



Genetic Diversity Analysis of Linseed (*Linum usitatissimum* L.) at Bilaspur Plain Region of Chhattisgarh

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Abstract

The present investigation was carried out with 60 genotypes including 4 checks (KIRAN, DEEPIKA, PADMINI, and INDIRA ALSI) and 56 entries. The experiment was laid down in medium black soil under rainfed conditions during rabi season with statistical design, Augmented Block Design comprising 07 blocks, each block consists of 8 genotypes with 4 checks total of 12 plots. The linseed was classified into 5 clusters. Cluster I was the largest, containing of 18 genotypes followed by cluster IV comprising 17 genotypes, cluster V with 13 genotypes, cluster II comprising 7 genotypes, while cluster III with 5 genotypes.

The highest intra cluster distance was recorded for cluster III (2123.64) (46.08), followed by cluster V (1640.66) (40.50), cluster II (1572.96) (36.66), cluster IV (1539.42) (39.23), while the lowest intra cluster distance was observed for cluster I (1411.20) (37.56). highest inter-cluster distance was recorded between cluster II and III, followed by clusters III and V, cluster III and IV, cluster I and II, cluster I and V, cluster I and III, cluster II and IV, cluster I and IV, cluster II and V, while the lowest inter cluster distance was observed between cluster IV and V. Genotypes in cluster I demonstrate largest genetic diversity within the cluster be comparable to the genotypes be the member of other clusters. Thus, hybridization can be taken among all these genotypes to getting useful in F₂ generations for the yield and yield contributing characters.

Keywords: D2; Linseed; Genetic; Diversity

Introduction

Linseed (*Linum usitatissimum* L.) (2n = 30), commonly called as Flax is an autogamous crop (primarily self-pollinating). Its centre of origin is India. It is dominantly self-pollinated crop but less than 2% cross-pollination occurred due to pollinator's activity. It is widely grown species with huge economic impact. The current oilseed varieties contain 33 - 45% oil and 24% crude protein significantly more than fiber varieties [1]. Its oil is mainly composed

of five fatty acids namely, palmitic acid-6%, stearic acid-2.5%, oleic acid-19%, linoleic acid-24%, and linolenic acid-55 - 57% (Cloutire, et al. 2011). It has drying and hardening properties, which is issued from its high linolenic acid content. About 20% of the total linseed oil produced in India is used for consumption and the rest about 80% goes to industries for the manufacture of paints, varnish, oil cloth, linoleum, printing ink, putty, hair gels, medicines and polymers [2,3].

The study on genetic divergence analysis using techniques like Mahalanobis D2 or nonhierarchical were applied to assess genetic variability present in the 56 genotypes along with four checks (KIRAN, DEEPIKA, PADMINI, INDIRA ALSI) used in this experiment. Similar works have also been reported by [4-8]. The genetic variability more will be the chance to expect improvement through suitable selection process [9].

Materials and Methods

The experiment was conducted at Instructional Farm of BTC College of Agriculture and Research Station, Bilaspur, a constituent college of Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh). Bilaspur district is located in NW part of Chhattisgarh and is bounded by North latitudes 21°47' and East longitudes 23°8' and 81°14' and 83°15' with an altitude of 265 meters above the mean sea level. This place falls under "Plains of Chhattisgarh". Chhattisgarh state comes under dry moist, sub humid zone and termed as the seventh agro climatic zone of India.

The field investigation was carried throughout rabi 2020 at the Instructional Farm of BTC CARS, Bilaspur, C.G The experiment was laid out in an Augmented Block Design with total 07 blocks each block consists of 12 plots. The trial was regulated in medium black soil under rainfed conditions during rabi season of 2019-20. The experimental material utilized for present investigation consisting 56 genotypes including 04 checks of linseed.

The plot size 1m x 1m entry represented 03 rows of 1 meter lengths. Recommended intercultural operations were validated to growing the crop. For recording the observations Five plants are selected randomly on 14 characters viz. days to 50% flowering, plant height (cm), days to maturity, number of capsule per plant, number of seed per capsule, number of branches per plant, capsule length (mm), capsule width (mm), seed length (mm), seed width (mm), biological yield, harvest index (%), 1000 seed wt (gm), seed yield (gm).

The genetic divergence in 60 genotypes was estimated by using Mahalanobis D2 statistics [10] and statistical analysis was done from SPAR 2.0 software, following

$$D2 = \lambda I_j \delta_i \delta_j$$

Where:

λ Ij = Reciprocal matrix to the common dispersion matrix.

