

# STUDIES ON GENETIC DIVERSITY IN LINSEED (*LINUM SITATISSIMUM L.*)

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## KEYWORDS

Genetic diversity  
D<sup>2</sup> analysis  
linseed  
*L. usitatissimum*  
Cluster distance

## Received on :

19.04.2016

## Accepted on :

25.10.2016

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## ABSTRACT

The D<sup>2</sup> analysis of 35 linseed (*Linum usitatissimum L.*) genotypes grown at Raipur, IGKV, Chhattisgarh, revealed into eight clusters indicated the existence of large amount of diversity in the present germplasm. The highest inter cluster distance between were obtained cluster VII and cluster II (5.29) followed by cluster II and cluster I (5.02), cluster VI and cluster I (4.99) and cluster VIII and cluster VII (4.97). The lowest inter cluster distance was found between cluster VI and cluster I (2.76). The inter cluster value varied from a range of 5.29 to 2.76, whereas the intra cluster distance varied from 3.61 to 8.17. It's indicated wide range of diversity in term of genetic distance (D<sup>2</sup>). The maximum intra cluster distance shown by cluster VII followed by cluster III, suggesting that the genotypes in those clusters were relatively more diverse. A maximum of thirteen genotypes were accommodated in clusters V followed by Cluster I, II, III, IV, VII, and VIII included five, two, four, three, four, two and again two genotypes, respectively. The study indicated that while planning hybridization programmes, genotypes like CI-2006 and EC-1066 from cluster II (for characters such as plant height, capsule size, seed size, earliness, harvest index, seed yield/ plant); EC-41659 and EC-41741 of cluster VII (for plant height, number of seed/ capsule, seed size) are expected to give promising and desirable recombinants in segregating generations as they possess desirable features.

## INTRODUCTION

Linseed (*Linum usitatissimum L.*) belongs to genus *Linum*, the only species that has economic agronomically values under Linaceae family. It has two different forms that are used: for fiber (namely fiber flax) and for oil production (namely oil flax, or linseed) Kurt. (1996). Linseed is the important *Rabi* oilseed crop in India having several uses. It is mainly cultivated in central India, however it's cultivation spreads from Himalayas to Karnataka. The crop is originated in Southwest Asia, Vavilov. (1935). Linseed has been providing a variety of health benefits, Thompson and Cunnane. (2003). The components that contribute the health benefits include lignans (up to 13 mg/g flaxseed),  $\alpha$ -linolenic acid (ALA), and nonstarch polysaccharides. ALA, a polyunsaturated lipid, accounts for 52% of the fatty acids in the oil. This crop it has been in cultivation since ancient times for seed as well as for oil.

Despite the importance of this crop, only limited breeding work has been done and very little attention has been given for its genetic improvement in the past, in order to enhance the productivity levels of Linseed. Information on the nature and magnitude of genetic diversity present in the genotypes is a pre-requisite. To develop a new variety there is need of the magnitude of genetic variability in the base material and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants Kumar *et al.* (2012). Diversity in the germplasm is essential to meet different purposes of the crop such as increased yield Joshi and Dhawan (1986), wider

adaptation, desirable quality, pest and disease resistance Nevo *et al.* (1982). Multivariate analysis is an important technique for assessing the degree of divergence and the relative contribution of different characters to the total divergence Golakia and Makne (1992). The genetic distance between pair of genotypes offers the basis for understanding the structure of the diversity of any intra-species population. The multivariate analysis is a useful tool for choosing the parents for hybridization and has been well demonstrated by previous workers *viz.*, Badaya *et al.* (2015); Sachin *et al.* (2014); Shekhawat *et al.* (2014) and Kumar, *et al.* (2013a.). Therefore the present study was undertaken to classify and understand the nature and magnitude of genetic diversity present in 35 linseed (*Linum usitatissimum L.*) genotypes. However, the main objective of present study to identify genetic divergent parents, so as to select the potential parents for breeding programme to attain the anticipated improvement in oil yield of linseed.

