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Studies on Genetic Diversity, Correlation and Variability of the Linseed (*Linum usitatissimum* L.) Genotype

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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

The present investigation was carried out to assess the genetic advancement, heritability, genetic variability, correlation coefficient and the genetic divergence analysis in forty-five linseed genotypes for sixteen quantitative characters/traits during Rabi 2023-24 at field experimentation centre, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh by using Randomized Block Design in three replications. Moderate GCV along with For Test weight, capsule size, seed size, number of primary branches/plant, number of secondary branches/plant, and high heritability combined with high genetic advance as a percentage of mean was noted.

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Indicated that most likely the heritability might be due to additive gene effect and selection may be effective in segregating generation for improvement of these traits. Grain yield showed positive significance association with all 16 quantitative characters. Genotype EC-12082 (4.59 g) had maximum grain yield per plant followed by EC-1411CK, EC-990020, EC-10077. When choosing linseed, these traits ought to be prioritized in order to increase yield. According to Mahalanobis D2 analysis five different clusters were created from these genotypes with cluster I as largest cluster having 34 genotypes and rest of the clusters with solitary genotypes. Cluster-I exhibited the highest intra-cluster distance of 13.17 indicating significant variability and diversity within this cluster and the largest inter-cluster IV and III 148.01 followed by cluster-II and cluster- IV 118.46, cluster-IV and cluster-I 104.58. The study found significant genetic variability in 45 linseed genotypes, with traits like number of branches and seed size showing high heritability, suggesting effective selection for yield improvement and Cluster I having the highest intra-cluster variability and significant inter-cluster differences, highlighting its potential for targeted selection.

Keywords: Linseed; genetic variability; correlation; significance; diversity.

1. INTRODUCTION

An annual self-pollinating crop, linseed belongs to the Linaceae family (*Linum usitatissimum* L: 2n=30). It is believed that the genus Linum first appeared in the Middle East or India before spreading to Asia, Europe, and ultimately the New World (Soto-Cerda et al*.,* 2013). It is a great vegetarian source of Alpha-Linolenic Acid (ALA), an Omega 3 essential fatty acid, and has twice as much of it than fish oil. Due to their anti-inflammatory qualities, these important fatty acids can help prevent a range of chronic illnesses, including diabetes, arthritis, and heart disease (S. Sarkar and A. Sarkar, 2017). Linseed, also known as flax, is cultivated in temperate regions globally and is typically planted in India between October's final week and November's first week. For optimal seed germination, temperatures of 25–30°C are preferred, while seed production thrives at 15–20°C. When grown for fiber, the crop requires cooler temperatures (10–19°C) and high humidity levels (76%), and it is sensitive to frost (Singh and Manibhushan, 2018). Because of its high linolenic acid concentration (45–60%), which gives it drying and hardening qualities, the oil is mostly utilized in industrial processes including the manufacturing of printing inks, paints, varnishes, and soaps (Wakjira, 2007).

It is necessary to first evaluate the variability of yield and its component aspects in order to plan an appropriate breeding strategy for genetic improvement. Genetic metrics such as the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) can be used to determine the level of diversity in the germplasm. In order to forecast the outcome of selecting the optimal genotypes for yield and the attributes that contribute to it, heritability in conjunction with high genetic advancement would be a more beneficial tool. It assists in figuring out how the environment affects how a character's genotype and dependability are expressed (Kumar et al., 2015).

Crop diversity allows plant breeders to select suitable parents and analyse the kind and quantity of genetic variation present in the germplasm to produce new and improved cultivars with desired features. (Govindaraj et al., 2015).

