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

Kajal Samantara[1*], Sourav Ranjan Mohapatra[2] and B. D. Pradhan[3]

[1]Department of Genetics and Plant Breeding, Centurion University of Technology and Management, Odisha, India
[2]Division of Genetics and Tree Improvement, Forest Research Institute, Dehradun, Uttarakhand, India
[3]Department of Plant Breeding and Genetics, Orissa University of Agriculture and Technology, Bhubaneswar, Odisha, India

**Corresponding author*

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A B S T R A C T

In this experiment 55 linseed genotypes were evaluated to determine genetic diversity by Mahalanobis D^2 statistics during rabi 2018-19 at the Department of Plant breeding and Genetics, Orissa University of Agriculture and Technology, Odisha India. It revealed that 55 genotypes were grouped into eleven clusters. Result envisaged that genotypes grouped within a particular cluster are more or less genetically similar. Genotypes grouped into cluster I were showed maximum intra-cluster diversity while maximum inter-cluster diversity was observed between cluster XI and V followed by cluster XI and X. So, it could be suggested that hybridization program involving genotypes from the farthest diverse clusters (Cluster XI and V and cluster XI and X) are likely to achieve wider and desirable heterotic recombinants or even transgressive segregants.

Introduction

Linseed (*Linum usitatissimum* L.2n =2x= 30) otherwise called as flax, belongs to family Linaceae and order Geranite. It is a resourceful crop, used for fiber as well as oil (Chauhan *et al.*, 2009). Linseed a conventional oil seed crop has a great economic potential, used in various agro based industries to manufacture paints, varnishes, clothes, patent leathers, printer inks, enamels, stickers, tarpaulins, soaps, linen fabrics, linen threads, canvas bags, quality papers etc. (Savita, 2006). Linseed has numerous medicinal properties for which it is used in local medicines as demulcent, emollient and laxative and is taken orally in bronchial infection and diarrheal (Shafi, 1994). Due to its versatile use there is a high demand of linseed by various industries but

still the production is very low as per its demand, due to lack of high yielding varieties. To overcome the problem of poor yield levels on linseed, development of high yielding varieties becomes the top priority.

Studies on genetic diversity is a basic criterion for the crop improvement as selection of suitable divergent parents for hybridization offer great possibility of obtaining desirable segregants in the segregating generations (Moll and Robinson, 1962).Considering these facts in view, the present investigation was carried out to identify the divergent genotypes of linseed germplasm using Mahalanobis D^2 or non-hierarchical Euclidean cluster analysis for future breeding programme.

Materials and Methods

The present investigation involving 55 accessions of linseed genotypes that includes released varieties advanced breeding lines and local cultivars. The test materials were planted in Randomized Block Design with 2 replications during Rabi season 2018-19.Each genotype was grown in two lines of 3 meters row length and the inter and intra row spacing was maintained as 30cm and 10cm respectively at experimental section of Department of Plant Breeding and Genetics, Orissa University of Agriculture and Technology, Bhubaneswar. Recommended agronomic practices were followed to raise the crop. Five competitive plants from each genotype were selected randomly to record observations on nine traits viz., Days to 50 per cent flowering, Days to maturity, Plant height (cm), Number of branches per plant, Number of primary branches per plant, Number of capsules per plant, Number of seeds per capsule, 1000 seed weight (g), Seed yield per plant (g).The collected data were subjected to analysis of Genetic divergences in fifty five genotypes by using Mahalanobis D^2 statistics, (1936) following Rao (1952). Inter and intra-cluster distances were calculated by method as suggested by Rao (1952).

Results and Discussion

In the present investigation, 55 genotypes of linseed were grouped into eleven distinct non-overlapping clusters (Table 1). All the 55 genotypes of Linseed were distributed into eleven clusters on the basis of D^2 values hence the genotypes within a cluster have comparable D^2 value than other clusters. The maximum numbers of genotypes (27) were present in cluster I and it became the largest cluster of all. Both Cluster II and IV contained a total of 6 genotypes each. Cluster VI retained 4 genotypes followed by Cluster III and V which possessed 3 genotypes as well and at last the whole clustering pattern revealed four such single genotypic clusters which were far more divergent than others (Table 1).

