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Genetic diversity (D^2) analysis in Linseed (*Linum usitatissimum* L.)

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Abstract

The characters, days to 50% flowering, plant height, biological yield per plant and capsules per plant contributed more than 86% of the total genetic divergence. Mahalanobis D^2 statistics revealed considerable genetic diversity among the genotypes. The 35 genotypes grouped into six clusters. This envisaged that the genotypes grouped within a particular cluster are more or less genetically similar to each other and apparent wide diversity is mainly due to the remaining genotypes distributed over rest of the other clusters. Genotypes belonging to cluster III (A-49, L-14, A-449, A-434 and 5620-A) exhibited maximum genetic diversity within the cluster as compared to the genotypes belonging to other clusters. Hence, hybridization could be taken up among these genotypes for obtaining desirable sergeants for the yield and yield component traits. On the basis of high inter cluster distance, hybridization programme could be taken up between the varieties of cluster II (A-210, Banner, A-10-2-2 and 191 RR 9/2) and cluster IV (LC-185, A-385 and LC-2063) and also between the varieties of cluster II (A-210, Banner, A-10-2-2 and 191 RR 9/2) and cluster VI (A-404, L-108, ARNY and NP-23K) for expecting the transgressive sergeants *visa-vis* a chance for selecting genetically variable genotypes for improvement in linseed. Heterotic cross combinations could also be exploited for development of hybrid in linseed. Genotypes from these clusters may be selected for hybridization programme, on the basis of their high *per se* performance for yield and yield contributing traits.

Keywords: Clusters, genetic diversity, genotypes, heterosis, hybrids and Linseed

1. Introduction

Linseed (*Linum usitatissimum* L.) commonly known as *Alsi*, belongs to the genus *Linum* of the family Linaceae having 13 genera. Out of these only *Linum usitatissimum* (with diploid chromosome $2n=30$) is the only cultivated species of genus *Linum*. All other species in this genus are wild and are less important economically. The genetic divergence analysis using techniques like Mahalanobis D^2 or non-hierarchical Euclidean cluster analysis, classify the genotypes into homogenous group per cluster with little within cluster diversity, while diversity between two clusters is usually high. Thus representative genotypes from diverse clusters taken for utilization in hybridization programme depend upon breeding objectives.

2. Materials & Methods

The present investigation involving thirty-five genotypes of linseed was undertaken to examine the genetic variability, heritability, genetic advance, correlation coefficient, path coefficient analysis and genetic divergence. Thirty five genotypes of linseed were sown in a Randomized Complete Block Design with three replications during *rabi* season 2015-16. Each genotype was sown in 3 rows plot of 3 meters length, spaced 20 cm apart with plant to plant distance of 5-6 cm at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (UP). Observations were recorded for days to 50 per cent flowering, plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, days to maturity, biological yield per plant (g), seed yield per plant (g), harvest index (%) and 1000 seed weight. All recommended agronomic practices and plant protection measures were followed to raise the good crop. The genetic divergence in thirty five genotypes was estimated by using Mahalanobis D^2 statistics, (1936) following Rao (1952) [15]. Inter and intra-cluster distances were calculated by Ward (1963), method as suggested by Rao, (1952) [15].

3. Results & Discussion

The analysis of genetic divergence among 35 genotypes of linseed was carried out following the method of Mahalanobis ' D^2 ' statistics as described by Rao (1952) [15].