Rao (1952) and Murty & Anunachalam (1966) provide Mahalanobis D2 multivariate analysis of quantitative traits-based statistics as a powerful technique. The possibility of successfully choosing desired plant types through efficient breeding and selection processes increases with population variability and diversity. Breeders can find viable candidates with desired qualities by knowing the degree of variability and variation in the genotypes. This enables them generate superior crop varieties that better satisfy the needs of consumers and agriculture. The complex characteristics of seed yield are influenced by both hereditary and environmental factors. India typically produces less linseed than other nations; therefore, breaking through the current yield barrier and creating high-yielding cultivars would be necessary to increase production. The scope of irrigated linseed is greater than that of rainfed linseed. So, variability of different type of genotype on the basis of yield parameter helps to select the suitable quality of genotype in Prayagraj region.

2. MATERIALS AND METHODS

The experiment was carried out in the experimental farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences, Prayagraj (Uttar Pradesh). During the Rabi season of 2023–2024, 43 linseed genotypes and two common check varieties, NEELAM and SHEKHAR, were evaluated using a Randomized Block Design with three replications. The distance between plants is 10 cm, while the distance between rows is 30 cm. Every genotype was cultivated in a single 1.5-meter line. The crop was effectively grown by applying all necessary and advised agronomic techniques. In order to reduce border impacts, five competitive random plants were chosen from each plot and tagged to exclude border plants. Five randomly chosen plants from each plot had their data averaged according to certain characters, and this data was then subjected to a number of statistical tests. Plant height, number of primary and secondary branches, number of capsules per plant, size of capsules, number of seeds per capsule, size of seeds, 1000 seed weight (gm), seed yield per plant (gm), biological yield (gm), number of seeds per plot (gm), number of seeds per ha (Kg), harvest index, and days to first flowering, days to 50% flowering, and days to maturity are the 16 characters for which data was made.

2.1 Statistical Analysis

The recorded data was subjected to an analysis of variance (Panse and Sukhatme, 1985). The variability parameters were determined using the recommendations made by Johnson et al. (1955); Burton and Devane (1953). Genetic divergence using D^2 Statistics (Mahalanobis, 1936).

3. RESULTS AND DISCUSSION

"Studies on Genetic Variability, Correlation and Diversity in Linseed (Linum usitatissimum L.) Genotype" is the title of the investigation. The results of this study supported the findings from the analysis of variance for pooled data, which indicated that there is a large variation in the genotypes for every character under investigation. Significant mean squares owing to seed yield and attributed attributes demonstrated the existence of considerable diversity in the material tested for the improvements of various traits, as shown by Table 1, which also showed that there is a considerable variety among the germplasm. There is a great degree of variability among the genotypes, as evidenced by the analysis of variance for 16 characters, which revealed very significant differences among 45 genotypes for all the traits analysed.

Table 1 shows the characteristics under study, including heritability, genetic advancement, genotypic and phenotypic coefficients of variation (PCV and GCV), expressed as a percentage of mean. Variability is a crucial factor to take into account in every crop improvement program. The assessment of genotypic and phenotypic variation, heritability (h2), phenotypic coefficient of variation (PCV), genotypic advance, and genetic gain for various quantitative variables are used to measure it. For every character (Table 1), the phenotypic coefficient of variation was greater than the genotypic coefficient of variation, suggesting that the environment influences genetic expression. Similar result reported by Mohapatra et al. (2017). These parameters earn attention in selection for enhancement in concerned traits. Both genetic and environmental variation contribute to the observable phenotypic variability. It varies depending on the surroundings. The genotypic variance, ranged from 0.27 to 1079.04. The genotypic variance was highest for Seed yield per ha (Kg) (1079.04) followed by Days to maturity (47.96), Capsules per plant (12.53) and Days to 50% flowering (7.04). The phenotypic variance, ranged from 0.39 to 3661.7. The Seed yield per ha recorded maximum phenotypic variance (1079.04) followed by Days to maturity (52.77), Capsules per plant (40.91) and Days to first flowering (12.12). For the 16 traits under study, the general estimates of heritability varied from 16.66 (seed yield per plot) to 90.886 (days to maturity). elevated heritability (common sense) (≥60%) was recorded for Days to maturity (90.886), Number of primary branches (79.73), Number of secondary branches (77.155), Test weight (72.421), Capsule size (70.123), Seed size (68.895) and Days to 50% flowering (63.64). Moderate heritability (broad sense) (30-60 %) was observed for Seeds per capsule (35.89) and Capsules per plant (30.61) Low heritability (broad sense (≤30) was observed Seed yield per ha (29.468), Plant height (25.967), Harvest Index (21.029), Days to first flowering (21.027), Biological yield (20.957), Seed yield (20.928) and seed yield per plot (16.66) This suggests that non-cumulative gene action governs the features and that environmental factors have a greater influence. These findings were reported by Sharma et al. (2016). Genetic advancement as a percentage of mean ranged from 25.65 (number of major branches) to 1.35 (harvest index). Test weight (25.39), seed size (20.32), and number of primary branches (25.65) all showed high genetic advance as a percentage of mean (≥20). For capsule size (19.80), number of secondary branches (19.53), and days to maturity (12.28), a moderate genetic improvement was noted as a percentage mean (10–20). The remaining characteristics all displayed modest genetic advancement as a percentage of mean (≤10).

