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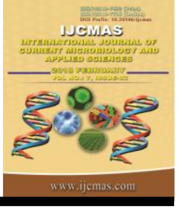

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Diversity Analysis in Linseed (*Linum usitatissimum* L.)

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ABSTRACT

In this experiment 66 linseed genotypes, along with three check varieties (T-397, Mukta and Hira) were analyzed for genetic diversity by Mahalanobis D^2 statistics. Presence of diversity pave way for exploitation of genotypes in breeding programme intended to improve yield and yield attributing traits. The cluster analysis grouped 66 linseed genotypes into 9 distinct clusters. Genotypes grouped into cluster II were showed maximum intra-cluster diversity while cluster V showed minimum intra-cluster diversity. The maximum inter-cluster diversity was observed between cluster VIII and V while minimum inter-cluster diversity was observed between cluster IV and III. From cluster mean value, genotypes in cluster VI, VII and IV deserve consideration for their direct use as parents in hybridization programs to develop high yielding linseed varieties. Thus, hybridization among these cluster pairs is recommended for getting high transgressive segregants in F2 generation.

Keywords

D^2 statistics, Linseed, Inter-cluster, Intra-cluster

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Introduction

Linseed is a versatile crop, used for fiber and oil both. Linseed oil has various industrial and medicinal uses (Chauhan *et al.*, 2009).

Linseed has an increasing demand in agro based industries but still the average productivity is very low as compared to other countries, due to lack of high yielding varieties. The major causes behind low production are cultivation of linseed mainly in marginal land coupled with disease, insect-pest problems and also poor crop management. Few high yielding varieties of linseed are available, which suffers from various biotic and abiotic stresses.

The studies on variation in the germplasm are very useful for developing high yielding, disease and insect- pest resistant cultivars. The selection of suitable divergent parents for hybridization is required because the cross involving diverse parents offer great possibility of obtaining desirable segregants in the segregating generations (Moll and Robinson, 1962).

With comprehension of aforementioned details, a study on genetic divergence analysis using techniques like Mahalanobis D^2 or non-hierarchical were applied to assess genetic variability present in the 66 genotypes along with three check varieties (T-397, Mukta and Hira) used in this experiment. Similar works have also been reported by (Payasi, 2000; Diederichsen, 2001; Adugna and Labuschagne, 2004; Mahto, 2004; Begum *et al.*, 2007). Higher the genetic variability more will be the opportunities to expect improvement through appropriate selection procedure(s) (Muhammad *et al.*, 2003). The study indicated that the different clusters showed considerable difference in inter-cluster group means of 10 characters and genotypes having distinctly different mean performance for various characters and were separated into different clusters.

Based on the high inter cluster distance between cluster VI and I, hybridization between genotypes of these two cluster VI (ICAR Sel.-1) and cluster I (L-9, No-314, H-660, Lck-87042, NDL-2005-22, GS-335) may produce promising genotypes in segregating generations.

Materials and Methods

The experimental material comprising 66 linseed germplasm lines along with three checks (T-397, Mukta and Hira) were planted in augmented block design. The experimental field was divided into three blocks of twenty four plots. The checks were distributed randomly in each block. Observations on the following characteristics were recorded on the basis of five plants randomly selected. The analysis of variance for different characters in Augmented Block Design was done according to Federer (1956).

Genetic divergence was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973). According to Beale (1969) each observation in cluster analysis is initially allocated to its closest cluster center. The means of clusters are then calculated and are taken to new cluster centers. The recommended cultural practices were followed to raise a good crop.

Results and Discussion

The distribution of 66 linseed genotypes in nine clusters is given in (Table 1). Kanchan and Rao (2008) observed nine clusters too while analyzing 90 genotypes. The highest number of genotypes appeared in cluster III which contained 11 entries followed by cluster VI having 10 entries. Cluster VII possess 9 entries, while cluster IX were constituted of 8 lines. Cluster IV having 7 entries. Cluster I and II possessed 6 lines. Cluster VIII having 5lines. Cluster V was represented by 4 entries. The estimates of intra and inter cluster distance for 10 characters are presented in Table 2. The highest intra-cluster distance was observed in case of cluster II (14.53), followed by cluster III (10.88). The lowest intra-cluster distance was noted for cluster V (5.74) followed by cluster VIII (6.85). The maximum inter cluster distance was observed between cluster VIII and V (56.00) followed by cluster VI and V (45.92). The minimum inter-cluster distance was observed between cluster IV and III (13.86) followed by cluster IX and VI (15.38).

Cluster mean for 10 characters are presented in Table 3. The genotypes of cluster VI were responsible for highest cluster mean for days to 50% flowering (89.64 days) followed by entries of cluster VIII (87.37 days) and cluster IV (85.27 days). The genotypes, with early flowering were concentrated in cluster XI (62.57 days). The highest cluster mean for plant height was observed in case of cluster VIII (89.60 cm) followed by cluster VII (74.60 cm). The lowest cluster mean for plant height was found in case of cluster IX (46.53 cm).

Considering the variation in number of primary branches per plant cluster IV (6.14) showed highest mean value while, cluster IX (3.51) had lowest value for number of primary branches per plant.

