodging. The secondary branch showed a significant positive correlation between thousand-seed weight and the primary branch.

Additionally, the following traits were showed positive and non-significantly correlated with each other: maturity and flowering dates, plant height, lodging, primary branch, plant height and lodging, secondary branch, days to flowering, capsules per plant, flowering date, days to maturity, tiller per plant, primary

branch, harvest index, primary branch, and harvest index, biomass, number of flowering dates. Similarly, the following variables were negatively non-significantly correlated with each other: Days to maturity with Days to flowering, Plant height with Days to flowering, Lodging with Days to flowering, Primary branches with Days to flowering, maturity date, Plant height and Lodging, Tiller per plant, and Capsules per plant; Thousand seed weight with maturity date, Plant height, Tiller per plant, and Harvest index; and Seed yield, Oil content, and Oil yield with Primary branch, Secondary branch, and Capsules per plant.

Table 12. Genotypic correlation

Traits	DF	DM	PH	Lod	TSW	TN	PB	SB	CP	HI	BM (ton)	OC%	SY/Ha (ton)	OY (ton)
DF														
DM	-0.174													
PH	-0.113	0.571**												
Lod	-0.051	0.372**	0.683**											
TSW	0.037	-0.249*	-0.291*	-0.585**										
TN	0.045	0.220	0.122	0.266*	-0.268*									
PB	-0.271*	-0.197	-0.165	-0.122	0.208	0.075								
SB	-0.373**	-0.490**	-0.394**	-0.136	0.366**	-0.408**	0.264*							
CP	-0.098	-0.116	-0.491**	-0.418**	0.069	-0.263*	-0.164	0.466**						
HI	0.057	0.260*	0.218	0.185	-0.173	0.145	-0.122	-0.069	0.101					
BM (ton)	-0.127	-0.228	-0.105	-0.143	0.333**	-0.196	0.058	0.176	-0.092	-0.708**				
OC%	0.023	0.138	0.288*	0.175	0.216	0.058	-0.124	0.001	-0.177	0.464**	0.225			

SY/Ha(ton)	0.023	0.138	0.288*	0.175	0.216	0.058	-0.124	0.001	-0.177	0.464**	0.225	0.667**	
OY (ton)	0.049	0.102	0.296*	0.210	0.178	0.084	-0.091	-0.052	-0.228	0.433**	0.240*	0.988**	0.988**

Key: BM= biomass, NCPP=capsule per plant, DF =Days to flowering, DM= Days to maturity, HI= harvest index, Lod=lodging (%), OC=oil content, OYH= oil yield, PBPP=primary branch, PH=plant height, SBPP =secondary branch, SYPha=seed yield, TPP= Number of tillers per plant, and TSW= thousand seed weight.

4 CONCLUSIONS AND RECOMMENDATIONS

In Ethiopia, plant-based oil imports have become the number one problem for the government to satisfy the needs of a growing population and economic inflation. To buffer the markets, the country imports 98% of its demand from abroad, and only 2% of the demand is covered by local production. The limited number of released varieties and low productivity compared to the world average of linseed varieties were additionally becoming a significant issue for emerging oil factories in Ethiopia. So, the study of genetic variability and trait association among linseed genotypes may be a pillar and starting line to spot and choose high-yielding, tolerant, or resistant to biotic and abiotic factors breeding planting materials to develop the best varieties in general. An experiment was done to determine the degree of genetic variability and trait relationship with seed yield. 35 linseed genotypes were evaluated using a 5x7 alpha lattice design during the main cropping season of 2023 at the Holeta Agricultural Research Center.

The analysis of variance showed highly significant ($P \leq 0.01$) differences among the tested genotypes for all traits studied. Descriptive statistical analysis also showed the presence of a wide range of phenotypic variation among the studied genotypes. PCV and GCV values showed there was significant and tremendous variability among the studied genotypes for the respective traits of interest. The highest heritability, coupled with high genetic advance as a percentage of the mean, was observed for oil yield, oil content, seed yield, harvest index, capsule number, primary branch, tiller number, thousand seed weight, and biomass.

Multivariate analysis shows that the first five principal components were found to be significant, having Eigenvalues greater than one and accounting for about 77% of the gross genetic variation of the genotypes. The studied genotypes were grouped into five clusters with different traits. Out of 35 genotypes, 51.43% were grouped in cluster 1, followed by 17.14%, 14.29%, 14.29%, and 2.86% for cluster 2, 3, 4, and 5, respectively. Inter-cluster distances were highly significant, but intra-cluster distances were non-significant. So, we can conclude that based on the studied traits of interest, the 35 Linseed genotypes are genetically divergent.

A highly significant and positive phenotypic correlation was observed between seed yield and harvest index, oil content, and oil yield; also, a significant negative correlation was observed between traits of interest. Similarly, a non-significant correlation was also observed for some traits. A highly Significant and positive genotypic correlation was observed between seed yield and harvest index and oil content; also, a significant correlation was observed with plant height. Similarly, non-significance was also recorded from other traits.

Genotypes from divergent clusters are a recommended source of parental material for linseed improvement through hybridization. However, a season experiment would not reveal genotypes' variability and the real association of traits in response to the environment, because quantitative traits are polygenic and profoundly highly influenced by the environment. Thus, repeating this experiment across multiple locations for at least two consecutive cropping seasons is better to find concrete results. In addition, a comprehensive study supported by molecular data is recommended for the identification of novel genes responsible for important traits for linseed variety improvement. Generally, further work should be made to improve linseed genetic variability across the country, by employing germplasm collection from potential areas, introduction from potential countries, and a strong crossing program for specific traits should be initiated.

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Author contributions

TMT Conceptualization, selected genotypes, data collection, data analysis, result interpretation, manuscript drafting, final manuscript approval, GNG designed the experiment, selected genotypes, editing, and final manuscript approval, and FEJ designed the experiment, data collection and entry, selected genotypes, editing, and final manuscript approval.

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Declarations Consent to Participate

Not applicable.

Declarations Consent for publication

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