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Genetic-morphological Characterization and Diversity Analysis of Linseed (*Linum usitattissimum* L.) Germplasm

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: To study morphological and genetic diversity among 100 Linseed (*Linseed usitassimum* L.) germplasm accessions.
Study Design: Augmented RBD Design in five blocks with four checks.
Place and Duration of Study: College of Agriculture, IGKV, Raipur, Chhattisgarh. During *rabi* 2020-2021 and *rabi* 2021-2022.
Methodology: A total of 100 linseed germplasm accessions and four standard checks were studied by examining 10 quantitative traits which contribute to yield and its attributing traits. And observations recorded.
Results: Outcome of the study revealed that analysis of variance for 10 quantitative characters showed differences for various characters. Results from genetic variability analysis state that the highest GCV/PCV was recorded for the traits 50% flowering, secondary branches plant^{-1}, no. of capsules plant^{-1}, and seed yield plant^{-1}. Highest heritability was observed for all the traits under study. Highest heritability coupled with the highest genetic advance as percent was reported for 50% flowering, followed by secondary branches plant^{-1}, no. of capsules plant^{-1}, 1000 seed weight (g), and seed yield plant^{-1}. Seven accessions such as LCK-9406, NL-126, Sumerpur Local, SJKO-8, L-103, EC-397752, R.S.-6 were recorded as having the highest oil content (%) greater than

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>42%. The highest seed yield plant^{-1} along with the highest oil content (%) was recorded in four accessions such as Sumerpur Local, EC-397752, LCK-9406, SJKO-8.
Conclusion: The linseed accessions used in the current study showed significant variability for most of the characters. Observed accessions having the highest seed yield (g) and oil content (%) can be further utilized in the breeding programs based on breeder requirement.

Keywords: Augmented RBD; coefficient of variation; ANOVA; Tukey's method; linseed germplasm; genetic diversity.

1. INTRODUCTION

Linseed is also called Flax which is grown for fiber purposes. Botanically linseed is called *Linum usitatissimum* L. with the somatic chromosome complement, 2n=30, and belongs to the genus Linum in the family Linaceae. Linseed is believed to be originated from the Middle East and subsequently introduced to the other parts of the world. Linseed is a dual-purpose crop and today it is grown for oil and Flax fiber extraction. Huge diversity of present flax was obtained by domestication by our forefathers for centuries through disruptive selection which led present flax into oil seeded and fibrous plants Falx types are tall in stature with less number of primary and secondary branches whereas linseed types are cultivated for seed and oil purposes. Linseed contains the highest oil content among the crop plants grown with 36-40% which is also the richest source of PUFA (Poly Unsaturated Fatty Acids). Oil extracted is mainly used for industrial purposes for the manufacturing of paints, varnishes, soaps etc.., as it is having drying and hardening properties from the high linolenic acids (45-60%) [1,2] whereas low linolenic acid is preferable for human consumption. The fiber is known for its good quality having high strength and durability, therefore, used in the manufacturing of cloth, water-resistant pipes, paper and strawboard. The fiber is known for its good quality having high strength and durability, therefore, used in the textile industry, liquid proof pipes, paper and strawboard.

Although the area, production, and productivity of linseed in India during 2020-2021 is the productivity of 637 kg/ha with an area of 174.87 thousand tons per hectare and in Chhattisgarh the productivity of 384 kg/ha with an area of 12.82 thousand tons per hectare (Indiastat, 2021). With the availability and presence of low genetic variability, there is a need for characterization and evaluation of germplasm accessions through the introduction of new germplasm, collection of local landraces, and by the adoption of interspecific hybridization. Germplasm serves as the most valuable reservoir in providing needed attributes for developing superior varieties. Characterization involves estimating existing variability across the population of individuals [3]. Moreover, morphological diversity characterization studies have a relevant role in the management of crop diversity. So, it is required to conserve the diverse genotypes and also to explore the diversity studies of linseed for further breeding purposes.

2. MATERIALS AND METHODS

The present study was conducted at the research cum Instructional farm, Indira Gandhi Krishi Vishwavidyalaya, (IGKV), Raipur, India. A total of 100 linseed genotypes were used in the present study. The experiment was conducted during the 2020-2021 *Rabi* and 2021-2022 *Rabi* in an Augmented RBD design and observations were recorded for various quantitative characters and data analysis for various agro-morphological traits was done as per the standard statistical procedures. By using the RStudio, an Analysis of variance was done for pooled data in Augmented RBD design as per Federer [4], variability parameters were worked out as suggested by Burton and De Vane [5]; Johnson et al. [6], Four standard checks namely Neelum, Kiran, RLC-148(Varsha alsi) and RLC-153 were used in this study. Climatological data on temperature, rainfall, rainy days, relative humidity (RH) and sunshine hours were recorded at the Meteorological Observatory Unit, Department of Agro-meteorology, IGKV, Raipur during the cropping period. Favorable weather conditions were noticed during the crop growth and investigation of the current study.

