

## Analysis of Genetic Diversity in Linseed (*Linum usitatissimum* L.) Genotypes

Subhash Chand<sup>1\*</sup>, Sandhya<sup>2</sup>, Manoj Kumar<sup>2</sup>, Yamini Tak<sup>3</sup> and H.P. Meghwat<sup>4</sup>

<sup>1</sup>M.Sc. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Ummadganj, Agriculture University, Kota (Rajasthan), India.

<sup>2</sup>Assistant Professor, Department of Genetics and Plant Breeding, Agricultural Research Station, Ummadganj, Agriculture University, Kota (Rajasthan), India.

<sup>3</sup>Assistant Professor, Department of Biochemistry, Agricultural Research Station, Ummadganj, Agriculture University, Kota (Rajasthan), India.

<sup>4</sup>Assistant Professor, Department of Entomology, Agricultural Research Station, Ummadganj, Agriculture University, Kota (Rajasthan), India.

(Corresponding author: Subhash Chand\*)

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**ABSTRACT:** The present investigation was carried out to determine genetic diversity among thirty Linseed (*Linum usitatissimum* L.) genotypes during Rabi 2019-20 at Research farm, College of Agriculture, Agriculture University, Kota. Divergence analysis is helpful in identifying diverse parents for realizing high heterotic effects with transgressive segregants in later generations. Thirty genotypes were grouped into six clusters. Cluster I constituted maximum number of genotype followed by cluster III, cluster II, cluster V, cluster IV and cluster VI. Cluster V (173.32) had the highest intra-cluster distance followed by cluster I (112.05), cluster III (85.66), cluster II (69.72), cluster IV (0.00) and cluster VI (0.00). Cluster IV and VI (1728.35) had the highest inter-cluster distance followed by cluster I and VI (1062.19) and cluster III and IV (947.45). Suggested that the genotypes from these cluster may use hereafter be as a parents for future hybridization programme to obtain heterotic recombinants or even transgressive segregants.

**Keywords:** Cluster analysis, D<sup>2</sup> statistics, Linseed, Genetic Diversity.

### INTRODUCTION

Linseed (*Linum usitatissimum* L.; 2n=2x=30), commonly known as flax, belongs to family "Linaceae". It is used for fiber and oil (Chauhan *et al.*, 2009). Linseed oil has many industrial and medicinal utilities (Kumar *et al.*, 2018). Linseed oil cake also contains very good nutritive feeding value for animals (Bibi *et al.*, 2015). It is an amazing source of essential fatty acids and alternate source of omega-3 fatty acids and contains about 33 to 47% of oil content which may vary. Though there is high demand for linseed, still the linseed production is unable to meet its demand. The major causes behind its low production can be due to marginal cultivation of linseed and prone to biotic and abiotic stress (Kumar *et al.*, 2018).

Therefore, studies on genetic diversity prove to be an essential criterion for the crop improvement since selection of suitable divergent parent for hybridization offer great possibility of obtaining desirable segregants in the segregating (Samantara *et al.*, 2020). Mahalanobis D<sup>2</sup> statistic is useful for qualifying the degree of divergence among genotypes. In the present investigation, an attempt is made to understand the nature and magnitude of genetic divergence and to select divergent parents for hybridization programs. Different scientists have highlighted the value of parental diversity in optimum magnitude to obtain

superior genotypes in the segregating generations (Srivastava *et al.*, 2009; Tyagi *et al.*, 2015).

### MATERIAL AND METHODS

Thirty genotypes of linseed were sown in a Randomized Complete Block Design with three replications during Rabi 2019-20 at Research farm, College of Agriculture, Ummadganj, Agriculture University, Kota (Rajasthan). Observations were recorded for 12 characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, test weight (g), biological yield per plant (g), harvest index (%), oil content (%), protein content (%) and seed yield per plant (g). The genetic divergence in 30 genotypes has been estimated by using Mahalanobis D<sup>2</sup> statistics (1936) with inter and intra cluster distances, as suggested by Rao (1952).

### RESULTS AND DISCUSSION

Thirty genotypes of linseed were grouped into six distinct non-overlapping clusters (Table 1). Cluster I constituted maximum numbers of 20 genotypes (JLT-204, JLT-215, PKDL-73, PKDL-72, NL-126, LBR-6, LMS-3, NL-165, BAU-06-17, NDL-2005-29, BAU-06-5, OLC-99-57, RRN-2, PKDL-74, NDL-2005-24, RRN-1, NDL-2005-16, SLS-68, BAU-06-8 and NL-

260) followed by cluster III with 4 genotypes (PCL-1-106, PCL-35-06, NDL-2005-34 and NDL-2005-26), cluster II with 2 genotypes (LC-2279-4 and PKDL-75), cluster V with 2 genotypes (LCK-6028 and RLC-112) and while rest of the cluster IV and VI contained single genotype each (LMS-149-4 and NDL-2005-17). Distribution pattern of all the genotypes in six clusters showed the presence of considerable genetic diversity among them for all the traits under considerable.

Inter and intra-cluster distances were present in Table 2. The maximum intra-cluster distance was observed in cluster V (173.32) followed by cluster I (112.05), cluster III (85.66) and cluster II (69.72). While it was zero for cluster IV and cluster VI. Maximum inter-cluster distance was found between cluster IV and VI (1728.35) followed by cluster I and VI (1062.19) and cluster III and IV (947.45) while minimum inter cluster distance was recorded between cluster I and II (164.09). The greater the distance between two clusters, wider the expected genetic diversity. Similar studies done by Thakur *et al.* (2021); Kumar *et al.* (2017); Nizar and Mulani (2015); Begum *et al.* (2007).