## MATERIALS AND METHODS

The material for the present study Research cum Instructional Farm under AICRP on Linseed, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India (altitude of 289.60 m above mean sea level, and 24°45'N and 84°15' E). Experiment was conducted in medium black soils Consisted under rainfed conditions. The experiment material for present study was comprised of 35 linseed germplasm accessions and three checks T-397(NC), Padmini (ZC) & Indira Alsi-32 (ZC) was carried out during *Rabi* 2014 -15. The experiment

was laid out in an randomized block design with three replications, and all the three checks. Each genotype was grown in plots of 2 rows of 3 m length at spacing of 30 cm between row and 30 cm between plants in a row. Fertilizer was applied @ 40 kg N, 20 kg P<sub>2</sub>O<sub>5</sub> per hectare. The observations were recorded for twelve agro-morphological characters *viz.*, days to 50% flowering, plant height (cm), number of primary branches/ plant, number of capsules/ plant, capsule size (mm), number of seeds/ capsule, seed size (mm), 1000 seed weight (g), days to maturity, biological yield (g), harvest index (%) and seed yield/ plant (g). Observations were recorded in five randomly selected plants of each accession. With the development of advanced biometrical techniques, several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives, of which the data were subjected to the Multivariate analysis was done utilizing Mahalanobis (1936) D<sup>2</sup> statistics and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). Data of each character was subjected to analysis to calculate means, minimum and maximum values, variances and standard errors (SE) through MS Excel Software.

## RESULTS AND DISCUSSION

A clear understanding of the extent of variability prevalent for each character in germplasm would simply for improving characters through selection. Hybridization programme where selection of genetically diverged parent is important to get wide array of recombination, the knowledge of genetic diversity among the accessions of germplasm is necessary. Basic descriptive statistics for 12 characters was presented in Table 1. Cluster I include five genotypes whereas cluster II, III, IV, VII,

and VIII included 2, 4, 3, 4, 2 and 2 genotypes, respectively. Cluster V include 13 genotypes. The clustering pattern showed that genotypes collected from the same geographic region were found to be distributed in several cluster, except cluster V. Genotypes from same geographical locations fell into different clusters and vice-versa indicating that clustering of populations did not follow their geographic or location distribution Shekhawat *et al.* (2001) and Singh, *et al.* (2006). This suggested that genetic drift and selection in different environments seems to be a cause of greater diversity rather than geographical isolation. Therefore, it is suggested that parents should be selected on the basis of total divergence for the characters used for an overall improvement in the yield. It was also earlier observed by Murty and Arunachalam (1996). Keeping this in mind, parents should be selected based on diversity.

Classification of these 35 linseed genotypes into eight clusters indicated the existence of large amount of diversity in the present germplasm. As a result, careful selection of parents from these 35 genotypes that have optimum genetic divergence might be desirable to produce heterotic progenies. Main and Bhal (1989) reported that the parents separated by D<sup>2</sup> value of medium. Magnitude generally should higher heterosis. Linseed accessions in different clusters with prominent traits were described in (Table 2). Accessions of group I were characterized as higher seed size (mm), capsule size (mm), number of primary branch per plant, capsule size (mm), seed size (mm), days to maturity, seed yield per plant (g). The inter and intra cluster distance for all the trait represented in table 3.

The highest inter cluster distance between were obtained cluster VII and cluster II (5.29) followed by cluster II and cluster I (5.02), cluster VI and cluster I (4.99) and cluster VIII and

**Table 1: Variation in quantitative traits of linseed accession**

Sr.No.	Variables	Minimum	Maximum	Range	Mean	SE
1	Days to 50 % flowering	51	65	14	60.70	2.75
2	Plant height (cm)	41	55	14	46.28	3.11
3	No of primary branches/ plant	2	4	2	2.96	0.24
4	No of capsules/ plant	21	33	12	26.11	2.59
5	Capsule size (mm)	5	6	1	5.46	0.25
6	No of seeds/ capsule	6	9	3	8.42	0.23
7	Seed size (mm)	4	5	1	4.09	0.12
8	Seed weight (g)	4.13	5.62	1.49	4.94	0.19
9	Days to maturity	113	122	9	119.52	2.52
10	Biological yield (g)	3.13	4.71	1.58	3.57	0.21
11	Harvest index (%)	31.31	56.73	25.42	42.14	2.41
12	Seed yield/ plant (g)	0.48	2.48	2	1.16	0.12