The experimental field was well prepared with a recommended package of practices. Proper irrigation was given to the crop at the required time intervals and weeding is done to control the weeds and to keep the crop free from weeds. Visual examination of the crop is done and

observations were recorded randomly for five plants in each plot. Data were recorded on five randomly selected plants for all the agronomic traits viz., days to 50% flowering, days to maturity, Plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, oil content (%) and seed yield plant^{-1}. Oil content (%) was recorded for 100 lines by using Soxhlet apparatus [7] at department of genetics and plant breeding, college of agriculture, IGKV, Raipur.

3. RESULTS AND DISCUSSION

The present study was done to utilize the maximum diversity exhibited by the germplasm. It is not a solitary vital for utilizing the appropriate attribute-based donors in breeding programs, but also important in the present era of conserving the linseed variability. Outcomes from this study conformation on conclusions by the study of analysis of variance (ANOVA) for pooled data showed that there is a significant difference among the genotypes for all the characters studied (Table 1), which indicated that there is a considerable variation existed among the germplasm and significant mean squares due to seed yield and attributing traits revealed the existence of considerable variability in the material studied for the improvements of various traits. The blocking effect (unadjusted) was significant for all the traits except for the days to maturity and primary branches plant^{-1}, and treatment (adjusted as well as unadjusted) was significant for all the traits except for fays to maturity and primary branches plant^{1}. However, the adjusted block effects were significant for all the traits except No. of capsules plant^{-1}, 50% flowering, days to maturity and primary branches plant^{-1}, secondary branches plant$^{-1,}$ and 1000 seed weight(g) indicating homogeneity evaluation of blocks. Similarly, effects due to checks were nonsignificant for all the traits except 50% flowering, days to maturity, and primary branches plant^{-1}, secondary branches plant$^{-1,}$ and 1000 seed weight(g). likewise, the mean squares due to checks v/s varieties were significant for all the traits except no. of capsules plant^{-1}, 50% flowering, days to maturity and primary branches plant^{-1}, secondary branches plant^{-1} and 1000 seed weight(g) indicating thereby that the test entries were significantly different from each other. The critical difference and standard errors of difference were computed (Table 2 and Table 3) for all the traits for comparison of adjusted means of test entries in the same block, test entries in a different block, checks, test entries, and checks. The present study results are in agreement with the findings of Adugna and Labuschagne [8] for characteristics like days to 50% flowering, number of primary branches plant^{-1}, no. of seeds per capsule, Tyagi et al.*[9]* for number of primary branches per plant, seed yield per plant^{-1}, Bindra and Paul [10] for characters like technical length, days to 50% flowering, no. of primary branches, seeds per capsule, seed yield per plant, Kumar et al. [11] for characters like number of primary branches and number of seeds per capsule.

Results from the ANOVA p-value were less than or equal to the significance level in some traits like seed yield plant^{-1}(g), hence we can reject the null hypothesis and conclude that not all of the population means are equal. We use the post hoc test of the seed yield (plant^{-1}g) trait to determine whether the differences are practically significant. Tukey's multiple comparison test is a method of post hoc test that can be applied to describe which means among a set of means vary from the rest (Table 5). In these results, every possible pair of means is compared to identify pair of treatments that are significantly different. The table shows that all the germplasms are presented using alphanumeric annotations that are assigned by "1" to "9" with "0" and "A" to "Z" capital letters with "a" to "z" small letters. Differences between means that share a letter are not statistically significant. The highest mean contenting germplasm RSJ-31 (9.045) with a group "m" letter and lowest mean contenting germplasm EC-718840 (0.762) with a group "1" alphabet, which indicates that the germplasm RSJ-31 has a significantly higher mean than germplasm EC-718840 and so on. Means of germplasm followed by the same letter in the table do not differ significantly. Similarly, check genotypes for seed yield plant^{-1}(g) all are not significantly different from each other. Similar analysis was also done by Pandey et al. [12].