δ_i = Difference between the mean values of the two populations for Ith character

δ_j = Difference between the mean values of the two populations for Jth character.

The parameter was determined as D2 [11].

$$D2 = \sum \sum \delta_{ij}$$

di dj = Sample estimate of Xij

Where:

δ_{ij} = Sample estimates of Xij

di = Sample estimates of δ_i

dj = Sample estimates of δ_j

Result and Discussion

The analysis of genetic divergence among 60 genotypes of linseed was carried out following the method of Mahalanobis 'D²' statistics as described by Rao [11]. The clustering was determined by Ward method (1963). The intra and inter cluster distances (D² value) were estimated by formula as proposed by Rao [11]. Also calculate the mean performance of the cluster for different characters.

In table 1, the clustering system of the genotypes is presented, Cluster I was the largest, containing of 18 genotypes followed by cluster IV comprising 17 genotypes, cluster V with 13 genotypes, cluster II comprising 7 genotypes, while cluster III with 5 genotypes.

In table 2, the cluster means for 14 quantitative traits were calculated and are presented. Days to 50 per cent flowering showed highest mean (65.52) in cluster number V followed by cluster IV (61.54), cluster I (59.89), and cluster III (59.20), while the lowest mean for this trait was recorded in cluster II (58.57). The days to maturity was observed maximum in cluster IV (95.17), followed by cluster I (94.83), cluster II (93.14), cluster III (93.00), and cluster V (87.90), and the maximum mean was presented by plant height in cluster I (64.22) followed by cluster III (63.20), cluster V (63.10), cluster II (55.14), whereas it was lowest in cluster IV (54.17). In Cluster V (12.57) the number of branches per plant showed maximum mean followed by cluster I (12.11), cluster VI (11.99), and cluster III (11.00), whereas cluster II (10.86) showed minimum mean for this trait. in cluster I (35.94) the number of capsule per plant exhibited maximum mean followed by cluster number III

Cluster	No. of genotypes	Genotype
	18	PYT,5, PYT,12, PYT,13, PYT,14, PYT,16, MLT,2, PYT,21, PYT,20, PYT,18, MLT,6, MLT,8, MLT,9, MLT,10, MLT,18, MLT,17, MLT,15, RALC,107, JLH,09
	7	PYT,8, PYT,6, PYT,1, MLT,1, PYT,17, R,3102, T,397
	5	PYT,9, PYT,10, MLT,5, MLT,7, MLT,13
	17	KIRAN, PADMINI, DEEPIKA, PYT,4, PYT,3, PYT,2, PYT,11, PYT,22, MLT,3, MLT,16, MLT,12, MLT,11, NL,97, PKDL,63, R,3148, R,552, LMH,62
	13	INDIRA ALSI, PYT,6, PYT,15, PYT,19, MLT,4, MLT,14, PKD,55, JLT,62, KARTIKA, R,4017, SHEETAL, RLCO4,06, RLC,05

Table 1: Grouping of 60 genotypes of linseed (*Linum usitatissimum* L.) in 5 clusters.

Characters	Cluster mean				
	1	2	3	4	5
Days to flowering	59.89	58.57	59.20	61.54	65.52
Days to maturity	94.83	93.14	93.00	95.17	87.90
Plant height (cm)	64.22	55.14	63.20	54.17	63.10
No. of branches per plant	12.11	10.86	11.00	11.99	12.57
No. Of capsule per plant	35.94	33.43	34.40	33.36	33.52
No. Of seed per capsule	8.28	8.71	8.80	8.14	8.53
Capsule length(mm)	8.46	7.76	8.04	8.04	8.14
Capsule width(mm)	7.11	7.06	7.24	7.21	6.88
Seed length(mm)	4.92	4.71	4.72	4.65	4.89
Seed width(mm)	2.48	2.66	2.72	2.35	2.72
Biological yield	230.57	135.63	308.26	190.40	162.78
HI (%)	47.41	61.43	41.85	46.05	38.83
1000 Seed wt (gm)	5.11	5.06	5.28	5.36	5.18
Seed yield(gm)	108.70	82.62	128.01	86.83	62.50

Table 2: Cluster mean for 14 traits of 60 genotypes in linseed (*linum usitatissimum* L.).