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The clustering was done following Ward method (1963). The intra and inter-cluster distances (D^2 value) and mean performance of the cluster for various characters were also computed. Based on D^2 value, 35 genotypes of linseed were grouped into six clusters. The clustering pattern of the genotypes is presented in Table-1. Cluster I was the largest, comprising of 10 genotypes (Nagarkot, BR-1, A-170, LC-54, BR-14, Baulk, Chambal, Neelum, Shikha and No-55) followed by cluster V with 9 genotypes (Kiran, Sheela, L-18,

LC-1044, Karam banda, L-43, NP-48, No-11 and LCK-88311), cluster III with 5 genotypes (A-49, L-14, A-449, A-434 and 5620-A), cluster II with 4 genotypes (A-210, Banner, A-10-2-2 and 191 RR 9/2), cluster VI with 4 genotypes (A-404, L-108, ARNY and NP-23K) and cluster IV with 3 genotypes (LC-185, A-385 and LC-2063). Similar findings were also observed by Deiderichsen *et al.* (2001) [5]. Adugna *et al.* (2004) [1], Begum *et al.* (2007) [2], Dandigadasar *et al.* (2012) [4], and Chahande *et al.* (2016) [3].

Table-1: Cluster mean values for ten characters of 35 genotypes in linseed.

S. No.	Characters	Cluster mean					
		I	II	III	IV	V	VI
1	Days to 50% flowering	65.467	66.250	75.067	78.222	77.259	75.417
2	Plant height (cm)	64.023	56.400	61.000	62.711	64.626	68.600
3	Primary branches per plant	6.670	5.283	5.480	7.022	6.089	6.600
4	Capsules per plant	145.233	106.183	147.907	190.244	158.681	197.900
5	Seeds per capsule	8.827	9.367	9.367	10.000	9.193	9.033
6	Days to maturity	136.033	134.500	134.067	136.333	135.852	134.333
7	Biological yield per plant (g)	23.120	18.917	20.273	32.022	26.444	29.783
8	Seed yield per plant (g)	8.147	7.467	8.207	9.333	9.348	10.617
9	Harvest index (%)	35.288	39.702	41.051	29.250	35.378	36.051
10	1000 seed weight (g)	6.297	6.102	6.022	5.843	6.123	6.285

In the present investigation the cluster mean for 10 quantitative characters were computed and are presented in Table-2. Days to 50 per cent flowering showed maximum mean in cluster number IV (78.222 days) followed by cluster V (77.259), cluster VI (75.417), cluster III (75.067), cluster II (66.250) and lowest mean for this character was observed in cluster number I (65.467days). The plant height exhibited maximum mean in cluster number VI (68.600 cm) followed by cluster V (64.626), cluster I (64.023), cluster IV (62.711), cluster III (61.000) whereas it was lowest in cluster number II (56.400 cm). The number of primary branches per plant reflected maximum mean in cluster number IV (7.022) followed by cluster I (6.670), cluster VI (6.600), cluster V (6.089), cluster III (5.480) whereas cluster number II reflected minimum mean value (5.283) for this character. Cluster number VI showed maximum cluster mean (197.900) for capsules per plant followed by cluster IV (190.244), cluster V (158.681), cluster III (147.907), cluster I (145.233) whereas it was lowest in cluster number II (106.183). Cluster number IV exhibited maximum mean (10.000) for number of seeds per capsule followed by cluster II (9.367), cluster III (9.367), cluster V (9.193), cluster VI (9.033) whereas it was minimum (8.827) in the cluster number I. The mean value for days to maturity was observed maximum (136.333) in cluster IV followed by cluster I (136.033), cluster V (135.852), cluster IV (134.500), cluster VI (134.333) whereas it was minimum (134.067) in cluster number III. The biological yield per plant, maximum mean value of (32.022g) was observed in cluster number IV followed by cluster VI (29.783g), cluster V (26.444g), cluster I (23.120g), cluster IV (20.273g) and minimum (18.917g) was reflected in cluster II for this character. For seed yield per plant, maximum mean value (10.617g) was observed in cluster number VI followed by cluster V (9.348g), cluster IV (9.333g), cluster III (8.207g), cluster I (8.147g) and minimum value (7.467g) was reflected in cluster II for this character. The mean value for harvest index was observed maximum (41.051%) in cluster III followed by cluster II (39.702%), cluster VI (36.051%), cluster V (35.378%), cluster I (35.288%) and minimum (29.250%) in cluster number IV. Cluster number I showed

maximum mean value (6.297g) for 1000-seed weight followed by cluster VI (6.285g), cluster V (6.123g), cluster II (6.102g), cluster III (6.022g) whereas it was noted minimum (5.843g) in cluster IV. Similar findings were also observed by Maho *et al.* (2004), Fulkar *et al.* (2007) [6], Kanchanand and Rao (2008) [7], and Khan *et al.* (2013) [8].