Genetic variability for the traits of interest is primary for crop improvement. The success of the breeding program depends on the quantum of genetic variability present in the population. Results from genetic variability analysis state that the highest GCV/PCV was recorded for the traits 50% flowering, secondary branches plant^{-1}, no. of capsules plant^{-1}, and seed yield plant^{-1} indicating the existence of a broad range of variability for those traits among the genotypes. Medium GCV with Medium PCV was noticed for the traits Plant height (cm), Primary branches

Table 1. Analysis of variance (ANOVA) for Augmented Block Design for pooled data *rabi* 2020-2021 and *rabi* 2021-2022

Source	Df	No. of capsules plant^{-1}	Days to maturity	50% flowering	Oil content (%)	Primary branches plant^{-1}	Plant height(cm)	Secondary branches plant^{-1}	No. of seeds capsule^{-1}	1000 seed weight(g)	Seed yield plant^{-1}
Block unadjusted	103	128.49 **	28.26 ns	780229.5 **	9.83 **	1.04 ns	25.36 **	9.34 **	0.69 **	0.82 **	6.13 **
treatment unadjusted	4	244.65 **	194.61 ns	1357059.01 **	11.07 *	3.95 ns	26.75 *	11.06 **	0.27 *	3.48 **	8.18 **
Block adjusted	4	16.78 ns	683.94 ns	6.26 ns	18.45 **	18.46 ns	45.04 **	0.08 ns	0.76 **	0.17 ns	0.88 **
Treatment (adjusted)	103	119.64 **	47.26 ns	727528.42 **	10.12 **	1.6 ns	26.07 **	8.91 **	0.7 **	0.69 **	5.85 **
Control	3	58.13 **	382.53 ns	16.13 ns	29.7 **	21.56 ns	75.38 **	0.54 ns	0.65 **	0.22 ns	0.41 *
Augmented	99	131.65 **	17.36 ns	808957.95 **	8.68 *	0.28 ns	23.41 **	9.7 **	0.66 **	0.85 **	5.98 **
test vs Augmented	1	26.93 ns	44.18 ns	276753.48 **	64.56 **	14.03 ns	68.68 **	0.41 ns	3.55 **	0.0035 ns	38.7 **
Test+Test vs Augmented	100	121.48 **	37.2 ns	749353.79 **	9.53 *	1 ns	24.59 **	9.17 **	0.71 **	0.71 **	6.01 **
Residuals	12	8.68	548.43	9.41	2.77	23.27	6.34	0.21	0.08	0.12	0.08

**= Significant at 5% = P=0.05, **= Significant at 1% = P=0.01*

Table 2. Comparison of critical difference for all traits of linseed germplasm

Comparison	No. of capsules plant^{-1}	Days to maturity	50% flowering	Oil content (%)	Primary branches plant^{-1}	Plant height(cm)	Secondary branches plant^{-1}	No. of seeds capsule^{-1}	1000 seed weight(g)	Seed yield plant^{-1}
A Test Treatment and a Control Treatment	7.86	62.49	8.19	4.44	12.87	6.72	1.21	0.74	0.94	0.78
Control Treatment Means	4.06	32.27	4.23	2.29	6.65	3.47	0.62	0.38	0.49	0.4
Two Test Treatments (Different Blocks)	10.15	80.68	10.57	5.73	16.62	8.68	1.56	0.96	1.22	1
Two Test Treatments (Same Block)	9.08	72.16	9.45	5.12	14.87	7.76	1.4	0.86	1.09	0.9

Table 3. Comparison of standard errors for all traits of linseed germplasm

Comparison	No. of capsules plant^{-1}	Days to maturity	50% flowering	Oil content(%)	Primary branches plant^{-1}	Plant height(cm)	Secondary branches plant^{-1}	No. of seeds capsule^{-1}	1000 seed weight(g)	Seed yield plant^{-1}
A Test Treatment and a Control Treatment	3.61	28.68	3.76	2.04	5.91	3.08	0.56	0.34	0.43	0.36
Control Treatment Means	1.86	14.81	1.94	1.05	3.05	1.59	0.29	0.18	0.22	0.18
Two Test Treatments (Different Blocks)	4.66	37.03	4.85	2.63	7.63	3.98	0.72	0.44	0.56	0.46
Two Test Treatments (Same Block)	4.17	33.12	4.34	2.35	6.82	3.56	0.64	0.39	0.5	0.41

Table 4. Genetic variability analysis for different characters of linseed germplasm

