Study on Genetic Divergence among Linseed (*Linum usitatissimum* L.) Genotypes

Prachi Singh[1]*, Sandhya[2], Manoj Kumar[2], B.K. Patidar[3] and D.L. Yadav[4]
[1]M.Sc. Scholar, Department of Genetics and Plant Breeding,
College of Agriculture, Agriculture University, Kota (Rajasthan), India.
[2]Assistant Professor, Department of Genetics and Plant Breeding,
Agricultural Research Station, Agriculture University, Kota (Rajasthan), India.
[3]Associate Professor, Department of Entomology,
Agricultural Research Station, Agriculture University, Kota (Rajasthan), India.
[4]Assistant Professor, Department of Plant Pathology,
Agricultural Research Station, Agriculture University, Kota (Rajasthan), India.

(Corresponding author: Prachi Singh*)
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ABSTRACT: An experiment was conducted to assess the magnitude of genetic divergence among 33 linseed genotypes including 3 checks using Mahalanobis' D^2 statistics in Randomized Block Design (RBD) at Agriculture Research Station, Ummedganj, Kota during *Rabi* 2023-24. Observations were recorded for 11 characters and based on D^2 statistics, the genotypes were grouped into 8 different clusters using Tocher's method. The results revealed that cluster I had maximum number of genotypes followed by cluster II and cluster VI while other five clusters were mono-genotypic. The highest intra-cluster distance was recorded for cluster VI, followed by cluster II and cluster I while the lowest intra-cluster distances were observed for remaining 5 clusters. Whereas the maximum inter-cluster distance was recorded between cluster IV and VIII, indicating a higher amount of genetic diversity available in genotypes of this clusters and can be utilized as parents for hybridization programmes.

Keywords: Genetic divergence, Cluster analysis, Mono-genotypic, Inter and intra cluster distance.

INTRODUCTION

Linseed (*Linum usitatissimum* L.) chromosome number, $2n = 30$, is one of the most important *Rabi* oilseed crops and belongs to genus *Linum*, which is a Latin term that means "very beneficial" (Naik *et al*., 2020). It is an annual plant belonging to family Linaceae and order Malphigiales, commonly known as "*Alsi*". It is presumed to have originated in South West Asia, particularly in India. *Linum usitatissimum* is the sole cultivated species grown by man, having 6000–7000 years of planting history and is one of the oldest crops under cultivation (Paul *et al*., 2020). Every part of the linseed has extensive and varied uses; linseed oil content varies from 33 to 45 per cent (Jaishri, 2021) and it is richest plant source of omega-3 (36–57 per cent) and omega-6 (18–24 per cent) that are nutritionally significant (Paul *et al*., 2020). It has been found that consumption of 25 g linseed on daily basis reduces risk of breast cancer (Kaur *et al*., 2023). For normal growth and development of linseed, cool climatic conditions are considered most suitable. The minimum and maximum temperature regimes should be 10ºC and 38ºC, respectively; therefore, October to November is suitable for sowing. Linseed is cultivated in most of the countries in the world. In India, linseed occupies about 219.86 thousand hectares with a production of 158.64 thousand tonnes and productivity

of 979 kg/ha (Annual Report of AICRP Linseed, 2022–2023). In Rajasthan, linseed is being cultivated in an area of 22.5 thousand hectares with a production of 24.2 thousand tonnes and productivity of 1070 kg/ha (Directorate of Economics and Statistics, DAC & FW, GOI, 2022-23). To thrive in any crop improvement programme, the pivotal factor is the analysis of the genetic diversity present, especially in the primary gene pool. It also plays an important role in effectively managing gene pool thereby conserving it. Among the different methods for evaluating genetic diversity, multivariate analysis, such as D^2 statistics, has proven useful in various breeding applications, notably in selecting the most diverse genotypes suitable for hybridization. Hence, this investigation was conducted to estimate the magnitude of genetic diversity available in 33 linseed genotypes.

MATERIALS AND METHODS

The experiment material consisting of 33 genotypes of linseed including three checks and was evaluated in Randomized Block Design (RBD) with three replications during *Rabi* 2023-2024 at Agriculture Research Station, Kota. Each genotype was laid in plot size of 4×1.2 m^2 with a spacing of 30×10 cm. All the recommended agronomic practices and plant protection

measures were timely adapted to raise a healthy plant population.