(34.40), cluster V (33.52), cluster II (33.43), whereas Cluster number IV (33.36) reflected minimum mean value for this character and maximum cluster mean for no. of seed per capsule exhibited in cluster III (8.80) Followed by cluster II (8.71), cluster V (8.53), cluster I (8.28), whereas it was lowest in cluster number IV (8.14). Cluster number I (8.46) showed maximum mean for capsule length (mm) followed by, cluster V (8.14), cluster III (8.04) and cluster IV (8.04) whereas it was minimum in the cluster number II (7.76), and maximum cluster mean for capsule width (mm) cluster III (7.24) followed by cluster IV (7.21), cluster I (7.11), cluster II (7.06) whereas it was lowest in cluster V (6.88). Number I (4.92) cluster

exhibited maximum mean for seed length (mm) followed by, cluster V (4.89), cluster number III (4.72) and cluster number II (4.71), whereas it was minimum in the cluster number IV (4.65). Cluster number III (2.72) and V (2.72) exhibited maximum mean for seed width (mm) followed by cluster II (2.66) and cluster number I (2.48), while it was minimum in the cluster IV (2.35). For biological yield (gm) per plant, maximum mean was recorded in cluster III (308.26) followed by cluster I (230.57), cluster IV (190.40), cluster V (162.78), and minimum mean was showed in cluster number II (135.63) for this trait. For harvest index (%), in cluster number II (61.43) maximum mean value was recorded, followed by cluster

I (47.41), cluster IV (46.05), cluster number III (41.85) and minimum mean value was showed in cluster V (38.83) for this character. For 1000 seed wt. (gm) maximum mean was recorded in cluster IV (5.36) followed by cluster number III (5.28), cluster number V (5.18), cluster number I (5.11) and minimum mean value was exhibited in cluster number II (5.06) for this character. The cluster number III (128.01) exhibited maximum mean for seed yield followed by cluster I (108.70), cluster IV (86.83), and cluster II (82.62), whereas it was minimum in the cluster number V (62.50).

In table 3, the present studies of average inter and intra cluster distance value was presented. The highest intra cluster distance was recorded for cluster number III (2123.64) (46.08), followed by cluster V (1640.66) (40.50), cluster II (1572.96) (36.66), cluster IV (1539.42) (39.23), while the lowest intra cluster distance was observed in case of cluster number I (1411.20) (37.56). Highest inter-

cluster distance was observed between cluster II and III, followed by cluster III and V, cluster III and IV, cluster I and II, cluster I and V, cluster I and III, cluster II and IV, cluster I and IV, cluster II and V, while the lowest inter cluster distance was observed between cluster IV and V. The maximum inter cluster distance showed that the genotypes of cluster II and III are not so closely connected, while the minimum inter cluster distance exhibited that the genotypes of cluster IV and V are closely associated. The maximum inter cluster distance indicated that genotypes of cluster II and III are not so closely related whereas the minimum inter cluster distance indicated that the genotypes of cluster IV and V are closely related. The crosses between genotypes be in to the clusters separated by lowest inter cluster distance are improbably to create optimistic recombinant in segregating generations. Ananda and Murty [12], also observed hybridization between lines be in to cluster separated by highest inter cluster distance in linseed.

Inter Distance/Intra (Bold) Distance Matrix among Clusters:					
	1	2	3	4	5
1	1411.204 (37.56)	11326.5325 (106.43)	7964.739 (89.24)	3595.2482 (59.96)	8313.4005 (91.17)
2		1572.9618 (39.66)	33835.1506 (183.94)	4669.1154 (68.33)	3226.7502 (56.80)
3			2123.6444 (46.08)	17271.8068 (131.42)	27139.2129 (164.73)
4				1539.4231 (39.23)	3037.531 (55.11)
5					1640.6627 (40.50)

Table 3: Average inter and intra cluster distance (D^2 value) among 5 clusters of 60 genotypes in linseed (*linum usitatissimum* L.)

Note: Diagonal values are intra - cluster divergence and off - diagonal values inter - cluster divergence. Values in parenthesis are the group distance (2) to be used for cluster diagram.

Conclusion

Genotypes be in to cluster I showed maximum genetic diversity within the cluster as comparable to the genotypes be the member of other clusters. Thus, hybridization can be taken among all these genotypes to getting useful segregants in F2 generations for the

yield and yield contributing characters. Among the high intercluster distances, hybridization programme can be taken up between the genotypes of clusters I and cluster II and also between the genotypes of cluster I and cluster III for predicting the transgressive sergeants visa-versa an opportunity for selecting genetically

variable genotypes for improvement in linseed. For improvement of hybrid in linseed, heterotic cross combinations can also be exploited. For hybridization programme genotypes from these clusters may be selected, according to their superiority for yield and yield attributing characters.

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