The analysis of the estimates of within and among cluster heterogeneity conferred by intra and inter cluster values admitted that the genotypes within a cluster had little divergence from each other as regards cumulative effect of 9 parameters under investigation. The cluster XI and cluster V found to possess greatest (304.90) inter cluster distance followed by cluster XI and X (280.71) and cluster VIII and V (277.32) indicated wide diversity between these clusters. It is therefore, suggested that crosses should be pursued between the genotypes belonging to cluster pairs separated by large inter-cluster distance. Thus the crossing between the genotypes belongs to cluster XI and cluster V may produce desirable transgressive segregants. Meanwhile the cluster X and cluster II (56.78) exhibited the lowest inter cluster distance followed by VII and cluster II (56.86) expressing less

divergence between the genotypes of these cluster pairs or we could say they were genetically similar to each other (Table 2).

Highest intra cluster distance was found in cluster I (50.60), followed by cluster III (45.03).The maximal intra cluster value marked greatest divergence amid several genotypes within the cluster. Cluster II (30.19) showed lowest intra cluster distance indicating minimum genetic diversity among the genotypes of that group. Therefore, the hybridization between genotypes belonging to the clusters possessing low inter cluster distances were unlikely to achieve heterotic recombinants in segregating generations So it is suggested to attempt crosses between the genotypes belonging to clusters separated by large inter-cluster distance. Ananda and Murty, (1968) also proposed hybridization between lines belonging to clusters separated by large inter cluster distance in linseed. Present finding is in accordance with the findings of earlier linseed worker like Nizar and Mulani (2015) and Kumar *et al.,* (2017).

The mean performance of all the nine quantitative traits of eleven clusters were studied which revealed that Cluster I containing 27 genotypes showed maximum cluster mean for plant height (61.74). The 3genotypes appeared in cluster III indicated highest cluster mean for number of branches per plant (4.43) as well for number of primary branches per plant (3.43).

Table.1 Clustering pattern of 55 linseed genotypes into different groups

Clusters	No. of Genotype	Genotypes included in the clusters
I	27	LMS-17-2K, OL-98-14-2, NL-119, SWETA, T-3-97, V1K2-99-44,LCK-2108, KARTIK, NL-97, V2K3-99-54-1,PADMINI-A,INDRALSI-32, ARPITA, NDL-205, OL-98-6-2,OL-98-13-1A,V1K2-99-57, V2K3-99-71-1, JLT-32, OL-98-13-2, JOWHAR,OLC-10B,OLC-11, NL-157, V1K2-99-48,OLC-10B, OLC-11, NL-157, RLC-93
II	06	PADMINI-B, OL-98-7-4, OL-98-64, OL-98-7-1, GARIMA, LMS-47-2K
III	03	OLC-51, OLC-50, SLA-52
IV	06	INDRA ALSI,PADMINI-C, OL-98-14-3, OL-98-13-1B, JLT-62, OL-98-15-3
V	03	OML-3, V1K2-99-40, SLS-51
VI	04	OLC-10A, L4K-9936, RLC-74, OL-98-15-2
VII	02	NDL-204, V2K3-99-70-1
VIII	01	OL-98-7-3
IX	01	RLC-95
X	01	SUVRA
XI	01	KIRAN

Table.2 Estimates of average intra and inter-cluster distances for the eleven clusters

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	50.60	85.92	87.72	89.04	120.78	78.20	120.01	95.71	101.04	105.71	150.34
II		**30.19***	152.99	104.14	130.95	133.73	56.86	127.47	167.79	56.78	163.08
III			45.03	158.13	119.91	123.70	134.81	143.61	76.04	112.11	268.38
IV				44.88	138.80	71.58	141.89	136.28	112.07	180.90	97.80
V					41.24	194.20	82.57	277.32	94.38	118.99	**304.90****
VI						37.42	203.72	103.29	113.34	175.56	120.73
VII							30.52	195.14	151.80	68.42	237.92
VIII								0.00	158.51	178.57	72.67
IX									0.00	180.90	220.69
X										0.00	280.71
XI											0.00