All the observations were recorded on ten randomly selected plants of each genotype for eleven characters *viz.,* plant height, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, biological yield, harvest index, test weight and seed yield per plant in each replication except for phonological characters *i.e.,* days to 50 per cent flowering, days to maturity and plant stand. These three characters were recorded on plot basis. These collected data were used to analyze genetic diversity using Mahalanobis's D^2 estimates and cluster genotypes were clustered using Tocher's method. The data analysis and diagram construction was done using Windostat (9.3 version) and R 4.30.

RESULTS AND DISCUSSION

In culmination to genetic relationship, based on relative magnitude of D^2 estimates the thirty three linseed genotypes were grouped into 8 distinct non-overlapping clusters and presented in Table 1. The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Out of all the clusters, cluster I had maximum number of genotypes *i.e.,* 15 namely RCRL-21-2, JSL 95, RL 18105, LCK 2109, RL 18114, BRLS 109-2, DLV-24, BRLS 109-5, SLS 142, LMS-2019-I-11, LCK 2037, RLC-190, RL 15580, LSL 93, and Pratap Alsi-2, followed by cluster II *i.e.,* 8 which includes genotypes RLC 192, T-397, RL-189, BRLS 109-2-1, RLC-191, LCK 2132, RLC 92, and LMS 9-2K and cluster VI consists of 5 genotypes *viz.,* LCK 2107, LMS-2019-I-4, Kota Alsi-6, RLC 184 and BAU-2021-06. While other five clusters comprised of only one genotype *viz.,* cluster III (BRLS 111-2), cluster IV (SLS 133), cluster V (DLV-23), cluster VII (RCRL-21-1) and cluster VIII (SLS 141). The average inter and intra cluster distances based on D^2 values is presented in the Table 2 and diagrammatically represented in Fig. 1. The intra cluster distance had ranged from 0 to 56.26. The maximum intra cluster distance was recorded for cluster VI (56.26), followed by cluster II (35.92) and cluster I (35.86) while cluster III, cluster

IV, cluster V, cluster VI, and cluster VIII had least intra cluster values *viz.,* zero as these clusters comprises of only one genotype each. The inter cluster distances ranged from 18.06 to 218.51. Samantara *et al.* (2020) reported the similar results in their respective studies.

The maximum inter cluster distance was recorded between cluster IV and VIII (218.51), followed by cluster V and VIII (204.56), cluster VII and VIII (167.2), cluster III and VIII (152.42), cluster II and IV (144.24), cluster II and V (135.81), cluster VI and VIII (135.29), cluster VII and VI (129.62), cluster II and VI (116.01), cluster III and V (111.38), cluster I and VIII (109.38), cluster III and VI (97.75), cluster II and VI (96.28), cluster II and III (93.72), cluster II and VIII (89.15), cluster V and VI (87.78), cluster III and VI (87.37), cluster IV and VI (80.78), cluster III and IV (79.33), cluster I and II (74.4), cluster I and VI (71.76), cluster I and V (61.28), cluster I and VII (58.17), cluster I and IV (57.5), cluster I and III (54.12), cluster IV and VII (52.19) and cluster V and VII (40.16). These findings were in agreement with the findings of Chand *et al.* (2022); Thakur *et al.* (2021) ; Sharma *et al.* (2018).

The cluster mean values for 11 different characters for eight clusters are presented in Table 3. Cluster IV consists of genotype (SLS 133) with a higher cluster mean for test weight, harvest index, and plant stand while cluster VI consists of genotypes (LCK 2107, LMS-2019-I-4, Kota Alsi-6, RLC 184, and BAU-2021-06) with higher cluster mean for seed yield per plant, biological yield, number of seeds per capsule and number of capsules per plant and genotypes included in these clusters could be utilized in hybridization programme for yield improvement. Cluster III (BRLS 111-2) was found earliest for days to 50 per cent flowering and days to maturity and the genotype included in it can be used as a donor for early maturing variety development programmes. Therefore, it is essential for a breeder to wisely combine all the targeted traits for a specific hybridization programme including selected genotypes from divergent clusters. These results are in conform with the results of Kumar *et al.* (2022); Meena *et al.* (2021); Ankit *et al.* (2019).
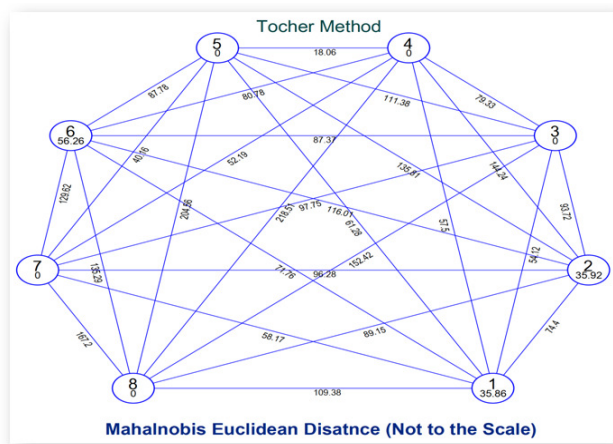

Fig. 1. Diagrammatic representation of cluster distances.