Table.1 Clustering pattern of 66 linseed genotypes on the basis of non-hierarchical Euclidean cluster analysis for 10 characters

No. Cluster	No. of Genotype	Genotype
1	6	L-9, No-314, H-660, Lck-87042, NDL-2005-22, GS-335.
2	6	GEWARGI 1-2, GS-179, No-1536, GS-229, L-67, H-31.
3	11	GS-415, NDL-2005-16, GS-30, NDL-2011-01, NDL-2011-8, NDL-2007-12, NDL-2005-34, NDL-2007-03, NDL-2005-23, NDL-2005-29, MUKTA.
4	7	H-15, Hy52 RR-9, L-103, L-120, Hyb-603-2, GS-145, Hy-262.
5	4	JRF, ICAR, NDL-2005-24, LC-54
6	10	Kanpur local, NP26 (SR) SK, No-1439, LW-81, H-49, NL-145, GS-436, No-3*RR 485, No-349, L-49.
7	9	L-48, Holden, No-335, L-98, GLC-1-1, GS-53, NDL-2011-09, GUNAUWAL local, No-45
8	5	KP-45, GS-81, JASIHI -1-3, NDL-2005-17, HIRA.
9	8	N-49, NDL-2007-09, NP-36, GS-361, GS-66, L-107, NDL-2011-02, T-397.

Table.2 Estimates of average intra and inter- cluster distances for the 9 clusters in linseed

	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**
I	**10.704**	18.686	23.087	17.684	21.929	17.942	23.640	25.454	17.312
II		**14.531**	19.286	25.399	25.489	24.060	19.000	25.272	23.273
III			**10.885**	13.865	19.632	28.173	20.904	35.759	20.560
IV				**8.101**	17.252	25.501	24.045	37.323	21.175
V					**5.743**	45.926	40.941	56.007	32.777
VI						**8.375**	16.350	18.839	15.384
VII							**8.200**	15.748	20.523
VIII								**6.854**	18.740
IX									**8.121**

Bold figure represent intra-cluster distance

Table.3 Cluster mean of 9 cluster for different characters in linseed

Cluster no.	**Days to 50% flowering**	**Plant height (cm)**	**Primary branches /plant**	**Secondary branches /plant**	**Capsules /plant**	**Seeds /capsules**	**Biological yield /plant**	**Harvest index (%)**	**Test weight (g)**	**Seed yield /plant**
I	84.174	63.950	4.982	51.962	64.450	6.786	6.595	4.400	20.783	20.945
II	68.097	51.744	4.615	44.410	60.056	6.010	6.352	5.474	23.252	23.713
III	77.982	65.945	4.588	29.073	44.648	6.764	7.039**	4.596	21.568	21.075
IV	85.278	67.658	6.149**	72.567	83.621	6.511	6.179	5.870	22.654	25.898
V	77.611	68.667	4.878	42.067	73.033	6.911	6.941	5.257	23.467	21.108
VI	89.644**	56.067	3.778	16.933	31.067*	6.711	6.982	3.436*	18.077*	19.251
VII	81.778	74.600	5.511	100.400**	93.400**	5.578	6.556	6.552**	22.673	28.744**
VIII	87.378*	89.600**	6.111	27.800*	48.800	8.978**	6.176*	4.292	24.133**	16.594*
IX	62.578	46.533*	3.511*	29.467	39.133	4.511*	6.552	3.882	22.090	18.334

Minimum value *
Maximum value **

The highest cluster mean for number of secondary branches per plant was observed in case of cluster VII (100.40) followed by cluster IV (72.56) while genotypes with very low number of secondary branches per plant were found to be grouped in cluster VI (16.93). The highest cluster mean for number of capsules per plant was exhibited by cluster VII (93.40) followed by cluster IV (83.62), while the lowest cluster mean of capsules per plant was produced by entries of cluster VI (31.06).The genotypes occurring in cluster VIII (8.97) and cluster V (6.91) showed highest mean for number of seed per capsule while the genotypes of cluster IX (4.51) were responsible for lowest means for number of seed per capsule. Cluster VIII (24.13g) followed by cluster V (23.46g) were comprised of entries which produced highest mean for biological yield per plant. The lowest cluster mean for biological yield per plant was observed for cluster VI (18.07g). The highest cluster mean for seed yield per plant was observed in case of cluster VII (6.55g) followed by cluster IV (5.87g). The lowest cluster mean for seed yield per plant was exhibited by cluster VI (3.43g)

The nine clusters in the aforesaid divergence analysis contained genotypes of heterogeneous origin frequently. The highest inter-cluster distance was observed between cluster VI and I, followed by cluster VI and III. The lowest inter-cluster distance was observed between cluster VIII and VII followed by cluster VIII and IV, which indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to the clusters separated by low inter cluster distances are unlikely to generate promising recombinants in segregating generations. Ananda and Murty, (1968) also proposed hybridization between lines belonging to clusters separated by large inter cluster distance in linseed. The intra-cluster group mean for 10 characters revealed considerable differences between clusters in respect of cluster means (Table 3). An examination of the estimates of within and between cluster diversity presented by intra and inter cluster D^2 values revealed that the genotypes of same cluster had little divergence from each other with respect to aggregate effect of 10 characters under study (Table 2). Therefore, the chances of obtaining good recombinants in segregating generations by crossing the members of same cluster are very low. It is, therefore, suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter-cluster distance. This finding is in agreement with the report advocating lack of definite relationship between genetic and geographic diversity in linseed (Murty and Ananda, 1968; Jeswani *et al.,* 1970; Asthana and Pandey, 1980; Srivastava *et al.,* 2009; Chauhan *et al.,* 2013).

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