Widerange of cluster mean value indicates the presence of variation among the studied genotypes. The mean values of twelve different characters for six clusters are presented in Table 3. Higher mean value in cluster II was observed for characters like protein content (20.35 %). Whereas, clusters IV had high mean values for number of primary branches per plant (4.53), plant

height (66.20 cm), and oil content (40.90 %) and also desirable for early flowering (67.00 days) and maturity (116.33 days). Cluster V for seed yield per plant (6.56 g), harvest index (41.71 %), test weight (8.88 g) and number of capsules per plant (95.23) Cluster VI for seed yield per plant (6.56 g), biological yield per plant (17.38 g), number of seeds per capsule (8.70). Therefore, hybridization between the selected genotypes form divergent clusters is essential to judiciously combine all the targeted characters. Earlier finding of Manhar *et al.* (2021); Thakur *et al.* (2021); Samantara *et al.* (2020); Tewari *et al.* (2020); Kasana *et al.* (2018); Kumar *et al.* (2018); Kumar *et al.* (2017); Tyagi *et al.* (2015); Nagaraja *et al.* (2010).

The contributions of per cent toward genetic divergence by contributions of twelve characters of thirty genotypes of linseed are given in Table 4. The character showed maximum contribution oil content (47.12%) followed by test weight (36.32%), protein content (10.11%), days to 50 per cent flowering (3.90%), seed yield per plant (1.14%), days to maturity (0.22%), plant height (0.22%), number of primary branches per plant (0.22%), number of seeds per capsule (0.22%), biological yield per plant (0.22%) and harvest index (0.22%). Similar finding were also reported by Manhar *et al.* (2021); Tewari *et al.* (2020); Kumar *et al.* (2017); Pali and Mehta (2016); Chaudhary *et al.* (2016); Tyagi *et al.* (2015).

**Table 1: Distribution of linseed genotypes in six clusters.**

Cluster	Number of genotypes	Genotypes
Cluster I	20	JLT-204, JLT-215, PKDL-73, PKDL-72, NL-126, LBR-6, LMS-3, NL-165, BAU-06-17, NDL-2005-29, BAU-06-5, OLC-99-57, RRN-2, PKDL-74, NDL-2005-24, RRN-1, NDL-2005-16, SLS-68, BAU-06-8, NL-260
Cluster II	02	LC-2279-4, PKDL-75
Cluster III	04	PCL-1-106, PCL-35-06, NDL-2005-34, NDL-2005-26
Cluster IV	01	LMS-149-4
Cluster V	02	LCK-6028, RLC-112
Cluster VI	01	NDL-2005-17

**Table 2: Estimates of average intra and inter-cluster distances for six clusters.**

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	112.05	164.09	586.72	193.92	346.91	1062.19
Cluster II		69.72	278.55	288.77	376.75	751.69
Cluster III			85.66	947.45	488.04	237.65
Cluster IV				0.00	782.00	1728.35
Cluster V					173.32	521.63
Cluster VI						0.00

**Table 3: Cluster mean of thirty genotypes of linseed for twelve characters.**

Cluster	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of capsules per plant	Number of seeds per capsule	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)	Protein content (%)	Seed yield per plant (g)
Cluster I	73.35	120.83	61.07	3.97	84.35	7.83	6.31	14.99	36.82	40.41	19.73	5.51
Cluster II	76.66	120.00	62.10	3.86	78.90	7.30 *	5.64	14.08*	34.37	37.50	20.35**	4.81
Cluster III	78.66	124.00	59.41	3.80*	82.91	7.85	6.32	16.01	33.73	32.75	19.15	5.39
Cluster IV	67.00*	116.33*	66.20**	4.53**	72.20*	7.73	4.52 *	14.65	29.12*	40.90**	19.44	4.26*
Cluster V	74.33	120.66	63.03	4.15	95.23**	8.38	8.88**	15.72	41.71**	39.43	19.93	6.56
Cluster VI	79.00**	125.66**	57.93*	4.00	94.06	8.70**	8.66	17.38**	37.80	31.70*	18.52*	6.56**
Minimum value*; Maximum value**												

**Table 4: Contribution (%) of twelve characters towards genetic divergence in linseed.**

Sr. No.	Source	Contribution (%)
1.	Days to 50 per cent flowering	3.90%
2.	Days to maturity	0.22%
3.	Plant height (cm)	0.22%
4.	Number of primary branches per plant	0.22%
5.	Number of capsules per plant	0.0%
6.	Number of seeds per capsule	0.22%
7.	Test weight (g)	36.32%
8.	Biological yield per plant (g)	0.22%
9.	Harvest index (%)	0.22%
10.	Oil content (%)	47.12%
11.	Protein content (%)	10.11%
12.	Seed yield per plant (g)	1.14%

## CONCLUSION

The experiment suggested that a considerable extent of genetic divergence was present among 30 genotypes of linseed. Cluster V had the highest intra cluster distance followed by cluster I, III and cluster II. The intra-cluster distance for cluster IV and VI was observed to zero since these contains one genotype. The highest inter-cluster distance was found between cluster IV and VI followed by cluster I and VI, cluster III and IV. Maximum mean value was observed in cluster II for characters like protein content. Clusters IV had high values for plant height, number of primary branches per plant, oil content and also desirable for early flowering and maturity. Characters viz., harvest index, test weight and number of capsules per plant had maximum values in Cluster V. Similarly, characters viz., number of seeds per capsule, seed yield per plant, biological yield per plant had maximum values in cluster VI. Therefore, hybridization between the selected genotypes form divergent clusters is crucial to wisely combine all the targeted traits. Nevertheless, maximum contribution to divergence was given by oil content, followed by test weight and protein content. Hence, these characters should be taken under consideration for future breeding program.

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**Conflict of Interest.** None.

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