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Assessment of Genetic Diversity in Linseed (*Linum usitatissimum* L.) Genotype Using D^2 Statistics

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Abstract

The present investigation was carried out to assess the genetic divergence analysis in forty-five linseed genotypes for sixteen quantitative characters 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. The mean sum of square due to genotypes showed significant differences for all the characters under study at 1% and 5% level of significance. According to Mahalanobis D^2 analysis these genotypes were classified into five distinct clusters with cluster I as largest cluster having 34 genotypes, followed by cluster III having 7 genotypes, cluster II having 2 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) highlighting substantial dissimilarity between these clusters suggesting its superiority in yield-related traits such genotypes could be hybridized and used to develop superior hybrids.

Key words : Linseed, Cluster, Genetic Diversity, D^2, Cluster Distance.

Linseed is an annual self- pollinated crop that is a member of Linaceae family (*Linum usitatissimum* L: 2n=30). Linum genus originated either in the Middle East or Indian regions and spread throughout Asia and Europe, and later into the New World (Soto-Cerda et al., 2013). *Linum usitatissimum* is only economically significant species of the family with semi dehiscent capsules type (Savita et al, 2011).Linseed (Flax) is a crop that is often grown in temperate regions around the world and is sown from the final week of October to the first week of November in India. The ideal temperature for seed germination is 25-30°C, and the ideal temperature for seed production is 15–20°C. However, a crop grown for fibre needs a lower temperature (10-19°C) and a high level of humidity (76%), and it is vulnerable to frost (Singh and Manibhushan, 2018).The oil has drying and hardening properties that emanate from the high linolenic acid (45-60%) content, and therefore it is mostly used for industrial purposes such as manufacturing of paints, varnishes, soaps, and printing inks (Wakjira 2007). The characterization and quantification of genetic diversity have been important objectives in evolutionary biology and genetic improvement initiatives. Genetic diversity is the key pillar of biodiversity and diversity within species, between species, and of ecosystems. Crop Diversity provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics by selecting suitable parents and analyzing the nature and magnitude of genetic variation present in the germplasm (Govindaraj *et al.*, 2015). The Complicated traits of seed yield is greatly impacted by both genetic and environmental variables. Since India's average linseed output is lower than that of other nations, there is a need to raise productivity by breaking through the current yield barrier and creating high yielding cultivars. The scope of irrigated linseed is greater than that of rainfed

linseed. Genetic diversity research helps choose parents for hybridisation in crop enhancement programs. Diverse parents are expected to provide increased hybrid vigour and variety in segregating populations based on overall fitness criteria.Measure the degree of divergence among group genotypes based on several traits and select efficient parents for hybridisation in outbreeding and self-pollinated crops. Mahalanobis D^2 statistics based on multivariate analysis of quantitative traits which is a powerful tool (Rao, 1952; Murty and Anunachalam, 1966).

Materials and Methods

Experiment conducted in the experimental farm of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology andSciences, Prayagraj (Uttar Pradesh). In the Rabi season of 2023-24, 43 linseed genotypes and two standard check varieties NEELAM and SHEKHAR were evaluated using Randomized Block Design with three replications. Genotypes were sown in 121.5 Net area. The crop was raised successfully by using all recommended and required agronomic practices. For the observations, five competitive random plants were selected from each plot and tagged excluding border plants to minimize border effects. Average mean was calculated of the data from five selected plants from each plot in respect of different characters and was subjected for various statistical analyses. Data was recorded for the 16 characters that is Plant height, Days to First Flowering, Days of 50% Flowering, Days to maturity, Number of Primary Branches, Number of Secondary Branches, Number of Capsule $Plant^{-1}$, Capsule size, Number of Seed $Capsule^{-1}$, Seed size, 1000 Seed weight (gm), Seed yield $Plant^{-1}$ (gm), Biological yield (gm), Seed yield $plot^{-1}$ (gm), Seed yield ha^{-1} (Kg), Harvest Index.