Trait	Mean	GCV	PCV	hBS	GAM
50% flowering	189.47	74.70	74.70	94.35	97.30
Days to maturity	111.59	3.12	3.73	81.74	82.46
Plant height(cm)	37.73	10.95	12.82	72.90	19.28
primary branches plant^{-1}	2.25	22.12	23.73	83.74	9.24
secondary branches plant^{-1}	6.16	50.01	50.55	97.88	102.07
No. of capsules plant^{-1}	22.44	49.41	51.13	93.41	98.53
No. of seeds capsule^{-1}	7.55	10.09	10.75	88.23	19.56
1000 seed weight(g)	6.21	13.71	14.84	85.35	26.13
Seed yield plant^{-1}	5.27	46.10	46.43	98.58	94.42
Oil content (%)	36.54	6.65	8.06	68.13	11.33

Table 5. HSD Tukey's method applies for all population mean comparisons for seed yield plant^{-1}(g)

Treatment	Adjusted Means	Group
EC-718840	0.762	1
CANADA	0.989	12
SJKO-6	1.066	123
LCK-9319	1.066	123
CI-1413	1.106	123
LCK-9325	1.106	123
S-203	1.366	1234
NL-126	1.458	12345
S-91-43	1.613	123456
BAU-9906	1.622	1234567
NDL-8809	1.752	12345678
BAU-08-07	1.780	12345678
GS-128	1.812	12345678
LC-2057	1.927	123456789
EC-4752	1.963	123456789
RJK-32	2.136	1234567890
LCK-9119	2.257	1234567890AB
LCK-9324	2.257	1234567890AB
RR-464	2.383	1234567890A
Raisa	2.389	1234567890AB
RLC-49	2.441	1234567890A C
A-236	2.599	1234567890ABCD
OL-98-13-9	2.855	1234567890ABCDEF
BAU-06-8	2.894	1234567890ABCDEF
Fzox Natural	2.894	1234567890ABCDE G
EX-304-1	2.948	1234567890ABCDEFGH
A-97	3.059	1234567890ABCDEFGHI
RLC-25	3.118	1234567890ABCDEFGHI
A-93	3.312	1234567890ABCDEFGHIJ
RL-910	3.419	234567890ABCDEFGHIJK
Punjab T-4	3.606	34567890ABCDEFGHIJKLM
EI-47-21-42	3.621	34567890ABCDEFGHIJKL N
BS-18	3.660	4567890ABCDEFGHIJKLMNO
OR-8-38	3.778	567890ABCDEFGHIJKLMNO
NPRR-449	3.879	567890ABCDEFGHIJKLMNO
RJK-34	3.888	4567890ABCDEFGHIJKLMNO
NPRR-272	3.925	567890ABCDEFGHIJKLMNO
NPRR-68R	4.061	7890ABCDEFGHIJKLMNOP
NPRR-61	4.127	7890ABCDEFGHIJKLMNOPQ
LC-2014	4.146	67890ABCDEFGHIJKLMNOPQ
NP-138	4.312	890ABCDEFGHIJKLMNOPQR
A-9-2-1	4.445	0ABCDEFGHIJKLMNOPQRS
NP-103	4.485	90ABCDEFGHIJKLMNOPQRS
NP-65	4.617	0ABCDEFGHIJKLMNOPQRST
EC-99056	4.638	0ABCDEFGHIJKLMNOPQRS
BR-26	4.736	ABCDEFGHIJKLMNOPQRSTU
KL-1	4.816	ABCDEFGHIJKLMNOPQRSTUV
NP-39	4.836	B DEFGHIJKLMNOPQRSTUVW
BAULK	5.027	CDEFGHIJKLMNOPQRSTUVWX
A-58	5.234	F HIJKLMNOPQRSTUVWXYZab
NP-30K	5.329	EFGHIJKLMNOPQRSTUVWXYZ cd
CI-1375	5.465	GHIJKLMNOPQRSTUVWXY a c e
B-81-81	5.578	IJKLMNOPQRSTUVWXYZabcdefg
EC-41595	5.753	KLMNOPQRSTUVWXYZabcdef h
JLT-90	5.814	JKLMNOPQRSTUVWXYZabcdefghi
EC-41495	5.894	KLMNOPQRSTUVWXYZabcdefghi
No.10	5.975	NOPQRSTUVWXYZabcdefghi
EC-22529	6.033	M OPQRSTUVWXYZabcdefghij
RKY-17	6.041	LMNOPQRSTUVWXYZabcdefghij