Table 2 The results of the genotypic correlation coefficient analysis demonstrated a significant and positive correlation between the amount of grain produced by each plant and the following variables: primary branches (0.544**), secondary branches (0.659**), capsules per plant (0.801**), seeds per capsule (0.437**), biological yield (0.842**), test weight (0.352**), capsule size (0.282**), seed size (0.268*), seed yield per plot (0.458**), seed yield per hectare (0.479**), and Harvest Index (0.221*).similar finding were reported by Savita, S. G. et al.(2011).

The exploration of genetic diversity in the available crop materials holds significant promise for enhancing crop improvement efforts, particularly concerning the characters of interest. A crucial aspect of this endeavour is the accurate estimation of genetic distance. One effective statistical tool for assessing genetic divergence is the Mahalanobis is D^2 Rao's (1952) description of statistics. The Ward method (1963) was utilized to determine the clustering. The formula suggested by Rao (1952) was used to measure the intra- and inter-cluster distances (D2 value). Compute the cluster's average performance for each character as well. It offers insightful information about the varied makeup of the population being studied. The study's conclusions, which are shown below, provide insight into the degree of genetic variety and can be an invaluable manual for upcoming breeding and selection initiatives.

The cluster pattern of 45 different linseed genotypes has been provided in Table 3 based on the performance of several traits. According to Mahalanobis D2 analysis all the 45 genotypes linseed were divided into five groups. This suggested that there was no correlation between genetic diversity and geographic distribution. Of them, cluster I had the most genotypes thirty-four while cluster III had seven, cluster II and cluster V had one, and cluster IV had two. Some previous researchers have discovered different clustering patterns in linseed (Pali & Mehta, 2016 and Patial et al*.,* 2019 and Kasana et al*.* 2018). The genotypes in all five clusters had the greatest values for seed yield per hectare, days to maturity, and capsule per plant, according to Table 5's mean value for each cluster.

Breeders' unidirectional selection pressure during the development program of the promising genotypes may have contributed to the divergence among genotypes within the same group or to different genotypes within the same cluster with different origins (Raina et al*.,* 2015). Cluster distance was divided into two categories: intra-cluster and inter-cluster distances. Table 4 displays the intra- and inter-cluster distances. Intra-cluster distance was highest in Cluster I (13.17), followed by clusters III and IV (11.26 and 7.94), with nil intra-cluster distances for the remaining clusters. The inter-cluster distance between cluster IV and cluster III was the largest at 148.01, followed by cluster IV and cluster I (104.58), cluster III and cluster V (54.88), and cluster V and cluster IV (53.71). The closest distance between clusters was found to be 15.46 between clusters II and III, then 19.09 between clusters I and V, 19.26 between clusters I and II, 31.377 between clusters I and III, and 31.99 between clusters I and III. Kumar and Kumar also reported similar results (2021). Clusters II and III have a close association based on the minimum inter-cluster distance, but clusters III and IV contain genotypes that are less closely related based on the maximum inter-cluster distance. Desirable segregates are probably produced by crossings between the number of clusters separated by a high inter-cluster distance. Pali & Mehta (2016) added that in order to further improve flax seed output and its constituent parts, crossing clusters with high mean values and high inter-cluster distances may aid in the accumulation of desired features.