Result and Discussion

The investigation entitled "Genetic diversity (D^2) analysis in linseed (*Linum usitatissimum* L.) Germplasm."Outcomes from this study conformation on conclusions by the study of analysis of variance 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

Table 1. Experimental Material

Directorate of Research, Sam Higginbottom University of Agricultural Technology and Sciences, Prayagraj, Uttar Pradesh.

SGB-1(DEEGAL)	EC-104265	A-39(80)(SGB-5)	A-199(181)(SGB-16)
EC-571	IC-15866	A-40(89)(SGB-6)	A-202B(183)(SGB-17)
EC-589	NP-RR-10	A-51(SGB-7)	A-203B(184)(SGB-18)
EC-1411CK	NP-22	A-60-(100)(SGB-8)	A-203(185)(SGB-19)
EC-10077	NP-23K	A-70(110)(SGB-9)	A-238(196)(SGB-20)
EC-12082	NP-RR-191	A-71(111)(SGB-10)	A-362(203)(SGB-21)
EC-41528	NP-RR-207	A-72(112)(SGB-11)	A-370(209)(SGB-22)
EC-41665	NP-RR-328	NEELAM(C)	A-459(265)(SGB-23)
EC-5328	A-4-1-(74)(SGB-2)	A-76(115)(SGB-12)	A-491(51)(SGB-24)
SHEKHAR(NC)	A-12-1-12(80)(SGB-3)	A-181(175)(SGB-13)	
EC-990017	NEELAM(FILLER)	A-195(178)(SGB-14)	
EC-990020	A-24-1-2(86)(SGB-4)	A-196(179)(SGB-15)	

Table 1. Analysis of Variance for different characterisitics in Linseed

Source	Mean Sum of Squares (MSS)		
	Replication (df=2)	Genotype (df=44)	Error (df=88)
Days to 50% flowering	5.1190	25.13**	4.02
Days to maturity	0.0520	148.695**	4.809
Plant height (cm)	7.0650	14.963**	7.291
Days to first flowering	19.1320	17.21**	9.568
Primary branches	0.3230	2.056**	0.161
Secondary branches	2.8710	15.982**	1.436
Capusles per plant	42.7180	65.954**	28.38
Seedsper capsule	0.6220	0.729**	0.272
Seed yield (g)	0.130	0.118*	0.066
Biological yield (g)	0.6790	0.614*	0.342
Test weight (g)	0.2340	1.052**	0.118
Capsule size(mm)	0.6370	2.367**	0.294
Seed size(mm)	0.080	0.917**	0.12
Seed yield per plot (gm)	51.1370	47.13*	29.461
Seed yield per ha (Kg)	4272.77	5819.85**	2582.74
Harvest Index (%)	2.7870	2.496**	1.387

*Significant at 5 percent level of significance

the improvements of various traits. The analysis of variance for 16 character Table 1 showed highly significant differences among 45 genotypes for all the characters observed, indicating the presence of considerable amount of variability among the genotypes.

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 statisticsas described by Rao (1952). The clustering was determined byWard method (1963). The intra and inter cluster distances (D^2 value) were estimated by formula as proposed by Rao (1952). Also calculatethe mean performance of the cluster for different characters. which provides valuable insights into the diverse nature of the population under study. The findings of the study, presented below, shed light on the extent of genetic variation and can serve as a valuable guide for future breeding and selection programs.

The cluster pattern of 45 different linseed genotypes has been provided in Table 2 and Fig. 1 based on the performance of several traits. According to Mahalanobis D^2 analysis all the 45 genotypes linseed were divided into five groups. This indicated that therewas no parallelism between geographical distribution and genetic diversity. Among them cluster-I had the highest number of 34 genotypes, cluster III had 7 genotypes, cluster-II and cluster-V had 1 genotypes and cluster IV had 2 genotypes. Different clustering patterns were also reported in linseed by some earlier workers (Pali and Mehta, 2017 and Patial *et al*., 2019 and Kasana *et al*. 2018). Mean value for each cluster Table 4 revealed that genotypes in all fivecluster had highest values for seed yield^{-1} hectare followed by days to maturity and capsule-1plant. Cluster analysis revealed wide range of geneticdivergence, which is useful for future hybridization breedingprogramme for getting desirable transgressive segregants.