**Maximum *Minimum (inter-cluster/ intra cluster) values

Table.3 Cluster mean of 55 genotypes of Linseed for nine characters

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/ plant	No. of primary branches/ plant	No. of capsules/ plant	No. of seeds/ Capsule	1000-seed weight(g)	Single plant yield(g)
I (27)	53.96	93.5	**61.74**	3.92	2.93	38.77	8.52	4.94	1.31
II (6)	50.58	**91**	60.13	4.02	3.02	37.05	6.37	5.13	1.24
III (3)	56.67	96.17	56.53	**4.43**	**3.43**	48.47	8.93	4.46	1.7
IV (6)	56.42	95.5	54.92	**3.37**	**2.38**	28.55	8.05	4.62	1.08
V (3)	**60.17**	101.17	61	3.93	2.93	43.4	7.1	4.77	1.19
VI (4)	53.13	94	**54.3**	3.7	2.67	33.05	**9.2**	4.12	**1.03**
VII (2)	55	94	58.05	4.4	3.4	41.4	**6.15**	5.43	1.34
VIII (1)	49.5	91	59.2	4.2	3.2	35.8	9.2	5.84	**1.78**
IX (1)	59.5	**105.5**	58.7	4.3	3.3	36.2	8.6	**4.39**	1.57
X (1)	**49.5**	92	59.2	4.2	3.2	**52.8**	6.4	4.98	1.4
XI (1)	51.5	92.5	54.8	3.4	2.4	**26.6**	9.1	**6.36**	1.12

Bold figures indicate minimum and maximum values

Table.4 Contribution (%) of nine characters towards genetic divergence of linseed

Sl. No	Characters	Contribution
1.	Days to 50% flowering	18.02
2.	Days to maturity	**4.98**
3.	Plant height (cm)	10.13
4.	No. of branches/plant	6.71
5.	No. of primary branches/plant	5.15
6.	No. of capsules/plant	14.24
7.	No. of seeds/capsule	**22.98**
8.	1000-seed weight (g)	11.14
9.	Single plant yield(g)	6.66

Bold figures indicate minimum and maximum values

The 6 genotypes falling in the cluster IV showed minimum mean for both number of branches per plant(3.37) and number of primary branches per plant (2.38).Cluster V comprising 3 genotypes exhibited highest mean for days to 50% flowering (60.17). The cluster VI represented by 4 genotypes revealed smallest mean for both plant height (54.3) and single plant yield (1.03) and highest mean for number of seeds per capsule. Cluster VII retained 2 genotypes showed minimum mean cluster for number of seeds per capsules (6.15). Cluster VIII contained 1 genotype revealed maximum cluster mean for single plant yield (1.78). The 1 genotype of Cluster IX exhibited greatest mean for days to maturity (105.5) and lowest mean for 1000 seed weight (4.39). Cluster X comprising 1 genotype revealed minimum cluster mean for days to 50% flowering (49.5) and maximum for number of capsules per plant (52.8). Likewise the single genotype of cluster XI indicated showed lowest mean for number of capsules per plant (26.6) and highest for 1000 seed weight (6.36) (Table 3).

A wide variation has been confirmed from one cluster to another in respect of cluster mean from the above observation, which pointed out that genotypes having distinct mean performance for various characters were separated into different clusters. Similar findings were also observed by Fulkar *et al.*, (2007) and Kanchan and Rao (2008).

Eleven parameters of 55 linseed cultivars contributed towards genetic divergence are presented in Table-4. Maximum contribution of character towards genetic divergence was observed by number of seeds per capsule (22.98%) followed by days to 50% flowering (18.02%), number of capsules per plant (14.24%). While low contribution of traits towards diversity can be seen for days to maturity (4.98%) and number of primary branches per plant (5.15%). It's been observed from the above that various characters contributed distinctively towards the diversity. These results are in conformity with Mahto and Singh (1996) and Abdul and Mulani (2015) for number of capsule per plant and number of seeds/ capsule that had higher contribution towards divergence.

In conclusion, an appreciable extent of genetic divergence was observed among 55 accessions of linseed. 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 booming seed yield

instead of those based on geographic diversity, which might not be a fruitful exercise for the finding of useful divergent parents.

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