Table 5 displays the cluster means for 16 characteristics across 45 linseed genotypes. Maximum days to 50% flowering (82.67), plant height (73.47 cm), days to first flowering (73.01), number of primary branches (8.97), number of secondary branches (29.36), number of capsules per plant (95.87), number of seeds per capsule (9.84), seed yield (4.60 gm), biological yield (10.58 g), test weight (5.61 gm), size of capsule (9.59 mm), seed size (5.84 mm), seed yield per plot (91.93 gm), seed yield per ha (1021.48 kg), Harvest Index (44.70), and number of days to maturity (118.33 days) were all recorded by Cluster IV. The variety observed in the

Table 1. Estimation of genetic parameters for 16 quantitative characters in linseed

Sl. No.	Genetic Parameters	Grand mean	Range	GCV	PCV	Heritability (%)	GA	GAM
1	Days to 50% flowering	77	71-83	3.42	4.29	63.641	4.36	5.62
2	Days to maturity	110	92-118	6.25	6.56	90.886	13.60	12.28
3	Plant height (cm)	67.41	62.52-75.97	2.37	4.66	25.967	1.68	2.49
4	Days to first flowering	69	64-75	2.28	4.98	21.027	1.51	2.16
5	Primary branches	5.7	4.74-9.2	13.94	15.62	79.733	1.46	25.65
6	Secondary branches	20.4	17.07-31.37	10.79	12.29	77.155	3.98	19.53
7	Capsules per plant	79.59	73.73-97.27	4.45	8.04	30.619	4.03	5.07
8	Seeds per capsule	8.39	6.73-9.87	4.65	7.76	35.894	0.48	5.74
9	Seed yield (g)	3.82	3.6-4.61	3.45	7.55	20.928	0.12	3.25
10	Biological yield (g)	9.01	8.49-10.88	3.34	7.30	20.957	0.28	3.15
11	Test weight (g)	3.85	3.07-5.7	14.48	17.02	72.421	0.98	25.39
12	Capsule size(mm)	7.24	6-9.84	11.48	13.71	70.123	1.43	19.80
13	Seed size(mm)	4.34	3.34-6	11.89	14.32	68.895	0.88	20.32
14	Seed yield per plot (gm)	76.3	72-92.1	3.18	7.80	16.66	2.04	2.68
15	Seed yield per ha (Kg)	847.47	800-1023.7	3.88	7.14	29.468	3.73	4.33
16	Harvest Index (%)	42.54	40.57-44.74	1.43	3.12	21.029	0.57	1.35

Note: GCV- Genetic Co-efficient of Variance; PCV- Phenotypic Co-efficient of Variance; GA- Genetic Advance; GAM- Genetic Advance Mean

Table. 2. Correlation coefficient between yield and its attributing traits in 45 linseed genotypes at genotypic level