The divergence among the genotypes belonging to the same group might be the diverse grouping of genotypes in same cluster with different origins might be due to unidirectional selection pressure practiced by the breeders during the development programme of the promising genotypes (Raina et al. 2015). Cluster distance was further classified into intra and inter cluster distances. The Table 3and despite in fig 2represents intra and inter cluster distances. The maximum intra cluster distance in cluster I (13.17) followed by cluster-III (11.26), cluster-IV (7.94) and rest of them had intra-cluster distance of zero. The maximum inter cluster distance was observed between cluster IV

and III (148.01) followed by cluster-II and cluster-IV (118.46), cluster-IV and cluster-I (104.58), cluster-III and cluster-V (54.88), cluster-V and cluster-IV (53.71). While the minimum inter cluster distance was observed between cluster II and cluster-III (15.46) followed by cluster-I and cluster-V (19.09), cluster-II and cluster-I (19.26), cluster-II and cluster-V (31.37) and cluster-I and cluster-III (31.99). Similar findings were also reported byKumar and Kumar (2021).The maximum inter cluster distance indicated that genotypes of cluster III and IV are not so closely related whereas the minimum inter cluster distance indicated that the genotypes of cluster II and III are closely related.The crosses between the number of clusters separated by high inter cluster distance are likely throw desirable segregates Pali and Mehta (2017) also suggested the crossing between those clusters with high mean value and high inter cluster distance would help to accumulate favourable and desirable alleles for further improvement in seed yield and its components in flax.

The cluster means for 16 characters among 45 linseed genotypes are presented in the Table 4 Cluster IV recorded 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), Capsules per plant (95.87), Seeds per capsule (9.84), Seed yield (4.60 gm), Biological yield (10.58 g), Test weight (5.61 gm), Capsule size (9.59 mm), Seed size (5.84 mm), Seed yield plot^{-1} (91.93 gm), Seed yield per ha (1021.48 kg) and Harvest Index (44.70) and Cluster-V recorded maximum Days to maturity (118.33 days)The diversity present in the germplasm is also supported by an appreciable amount of variation among cluster means for different

Table 2. Clustering pattern among 45 genotypes of linseed for various yield and yield related traits

Cluster group	No. 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 3. Cluster distances among five clusters in forty-five genotypes of Linseed

Cluster Distances	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

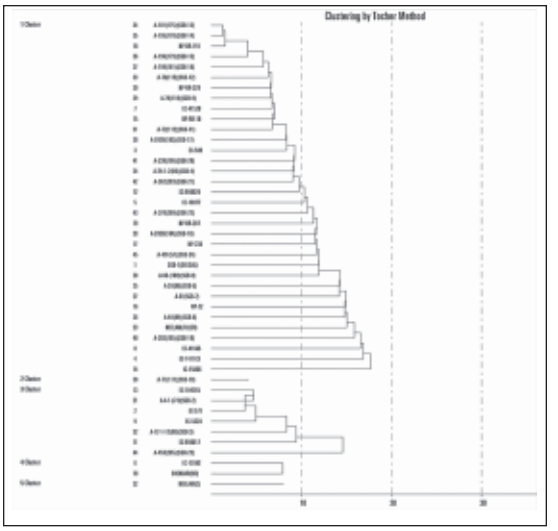

Fig. 1. Dendrogram representing clustering pattern among forty-five genotypes of Linseed.