**Table 2: Characteristics of linseed accession in clusters**

Sr.No.	Cluster No.	No. of genotypes in each cluster	% of lines	Prominent traits
1	I	5	14.2	Seed size, Seed yield per plant, Capsule size, Number of primary branch per plant.
2	II	2	5.7	Capsule size, Seed size, Days to maturity, Seed yield per plant.
3	III	4	11.42	Number of primary branch per plant, Number of capsule per plant, Days to maturity.
4	IV	3	8.57	Days to maturity, Biological yield.
5	V	13	37.14	Plant height, Number of seed per capsule, 1000 seed weight, Days to maturity.
6	VI	4	11.42	Number of capsule per plant, Days to maturity.
7	VII	2	5.7	Plant height, Number of seed per capsule, Seed size, Days to maturity.
8	VIII	2	5.7	Days to 50% flowering, Days to maturity, Harvest index.

**Table 3: Distances between cluster centroids**

Sr.No.	Cluster	I	II	III	IV	V	VI	VII	VIII
1	I	3.96	5.02	3.17	3.38	3.56	2.76	3.28	4.57
2	II		4.04	4.60	3.83	4.09	4.99	5.29	3.95
3	III			4.69	3.00	3.80	3.17	3.94	4.74
4	IV				4.35	3.17	3.56	4.16	3.95
5	V					4.27	3.40	3.98	3.14
6	VI						4.59	3.89	4.42
7	VII							8.17	4.97
8	VIII								3.61

**Table 4: Cluster mean for different twelve agro-morphological characters**

Sr. No.	Chara cters	Days to 50%Flow ering	Plant height (cm)	No. of primary branches / plant	No. of capsules / plant	Capsule size (mm)	No. of seed /capsule	Seed size (mm)	1000 Seed weight (g)	Days to Maturity	Biological yield (g)	Harvest index (%)	Seed yield/ plant (g)
Cluster													
1	1	62.33	45.22	3.36	23.11	5.44	8.71	4.08	5.32	118.88	4.2	34.83	1.52
2	2	51.22	48.44	2.11	26.11	6.22	8.44	4.36	4.6	115.44	3.49	56.73	1.46
3	3	53.66	45.44	3.51	27	5.33	6.22	4.08	5.09	117	3.69	36.13	1.16
4	4	55.55	44.77	3.22	23.1	5.33	8.22	4.02	4.42	117.11	3.55	43.75	0.63
5	5	62.33	47.44	3.22	27.77	5.4	9.36	4.06	5.28	121.44	3.31	46.08	1.27
6	6	61.88	42.33	3.22	29.81	5.33	8.33	4.04	5.24	120.44	3.63	36.05	0.54
7	7	63.11	55.55	3	23.11	5.55	9.44	4.19	5.06	121.22	3.74	33.26	0.81
8	8	64.44	44.33	3	26.66	5	8.22	4.01	4.13	122.33	3.28	54.96	0.7

**Table 5: Elite Linseed accession identified on the basis of important agro-morphological traits**

Sr.No.	Traits of interest	Range	Accession identified
1	Seed yield / plant (g)	e <sup>n</sup> 2	CI-1924, EC-511, FRW-9, GS-61, GS-129, CI-2006, EC-1066, CI-2204, CI-2260, EC-41628, EC-9901
2	Biological yield (g)	e <sup>n</sup> 1.58	CI-1924, EC-511, FRW-9, GS-61, GS-129, EC-41659, EC-41741, CI-2204, CI-2260, EC-41628, EC-9901
3	No. of seed /capsule	e <sup>n</sup> 3	EC-41659, EC-41741, EC-1386, EC-98994, EX-313-23, Fatehpur, FR-11, Gewargi-1-2, GIF-White, GS-27, GS-64, GS-85, NL-97(ZC), JLS-9(ZC), Padmini(ZC), CI-1924, EC-511, FRW-9, GS-61, GS-129
4	Days to 50 % Flowering	< 14	EC-1645, EC-41623, GIC-11-1, IA-32(ZC), EC-41659, EC-41741, FRW-12, FX-16

cluster VII (4.97). The lowest inter cluster distance was found between cluster VI and cluster I (2.76). The inter cluster value varied from a range of 5.29 to 2.76.