	Days to 50% flowering	Days to maturity	Plant height (cm)	Days to first flowering	Primary branches	Secondary branches	Capuslesper plant	Seeds per capsule	Biological yield (g)	Test weight (g)	Capsule size (mm)	Seed size (mm)	Seed yield per plot (gm)	Seed yield Per hectare (Kg)	Harvest Index (%)	Seed yield(g)
Days to 50% Flowering	1	0.1051	0.0856	0.727**	0.271*	0.316**	0.335**	0.278*	0.315**	0.239*	0.1295	0.1058	0.285**	0.325**	0.0417	0.339**
Days to Maturity		1	0.0715	0.0518	0.170*	0.1472	0.0747	0.211*	0.0688	-0.1091	0.1425	0.182*	0.1173	0.1294	0.149	0.1212
Plant height (cm)			1	0.0209	0.349**	0.390**	0.298**	0.1671	0.347**	0.173*	0.254*	0.198*	0.275*	0.341**	-0.0969	0.238*
Days to first Flowering				1	0.1662	0.1619	0.190*	0.1534	0.198*	0.1179	0.0894	0.0718	0.222*	0.181*	0.0063	0.200*
Primary Branches					1	0.748**	0.519**	0.456**	0.497**	0.454**	0.424**	0.425**	0.508**	0.538**	0.276*	0.544**
Secondary Branches						1	0.660**	0.425**	0.636**	0.494**	0.414**	0.436**	0.544**	0.621**	0.335**	0.659**
Capsules per Plant							1	0.442**	0.793**	0.339**	0.223*	0.212*	0.484**	0.493**	0.1072	0.801**
Seeds per Capsule								1	0.404**	0.264*	0.307**	0.324**	0.393**	0.382**	0.255*	0.437**
Biological yield (g)									1	0.326**	0.225*	0.1654	0.473**	0.480**	0.0428	0.842**
Test weight (g)										1	0.283**	0.332**	0.341**	0.359**	0.269*	0.352**
Capsule size(mm)											1	0.474**	0.299**	0.369**	0.286**	0.282**
Seed size(mm)												1	0.331**	0.341**	0.349**	0.268*

	Days to 50% flowering	Days to maturity	Plant height (cm)	Days to first flowering	Primary branches	Secondary branches	Capuslesper plant	Seeds per capsule	Biological yield (g)	Test weight (g)	Capsule size (mm)	Seed size (mm)	Seed yield per plot (gm)	Seed yield Per hectare (Kg)	Harvest Index (%)	Seed yield(g)
Seed yield per plot (gm)													1	0.482**	0.274*	0.458**
Seed yield per Hectare (Kg)														1	0.231*	0.479**
Harvest Index (%)															1	0.221*
Seed yield (g)																1

*Note: *Significant at 5% level, **Significant at 1% level*

Table 3. Clustering pattern among 45 genotypes of linseed for various yield and yield related traits

Cluster Group	Number of Genotypes	List of Genotypes
Cluster-I	34	A-181(175)(SGB-13), A-195(178)(SGB-14), NP-RR-191, A-196(179)(SGB-15), A-199(181)(SGB-16), A-76(115)(SGB-12), NP-RR-328, A-70(110)(SGB-9), EC-41528, NP-RR-10, A-72(112)(SGB-11), A-202B(183)(SGB-17), EC-589, A-238(196)(SGB-20), A-24-1-2(86)(SGB-4) and A-362(203)(SGB-21), EC-990020, EC-10077, A-370(209)(SGB-22), NP-RR-207, A-203B(184)(SGB-18), NP-23K, A-491(51)(SGB-24), SGB-1(DEEGAL), A-60-(100)(SGB-8), A-39(80)(SGB-5), A-51(SGB-7), NP-22,A-40(89)(SGB-6), NEELAM(FILLER), A-203(185)(SGB-19), EC-41665, EC-1411CK and IC-1 5866
Cluster-II	1	A-71(111) (SGB-10)
Cluster-III	7	EC-1 04265, A-4-1-(74) (SGB-2), EC-571, EC-5328, A-12-1-12(80) (SGB-3), EC-990017 and A-459(265) (SGB-23)
Cluster-IV	2	EC-12082 and SHEKHAR(NC)
Cluster-V	1	NEELAM(C)

Table 4. Cluster distances among five clusters in forty-five genotypes of Linseed