Treatment	Adjusted Means	Group
RLC-153(C4)	6.366	STUVWXYZabcdefghi
EC-1456	6.557	PQRSTUVWXYZabcdefghijklm
L-470-Eng	6.579	PQRSTUVWXYZabcdefghijklm
KANPUR-40/2	6.676	QRSTUVWXYZabcdefghijklm
EC-1453	6.677	QRSTUVWXYZabcdefghijklm
RLC-148(varsha alsi) (C3)	6.726	VWXYZabcdefghij
Kiran(C2)	6.770	WXYZabcdefghijk
Dingoahi	6.774	RSTUVWXYZabcdefghijklm
EC-1391	6.783	RSTUVWXYZabcdefghijklm
NL-97	6.852	RSTUVWXYZabcdefghijklm
L-106	6.868	RSTUVWXYZabcdefghijklm
CP-43	6.874	RSTUVWXYZabcdefghijklm
LCK-8605	6.891	RSTUVWXYZabcdefghijklm
Neelum (C1)	7.064	YZabcdefghijkl
L.S.-1	7.084	TUVWXYZabcdefghijklm
L-103	7.317	UVWXYZabcdefghijklm
NP-HYB-8	7.473	XYZabcdefghijklm
A-389B	7.473	XYZabcdefghijklm
LCK-9303	7.662	YZabcdefghijklm
A-195	7.729	ab efghijklm
65/12	7.734	YZabcdefghijklm
L-88-LHCK-7	7.742	YZabcdefghijklm
KFS-11	7.775	YZabcdefghijklm
R.S.-6	7.798	Z b d fghijklm
A-469B	7.822	YZabcdefghijklm
CI-1971	7.846	cdefghijklm
AYOGI	7.892	cdefghijklm
A-301	7.937	efghijklm
KL-230	7.948	hijklm
PKDL-55	7.948	hijklm
ILS-169	8.105	g ijklm
IC-AR-6	8.126	g ijklm
A-153	8.208	hijklm
EC-1393-1	8.248	hijklm
SJKO-8	8.566	jklm
LCK-9406	8.692	klm
SJKO-13	8.706	klm
EC-41770	8.738	lm
KLS-A-3	8.751	lm
RLC-40	8.855	lm
KLS-B-2	8.976	lm
EC-397752	8.981	lm
R.S.-2	9.000	lm
Sumerpur Local	9.003	m
RSJ-31	9.045	m

plant^{-1}, no. of seeds capsule$^{-1,}$ and 1000 seed weight (g) suggesting that some portion of variability was governed by environmental factors. Heritability values are categorized according to Robinson (1966) as low (50%), medium (50-70%), and high (>70%). Characters with high heritability are much less affected by the environment and hence higher probability of being transferred from parents to progeny (Table 4). These results confirm the findings of S Paul et al. [13], [14] and Mahto and Mahto [15].

High heritability was demonstrated by all the quantitative characters taken under study, however, maximum heritability was reported from 50% flowering, followed by days to maturity, primary branches plant^{-1}, secondary branches plant^{-1}, no. of capsules plant^{-1}, no. of seeds capsules^{-1}, 1000 seed weight(g), seed yield plant^{-1}and oil content (%). Highest heritability coupled with highest genetic advance as percent was reported for 50% flowering, followed by secondary branches plant^{-1}, no. of capsules plant^{-1}, 1000 seed weight (g), and seed yield plant^{-1} indicating that these traits are less influenced by environment and they are governed by additive gene action where simple selection is effective. High heritability coupled

with medium genetic advance as percent was reported for plant height (cm), no. of seeds capsule$^{-1,}$ and oil content (%) indicating that these traits are less influenced by environment and are governed by additive and non-additive gene action where selection is effective and heterosis breeding. High heritability coupled with low genetic advance as percent was reported for primary branches plant^{-1} indicating that these traits are highly influenced by the environment and are governed by non-additive gene action where selection is ineffective. These results confirm with the findings of Singh et al. [16] for seed yield/plant, Awasthi and Rao [17] for seed yield/plant, Kanwar et al. [18] for seed yield/plant, no. of primary branches, Choudhary et al. [19] for no. of primary branches, seed yield/plant.

4. CONCLUSION

The above-mentioned characters show a high estimate of genetic advance as the percent of the mean is governed by additive genes and selection for them will be rewarded. The linseed accessions used in this study revealed significant variability for most of the traits under study. Amongst, the genotypes studied high coefficients of variation were observed for most of the characters studied indicating the existence of sufficient variability. Out of 100 genotypes studied for various quantitative traits, seven genotypes such as, LCK-9406, NL-126, Sumerpur Local, SJKO-8, L-103, EC-397752, R.S.-6 were found to be having the highest oil content (>42%). The highest seed yield plant^{-1} and also oil content (%) was noticed for four accessions such as Sumerpur Local, EC-397752, LCK-9406, and SJKO-8.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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