Original Research Article

Evaluation of Genetic Diversity in Linseed (*Linum usitatissimum* L.)

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A B S T R A C T

In this experiment sixty linseed genotypes including three checks *viz.* RLC-133, RLC-143 and RLC-148 was evaluated to determine genetic diversity by Mahalanobis D^2 statistics during *rabi* 2022-23 at the Department of Genetics and Plant Breeding, IGKV, Raipur, C.G., India. It revealed that sixty genotypes were grouped into eight clusters. Result envisaged that genotypes grouped within a particular cluster are more or less genetically similar. Maximum inter-cluster distance was observed between cluster 7-8 (516.3), whereas minimum inter-cluster distance was observed between cluster 2-6 (28.35). The highest intra-cluster distances were observed between cluster 3-3 (67), whereas lowest intra-cluster between 2-2, 5-5, 6-6, 7-7 and 8-8. So, it could be suggested that hybridization program involving genotypes from the farthest diverse clusters (Cluster 7 and 8 and cluster 5 and 7) are likely to achieve wider and desirable heterotic recombinants or even transgressive segregants. The highest contribution in divergence was found in seed yield per plant (g), followed by number of capsules per plant and other traits.

Introduction

Linseed or flax (*Linum usitatissimum* L.) is a diploid (2n=30), self pollinated annual plant, having genome size of 368-373 Mb (Ragupathy *et al.,* 2011). It's valued for oilseed and fiber (Lay and Dybing, 1989), and belongs to linaceae family, comprising 14 genera and more than 200 species. Linseed has two origin centers i.e., South West Asia, mainly in India (Vavilov, 1935; Richharia, 1962) and the Mediterranean region of Europe (Darlington, 1963). Later it was introduced into New World (The

Americas) after extensive dissemination throughout Asia and Europe (Soto-Cerda *et al.,* 2013). The Mediterranean area near the Indian subcontinent holds *Linum's* highest biodiversity (Genesar and Morris, 2003; Fu, 2005; Kaur *et al.,* 2017), with Ethiopia as a secondary center (Wakjira, 2004). *L. usitatissimum* is distinct among Linaceae family for its economic importance. Seed yield directly affects crop profitability, while traits increasing oil content enhance value (Tadesse *et al.,* 2009). The cultivated species arise from a single domestication event from *L. bienne* (Allaby *et al.,* 2005). Early domestication

focused on annual growth cycle, reduced capsule shattering, and improved self-fertilization efficiency (Fu, 2011).

In spite of the numerous advantages of linseed, its cultivation is limited in only 195 thousand hectares area in India with the production and productivity level of 130 thousand tonnes and 666 kg per. ha (Ministry of Agriculture, Government of India, 2021-22). In Chhattisgarh, Linseed is cultivated over 11.5 thousand hectare area, with a production of 3.89 thousand tonnes and productivity of 338 kg per. ha (Source- Director's report of annual group meeting of safflower and linseed, 2022). A decreasing trend in the area, production and productivity in linseed was seen in India. So, there is an urgent need to find diverse linseed genotypes to identify donor(s) for different traits and utilizing these genotypes in different breeding programmes.

Genetic diversity is vital for stable linseed yields. The study of genetic diversity plays important role by providing basis in making selection of parents for hybridization programme in crop improvement programme. Linseed varieties with higher genetic diversity are more likely to exhibit stable yields across different growing seasons and varying agro-climatic conditions. It safeguards genetic resources, prevents erosion, supports yield enhancement (Joshi and Dhawan, 1986), resilience, quality, and pest resistance (Nevo *et al.,* 1982). Divergence assessment streamlines breeding line maintenance. Researchers emphasize diverse parents for superior generations (Rama kant *et al.,* 2011; Srivastava *et al.,* 2009; Tyagi *et al.,* 2015). Diversity analysis gauges genetic relationships (Patial *et al.,* 2019). Therefore, in this study genetic divergence on sixty genotypes has been examined using Mahalanobis D^2 statistics to assess the variation for yield and yield component traits in linseed.

Materials and Methods

In this investigation, sixty linseed genotypes from AICRP on Linseed, Raipur Chhattisgarh including three checks namely RLC-133, RLC-143 and RLC-

148 were evaluated for seed yield and its contributing traits in Randomized Block Design with three replications in plots of one row of four metres in length, with a row to row spacing of 30 cm and a plant to plant spacing of 10 cm during *rabi* 2022-23 at Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. To ensure sufficient germination, pre-sowing irrigation was applied. Prior to sowing, the experimental plots were carefully prepared, and Farm Yard Manure (FYM) was incorporated. Linseed cultivation followed the recommended fertilizer and manure application rates. Irrigation was provided as needed, and the trial was regularly weeded. Other necessary cultural practices were performed accordingly. Every accession was consistently monitored during the entire growing season at various growth stages, and any off types traits were removed. The observations were recorded on five randomly selected plants from each line for eleven quantitative characters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, number of seeds per plant, seed length (mm), seed width (mm), 1000 seed weight (g) and seed yield per plant (g).