Cluster Distances					
Clusters	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**
Cluster 1	13.17	19.26	31.99	104.58	19.09
Cluster 2	19.26	0.00	15.46	118.46	31.37
Cluster 3	31.99	15.46	11.26	148.01	54.88
Cluster 4	104.58	118.46	148.01	7.94	53.71
Cluster 5	19.09	31.37	54.88	53.71	0.00

Table 5. Cluster means among five clusters in forty-five genotypes of Linseed

	Days to 50% flowering	Days to maturity	Plant height (cm)	Days to first flowering	Primary branches	Secondary branches	Capusles per plant	Seeds per capsule
Cluster 1	77.13	113.13	67.10	69.64	5.55	19.91	78.45	8.33
Cluster 2	81.00	107.00	67.17	72.34	5.34	20.67	78.47	8.20
Cluster 3	77.00	97.76	67.00	69.77	5.45	19.78	79.79	8.25
Cluster 4	82.67	115.17	73.47	73.01	8.97	29.36	95.87	9.84
Cluster 5	80.67	118.33	69.17	72.67	6.34	23.27	85.27	8.67

	Seed yield (g)	Biological yield (g)	Test weight (g)	Capsule size(mm)	Seed size(mm)	Seed yield per plot (gm)	Seed yield per ha (Kg)	Harvest Index (%)
Cluster 1	3.77	8.90	3.75	7.13	4.31	75.33	836.95	42.51
Cluster 2	3.90	9.14	3.81	6.01	3.34	77.86	865.18	42.84
Cluster 3	3.77	8.96	3.86	7.16	4.15	75.24	835.98	42.14
Cluster 4	4.60	10.58	5.61	9.59	5.84	91.93	1021.48	44.70
Cluster 5	4.15	9.94	3.74	8.00	4.50	82.80	920.00	41.64