Table 2: Average intra and inter cluster distance (D^2 value) among six cluster in linseed.

Clusters	I	II	III	IV	V	VI
I	40.984	85.400	135.878	245.454	160.624	171.840
II		34.335	121.442	274.210	198.089	272.349
III			51.649	104.152	61.613	113.281
IV				23.653	62.396	84.128
V					36.773	59.511
VI						42.277

The average intra and inter cluster distance values have been given in Table-3. The maximum intra cluster distance (51.649) was observed for cluster III followed by cluster VI (42.277), cluster I (40.984), cluster V (36.773), cluster II (34.335) whereas the minimum intra cluster distance (23.653) was recorded in case of cluster IV. Maximum inter-cluster distance was found between cluster II and IV, (274.210) followed by clusters II and VI (272.349), cluster I and IV (245.454), cluster II and V (198.089), cluster I and VI (171.840), cluster I and V (160.624), cluster I and III (135.878), cluster II and III (121.442), cluster III and IV (113.281), cluster III and IV (104.152), cluster I and II (85.400), cluster IV and VI (84.128), cluster IV and V (62.773), cluster III and V (61.396) and the minimum inter cluster distance was recorded between cluster V and VI (59.511). The maximum inter cluster distance indicated that genotypes of cluster II and IV are not so closely related whereas the minimum inter cluster distance indicated that the genotypes of these cluster are closely related. The genotypes of cluster V and VI showed minimum inter clusters distances, hence these genotypes are closely related. Similar findings were also observed by Mesharm *et al.* (2008) [11], Nagaraja *et al.* (2010) [12], and Nizar & Mulani (2015) [13].

Table 3: Grouping of 35 genotypes of linseed in 6 clusters.

Cluster	No. of Genotypes	Genotypes
I.	10	Nagarkot, BR-1, A-170, LC-54, BR-14, Baulk, Chambal, Neelum, Shikha and No-55
II.	4	A-210, Banner, A-10-2-2 and 191 RR 9/2
III.	5	A-49, L-14, A-449, A-434 and 5620-A
IV.	3	LC-185, A-385 and LC-2063
V.	9	Kiran, Sheela, L-18, LC-1044, Karam banda, L-43, NP-48, No-11 and LCK-88311
VI.	4	A-404, L-108, ARNY and NP-23K

The contribution of 10 characters of 35 genotypes of linseed towards genetic divergence are given in Table-4. Maximum contribution of character towards genetic divergence was observed by days to 50% flowering (50.76%), followed by plant height (14.12%), biological yield per plant (10.59%), capsules per plant (10.25%), seeds per capsule (4.37%), 1000 seed weight (4.20%), harvest index (2.52%), days to maturity (2.02%). Whereas low contribution of characters towards genetic divergence were recorded for primary branches per plant (0.84%) and seed yield per plant (0.34%). Similar findings were also observed by Srivastava *et al.* (2009) [17], Pali & Mehta (2015) [14], Singh *et al.* (2015) [16], and Upadhyay *et al.* (2016) [18].

Table-4: Contribution (%) of ten characters towards genetic divergence in linseed.

S.N.	Source	Contribution (%)
1	Days to 50% flowering	50.76%
2	Plant height (cm)	14.12%
3	Primary branches per plant	0.84%
4	Capsules per plant	10.25%
5	Seeds per capsule	4.37%
6	Days to maturity	2.02%
7	Biological yield per plant (g)	10.59%
8	Seed yield per plant (g)	0.34%
9	Harvest index (%)	2.52%
10	1000 seed weight (g)	4.20%

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