Genetic diversity was studied following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952) using Windostat 9.30 ver. Tocher's method (Rao, 1952) was followed for grouping the sixty genotypes into different clusters.

Results and Discussion

The D^2 analysis allowed the sixty genotypes of linseed to be identified into eight distinct clusters with the assumption that those within the same cluster having smaller D^2 values among themselves than those belonging to other clusters (Table 1).

Cluster 3 was the biggest cluster consisting of twenty seven genotypes followed by the cluster 1 which was comprised of twenty four genotypes; cluster 4 comprised of four genotypes and cluster 2, cluster 5, cluster 6, cluster 7 and cluster 8 comprised

of only one genotype *viz.*, GP-2336, GP-691, GP-2831, IC-0526071 and IC-0498845, respectively during *rabi* 2022-23.The pattern of distribution of genotypes into various clusters is presented in Table 1.

Maximum inter-cluster distance was observed between cluster 7-8 (516.3), followed by between cluster 5-7 (482.65), cluster 6-7 (404.91), cluster 1-7 (328.79) and cluster 3-5 (296.75), whereas minimum inter-cluster distance was observed between cluster 2-6 (28.35), followed by between cluster 5-6 (38.84), cluster 2-5 (52.59), cluster 6-8 (84.18) and cluster 1-6 (84.57).

The highest intra-cluster distances were observed between cluster 3-3 (67), followed by between cluster 1-1 (52.54) and cluster 4-4 (36.31), whereas lowest intra-cluster between 2-2, 5-5, 6-6, 7-7 and 8-8. Intra (diagonal and bold) and inter-cluster distances among sixty genotypes is presented in Table 2.

The mean performance of all the eleven quantitative traits of eight clusters were studied which revealed that cluster 1 containing 24 genotypes showed maximum cluster mean for number of seeds per plant (339.80). Cluster 2 showed high cluster mean values for number of seeds per plant (448.13), cluster 3 showed high cluster mean for number of seeds per plant (644.21), cluster 4 showed a high mean value for number of seeds per plant (550.73), cluster 5 showed a high mean value for number of seeds per plant (310.07), cluster 6 showed a high mean value for number of seeds per plant (323.8), cluster 7 showed a high mean value for number of seeds per plant (773.87) and cluster 8 showed a high mean value for number of seeds per plant (352.67). Such degree of divergence was found by Sharma *et al.,* (2017); Kasana *et al.,* (2018); Ankit *et al.,* (2019); Terfa and Gurmu (2020) and Patel *et al.,* (2023). Hence, on the basis of divergence analysis the genotypes to be selected for hybridization programme.

The highest contribution in divergence was found in seed yield per plant (g), followed by number of capsules per plant, 1000 seed weight (g), number of primary branches per plant, number of seeds per capsule, number of seeds per plant, seed length (mm), days to 50% flowering, plant height (cm), seed width (mm) and days to maturity.

Table.1 Grouping of linseed genotypes in different clusters during *rabi* 2022-23.

Cluster Group	No. of Genotypes	List of Genotypes
Cluster 1	24	NEELA, RLC-143, IC-0499146, NEELUM, IC-0498872, IC-0525919, IC-0499201, IC-0498517, IC-0544571, R-5044, IC-0498884, IC-613907, R-5043, R-5038, IC-0525940, IC-0118874, IC-0498795, R-5046, IC-0498767, GP-52, GP-2861, IC-0096496, IC-0498706 & IC-0498922
Cluster 2	1	GP-2336
Cluster 3	27	RLC-133, RLC-148, IC-0305055, GP-68, GP-1018, GP-2087, IC-616878, IC-0420772, GP-1108, R-5045, GP-556, GP-829, GP-2191, R-5041, GP-2434, GP-2405, R-5034, IC-0525920, GP-895, EC-0041762, GP-722, GP-2006, IC-0525938, R-5035, IC-0499107, R-5033 & R-5036
Cluster 4	4	IC-0498400, IC-0498729, EC-993391 & IC-0597268
Cluster 5	1	GP-691
Cluster 6	1	GP-2831
Cluster 7	1	IC-0526071
Cluster 8	1	IC-0498845