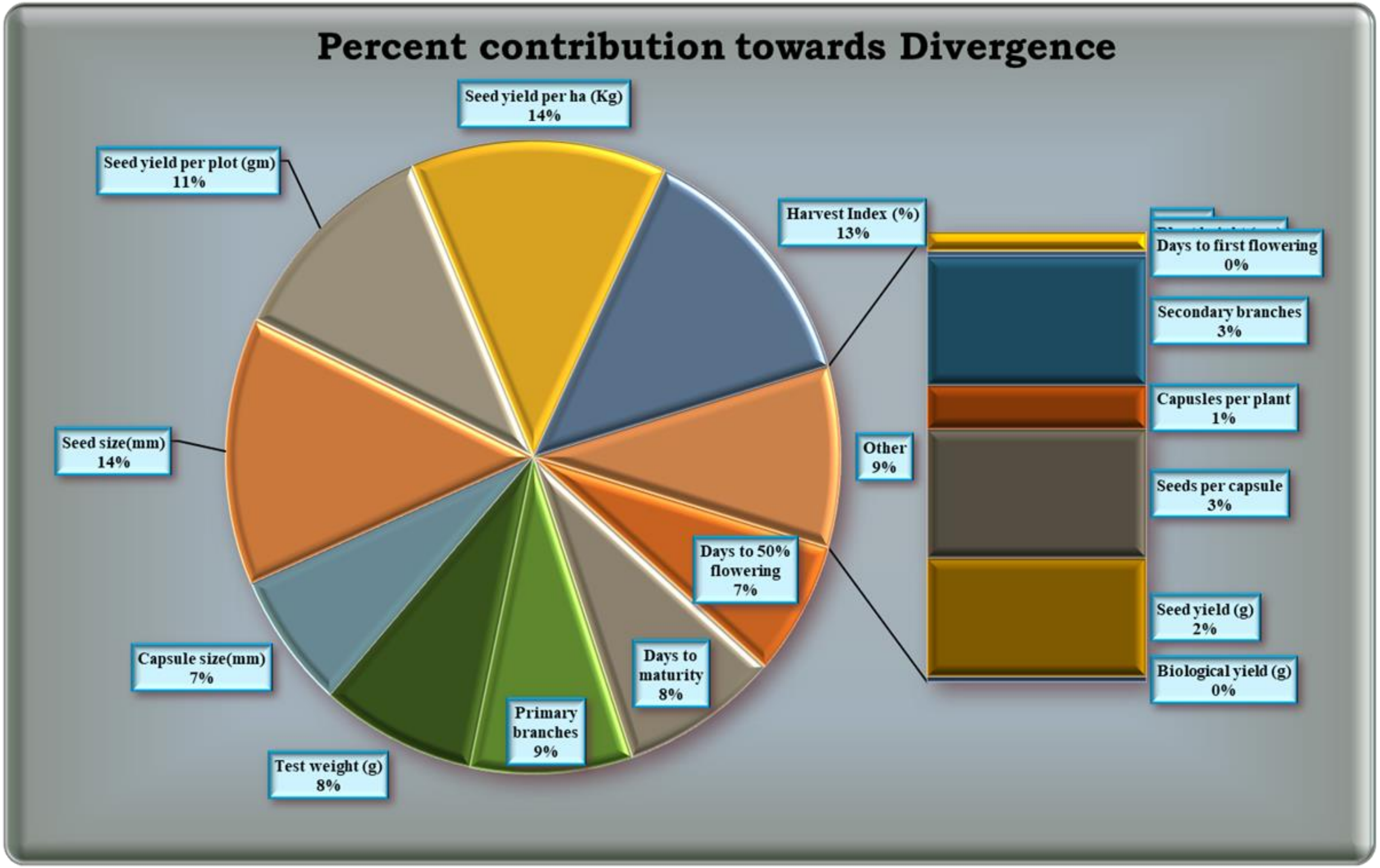

Fig. 1. Percent contribution of various traits among forty-five genotypes of Linseed

EC-12082

EC-1411CK

EC-990020

EC-10077

EC-41665

Fig. 2. Shows image of five best genotype for quantitative characters

germplasm is further supported by a significant degree of variation within cluster averages for numerous metrics. Similar findings were reported by Patial et al. (2019), Kaur et al. (2018), Kumar et al. (2018), and Nizar and Mulani (2015).

Fig. 1 displays the various characters' contributions to the overall divergence. Seed size (14 percent), followed by seed yield per ha (14 percent), harvest index (13 percent), seed yield per plot (11 percent), number of primary branches (9 percent), days to maturity (8 percent), test weight (8%), capsule size (7%), days to 50% flowering (7%), number of secondary branches (3 percent), seeds per capsule (3%), seed yield (2%), capsules per plant (1 percent), plant height (0.40 percent), days to first flowering (0.10 percent), and biological yield (0.10 percent) were the factors that contributed the most to divergence, with their corresponding times ranked first. Similar results were previously published by Kumar and Kumar (2021) and Nizar and Mulani (2015).

4. CONCLUSION

In the current investigation, notable differences were noted for every character. The current study's findings indicate that EC-12082 (4.59 g) had the highest recorded seed yield per plant, while EC-1411CK, EC-990020, and EC-10077 had the highest grain yield per plant. Additionally, EC-12082, EC-41665, and EC-990020 had the highest harvest index. Moderate PCV and GCV were observed for test weight, number of main branches, seed size, and capsule size. Days to 50% flowering, Plant height, Days to first flowering, primary branches, secondary branches, Capsules per plant, Number of seeds per capsule, Biological yield, Test weight, Capsule size, Seed size, Seed yield per plot, Seed yield per ha, and Harvest Index were all positively correlated with grain yield. According to Genetic divergence analysis cluster IV and III have highest inter-Cluster distance. Lastly, the contribution of Seed size (14%) and Seed yield per hectare (14%) is highest for genetic divergence.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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