Table 1: List of thirty three linseed genotypes groupedin to eight different clusters by Tocher's method.

Cluster Group	No. of Genotypes	List of Genotypes
Cluster I	15	RCRL-21-2, JSL 95, RL 18105, LCK 2109, RL 18114, BRLS 109-2, DLV-24, BRLS 109-5, SLS 142, LMS-2019-I-11, LCK 2037, RLC-190, RL 15580, LSL 93 and Pratap Alsi-2
Cluster II	8	RLC 192, T-397, RL-189, RL 15597, RLC-191, LCK 2132, RLC 92 and LMS 9-2K
Cluster III	1	BRLS 111-2
Cluster IV	1	SLS 133
Cluster V	1	DLV-23
Cluster VI	5	LCK 2107, LMS-2019-I-4, Kota Alsi-6, RLC 184 and BAU-2021-06
Cluster VII	1	RCRL-21-1
Cluster VIII	1	SLS 141

Table 2: Intra and inter cluster distances based on D^2 analysis.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**35.86**	74.4	54.12	57.5	61.28	71.76	58.17	109.38
Cluster II		**35.92**	93.72	144.24	135.81	116.01	96.28	89.15
Cluster III			**0**	79.33	111.38	87.37	97.75	152.42
Cluster IV				**0**	18.06	80.78	52.19	218.51
Cluster V					**0**	87.78	40.16	204.56
Cluster VI						**56.26**	129.62	135.29
Cluster VII							**0**	167.2
Cluster VIII								**0**

Table 3: Cluster mean values of seed yield and its contributing traits.

Cluster	Days to 50 per cent flowering	Days to maturity	Plant stand	Plant height (cm)	No. of primary branches per plant	No. of capsules per plant	No. of seeds per capsule	Biological yield (g)	Harvest index (%)	Test weight (g)	Seed yield per plant (g)
Cluster I	69.02	132.53	133.91	66.70	3.04	47.61	8.12	7.97	47.65	7.50	3.81
Cluster II	69.21	133.21	129.96	65.37	2.26	50.76	8.15	6.89	49.75	5.68	3.43
Cluster III	57.33	124.67	141.67	60.60	2.33	47.27	8.60	9.19	55.03	7.88	5.07
Cluster IV	66.33	128.33	143.33	59.87	4.73	52.25	8.70	9.54	56.91	8.15	5.43
Cluster V	68.33	128.33	135.33	64.35	4.89	61.87	7.46	9.39	45.30	7.70	4.25
Cluster VI	74.00	139.73	141.93	71.32	3.58	73.77	9.13	11.25	50.09	7.30	5.65
Cluster VII	64.00	130.33	125.67	66.85	4.20	45.04	6.90	6.35	38.56	6.91	2.45
Cluster VIII	75.33	143.00	133.00	95.45	2.32	43.85	8.73	8.57	36.72	5.82	3.14

CONCLUSIONS

The present investigation revealed that ample of genetic divergence was observed among 33 linseed genotypes. The earliest days to 50 per cent flowering and days to maturity were observed for cluster III. Cluster VI had genotypes with higher cluster means for biological yield, number of seeds per capsule, number of capsules per plant, and seed yield per plant whereas cluster IV had genotype higher cluster means for plant stand, harvest index, and test weight and lowest cluster mean for plant height. While a genotype having the maximum number of primary branches per plant was put into cluster V. Based on above mentioned analysis, it can be concluded that the genotypes should be selected from the divergent clusters for hybridization programme to obtain superior varieties with increasing yield.

FUTURE SCOPE

By conforming the above results at varied locations might help validate the unambiguousness of conclusions at its best. The study on genetic divergence lays out foundation for further hybridization programmes for improving varieties in respect of resilience against adverse climate and pathogens or insects hence stabilizing and increasing the yield of linseed crop.

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