Table.2 Intra (diagonal and bold) and inter-cluster distances among sixty genotypes for yield and its contributing traits in linseed during *rabi* 2022-23.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
				Cluster Distances				
Cluster 1	**52.54**	88.17	253.11	140.07	101.15	84.57	328.79	179.01
Cluster 2		**0.00**	119.99	144.15	52.59	28.35	252.60	90.07
Cluster 3			**67.00**	128.66	296.75	218.12	117.98	263.44
Cluster 4				**36.31**	281.86	200.44	123.10	286.36
Cluster 5					**0.00**	38.84	482.65	105.76
Cluster 6						**0.00**	404.91	84.18
Cluster 7							**0.00**	516.30
Cluster 8								**0.00**

Table.3 Cluster mean of eight clusters for seed yield and its component traits in linseed during *rabi* 2022-23.

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of capsules per plant	Number of seeds per capsule	Number of seeds per plant	Seed length (mm)	Seed width (mm)	1000 seed weight (g)	Seed yield per plant (g)
Cluster 1	58.14	108.74	49.24	2.91	42.00	8.14	339.80	4.51	2.30	5.83	1.28
Cluster 2	58.33	103.33	51.66	2.60	52.47	8.53	448.13	4.83	2.37	7.19	2.45
Cluster 3	59.00	105.37	48.80	3.96	76.81	8.37	644.21	4.57	2.32	6.04	2.70
Cluster 4	60.33	111.33	49.68	5.00	65.97	8.30	550.73	4.16	2.06	5.49	1.39
Cluster 5	50.00	93.00	51.00	2.00	36.00	8.54	310.07	5.05	2.34	8.91	2.15
Cluster 6	64.00	109.00	55.07	3.20	39.60	8.20	323.80	5.40	2.50	8.05	2.25
Cluster 7	62.00	112.00	47.80	2.87	90.33	8.53	773.87	3.96	2.15	4.59	1.76
Cluster 8	55.00	105.00	42.27	3.60	39.60	8.80	352.67	4.16	1.89	4.54	3.19

Table.4 Contribution of various yield and yield related traits to divergence during *rabi* 2022-23.

S. No.	Characters	Contribution in divergence %	Times ranked first
1	Days to 50% flowering	4.00	66.67
2	Days to maturity	1.00	16.67
3	Plant height (cm)	1.75	29.17
4	Number of primary branches per plant	7.68	128.00
5	Number of capsules per plant	19.00	316.67
6	Number of seeds per capsule	6.00	100.00
7	Number of seeds per plant	5.00	83.83
8	Seed length (mm)	4.04	67.33
9	Seed width (mm)	1.13	18.83
10	1000 seed weight (g)	10.40	173.33
11	Seed yield per plant (g)	40.00	666.67