The intra cluster distance varied from 3.61 to 8.17. The maximum intra cluster distance shown by cluster VII (8.17) having 2 genotypes namely, E C-41659 and E C-41741. Followed by cluster III (4.96) having 4 genotypes namely, C I-2204, C I-2260, E C-41628 and E C-99001.

These finding are in conformity to the findings of previous workers Begum *et al.* (2007), Diederichsen and Fu (2008), Dandigadasar *et al.* (2012), Khan *et al.* (2013), Kanwar *et al.* (2013).

The D<sup>2</sup> analysis indicated the presence of appreciable genetic diversity in the material. The inter cluster varied from 5.29 to 2.76 it clearly demonstrated considerable amount of genetic divergence present in material study. The intra cluster distance varied from 3.61 to 8.17. It's indicated wide range of diversity in term of genetic distance (D<sup>2</sup>).

The cluster mean of all the 12 characters presented in table 4. The highest cluster mean for days to 50% flowering was obtained cluster VIII (64.44) and lowest in cluster II (51.22).

Cluster VII had the highest cluster mean value for plant height (48.44) whereas, the lowest mean value exhibited in clusters VI (42.33). The cluster mean for number of primary branches/ plant was highest for cluster III (3.51) and lowest for cluster II (2.11). For number of capsules/ plant the highest cluster mean value was exhibited in cluster VI (29.81) and lowest in cluster I (23.10). Cluster II had the highest cluster mean for capsule size (6.22) whereas, the lowest mean value was exhibited in cluster VIII (5.00). Number of seeds/ capsule had the highest cluster mean was obtained in cluster VII (9.44) and lowest in cluster II (6.22). Highest cluster mean values for seed size were recorded in cluster II (4.36) and lowest in cluster VIII (4.01).

For seed weight highest cluster mean value was recorded in cluster I (5.32) and lowest in cluster VIII (4.13). Cluster VIII (122.33) had the highest cluster mean for days to maturity whereas, the lowest value was obtained in cluster II (115.44). For biological yield the highest cluster mean was recorded by cluster I (4.20) and lowest in cluster VIII (3.28). Cluster II (56.73) had the highest cluster mean value for harvest index whereas, the lowest value exhibited in cluster VII (33.26). For seed yield/ plant the highest cluster mean value was registered by cluster

IV (0.63) and lowest cluster in I (1.52). Important agromorphological traits like seed yield / plant (g), biological yield (g), number of seed /capsule and days to 50 % flowering, served as a greater yield potential criterion to select promising linseed genotypes having high yield with early duration (Table 6). Present results were in accordance with the findings of Khan *et al.* (2013), Kanwar *et al.* (2013) and Shekhawat *et al.* (2014).

This indicated that while planning hybridization programmes, genotypes like CI-2006 and EC-1066 from cluster II (for characters such as plant height, capsule size, seed size, earliness, harvest index, seed yield/ plant); EC-41659 and EC-41741 of cluster VII (for plant height, number of seed/ capsule, seed size); CI-1924, EC-511, FRW-9, GS-61, and GS-129 of cluster I (for 1000 seed weight, seed yield/ plant, number of primary branches/ plant, capsule size) are expected to give promising and desirable recombinants in segregating generations as they possess desirable features as seen from their cluster means. Therefore as Linseed is a self-pollinated crop though there is a potential for obtaining hybrid vigor by implementing hybridization programme between the genotypes of distinct group to obtain superior genotypes from the segregating generation.

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