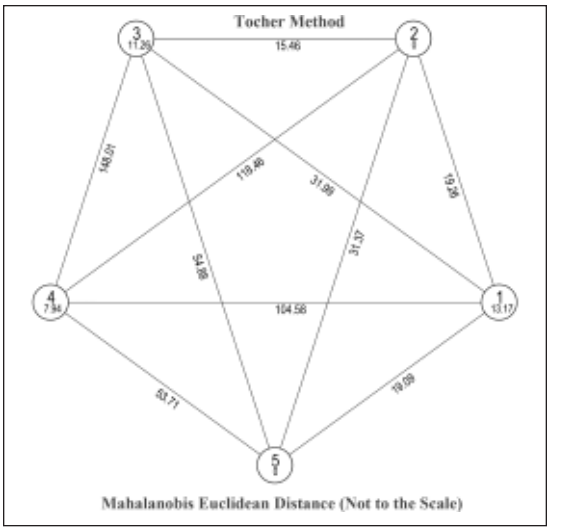

Fig. 2. Diagram represent the inter and intra cluster distance among five cluster.

traits. Diversity among the linseed germplasm was also reported earlier by Nizar and Mulani (2015), Kumar *et al*. (2018), Kaur *et al*. (2018) and Patial *et al*. (2019).

The contribution of different characters towards total divergence are presented in Table 5and depicted in Fig. 3 The highest contribution towards divergence with its respective times ranked first were reported for Seed size (13.64%) followed by Seed yield per ha (13.50%), Harvest Index (13.34%), Seed yield per plot (11.43%), Number of primary branches

Table 4. 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 plant^{-1}**	**Seeds capsule^{-1}**
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 plot^{-1} (gm)**	**Seed yield ha^{-1} (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

Table 5. Percent contribution of various traits among forty-five genotypes of Linseed

Source	Contribution %	Times ranked 1st
Days to 50% flowering	6.87	68.70
Days to maturity	8.32	83.20
Plant height (cm)	0.40	4.00
Days to first flowering	0.10	1.00
Primary branches	8.50	85.00
Secondary branches	2.65	26.50
Capsules per plant	0.91	9.10
Seeds per capsule	2.63	26.30
Seed yield (g)	2.44	24.40
Biological yield (g)	0.10	1.00
Test weight (g)	8.18	81.80
Capsule size(mm)	6.99	69.90
Seed size(mm)	13.64	136.40
Seed yield per plot (gm)	11.43	114.30
Seed yield per ha (Kg)	13.50	135.00
Harvest Index (%)	13.34	133.40

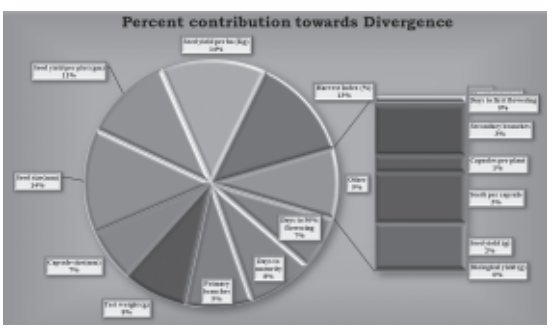

Fig. 3. Percent contribution of various traits among forty-five genotypes of Linseed

(8.50%), Days to maturity (8.32%), Test weight (8.18%), Capsule size (6.99%), Days to 50% flowering (6.87%), Number of secondary branches (2.65%), Seeds per capsule (2.63%), Seed yield (2.44%), Capsules per plant (0.91%), Plant height (0.40%), Days to first flowering (0.10%) and Biological yield (0.10%). Similar findings were also reported by Nizar and Mulani (2015) and Kumar and Kumar (2021).

Conclusion

Significant variation to all the characters were observed in the present study. According to Genetic divergence analysisall the 45 genotypes linseed were divided into five groups. Among them cluster-I had the highest number of 34 genotypes.Cluster IV and III have highest inter-Cluster distance (148.01) and Cluster I have highest intra-cluster distance (13.17). Lastly, the highest contribution towards divergence is of Seed size (13.64 %).

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