Fig.1 Dendrogram depicting relationships among the linseed genotype for eleven quantitative traits.
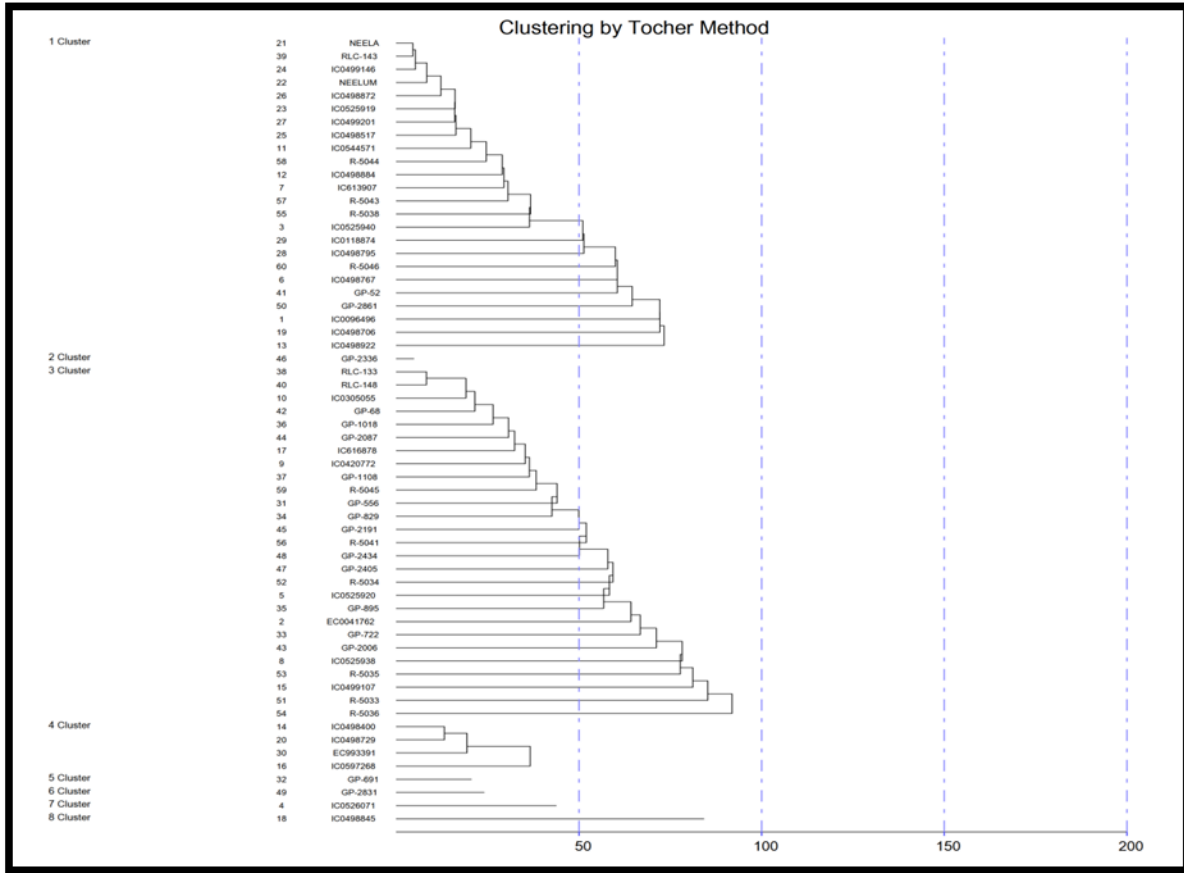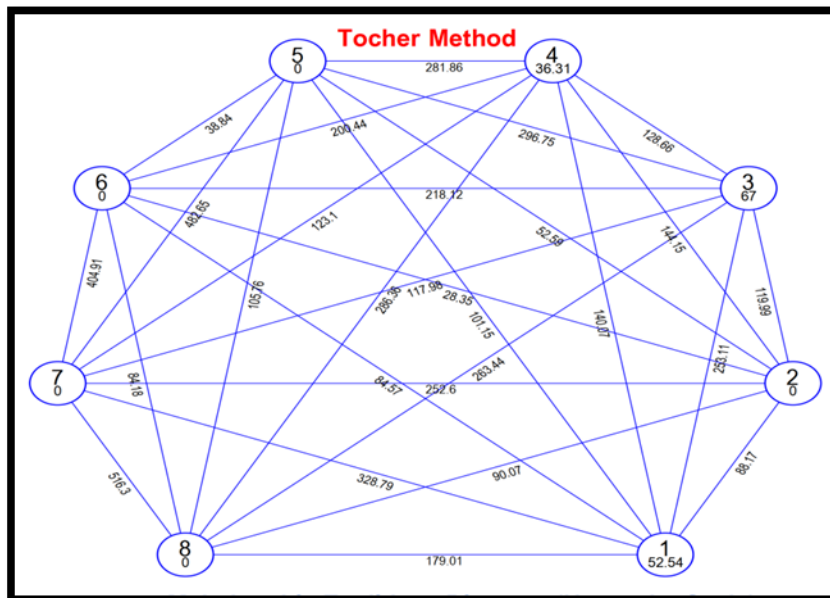

Fig.2 Intra and inter-cluster values of sixty genotypes of linseed during *rabi* 2022-23.

An appreciable extent of genetic divergence was observed among sixty genotypes of linseed. Hybridization between genetically diverse genotypes in linseed to generate promising breeding material has been suggested by Ananda and Murty, (1968).

On the basis of the above analysis it can be concluded that the selection of parental material for hybridization programme must be carried out from the farthermost clusters showing superior mean performance may help in obtaining transgressive segregants or heterotic cross, which may help in flourishing seed yield instead of those based on geographic diversity, which might not be a rewarding exercise for the finding of useful divergent parents.

Greater genetic divergence was found between cluster 7 and 8 followed by cluster 5 and 7 indicating that superior hybrids or recombinants can be realized by mating between the lines of these clusters in a specific fashion. Crossing between germplasms belonging to the same cluster might not be expected to yield desirable segregates. Further research on these selected germplasm will save a lot of time for the breeder in future.

Acknowledgement

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