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Extent and pattern of genetic diversity in linseed (*Linum usitatissimum* L) under irrigated ecology

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ABSTRACT

Sixty six genotypes of linseed were analysed for the morphological traits to investigate the genetic diversity between and within the genotypes. The field data was initially subjected to analysis of variance. There were highly significant differences among the genotypes for all the traits indicating the presence of variability among the genotypes and the possibility to undertake cluster analysis. The phenotypic divergence and relative importance were estimated by multivariate analysis. The cluster analysis classified linseed genotypes in to nine major groups. The maximum intercluster diversity was observed between cluster VIII and V. Based on mean performance of the genotypes and intercluster distance the crosses between ICAR Sel-1 and L-9, NDC 2005-34, H660, LCK 87042, NDL2005-22, GS335 is recommended to get use full transgressive sergeants in linseed.

Key words: Crosses, Diversity, Genotypes, Intercluster, Linseed

INTRODUCTION

Linseed/flax is among the oldest crop plants cultivated in temperate climate for the purpose of oil and fibre (Pali and Mehta, 2015). Recent genetic diversity studies suggest that flax may have initially selected as an oil seed crop. Linseed a minor crop is grown in a wide range of countries (47), climates, cropping situations and for many products. At present it is widely cultivated in Asia, Europe, Americas and Africa for oil and fibre. In South west Asia including Turkistan, Afghanistan, India, Nepal and Canada it is primarily cultivated for oil whereas in Russia, Egypt and Near the North western Europe it is mainly cultivated for the production of high quality fibre for making linen fabrics and several other products (Anonymous, 2017).

Breeding programmes is currently focused on enhancing oil content and nutritional value to meet the demand of nutraceutical market. The lustrous fibre of linseed coupled with strength, durability, blending quality with natural and artificial fibres has made its fibre an essential raw material for high value linen fabrics and paper industry for use of printed bank notes and cigarettes. Studies on variation in the germplasm are very useful for developing high yielding disease and insect pest resistant cultivars. The available germplasm serves most valuable natural reservoir in providing donor, parents for in corporating or importing the characteristics by genetic reconstruction of plant for developing high yielding crop varieties.

The proper evaluation of germplasm is essential for understanding its potential value as a breeding material as the success of any breeding programmes depends upon nature and extent of variability present in the germplasm collection. In view of these facts, large numbers of germplasm lines (sixty six) were evaluated in the present investigation.

MATERIALS AND METHODS

A total number of sixty six genotypes of linseed were used in the present study. All the genotypes including three checks T 397, Mukta and Hira were raised at Genetics and Plant Breeding Farm of N.D. University of Agriculture and Technology, Kumarganj, Faizabad (U.P.) during rabi session 2015-16under irrigated conditions for recording the data. The experiment was laid out in augmented block design. The experimental field was divided into three blocks of twenty four plots. The checks were distributed randomly in each block. Each plot consisted of double row of 5 meter length spaced 30 cm apart with plants to plant distance of 10cm observations on the ten traits were recorded viz: days to 50 % flowering, plant height (cm), number of primary branches / plant, number of secondary branches /plant, number of capsules / plant, number of seeds / capsule, biological yield per plant (g), seed yield per plant (g), harvest index (%)and test weight (g).

Five randomly selected plant were tagged from each row for taking observation of all the traits except days to 50% flowering which was recorded on line basis. The data recorded for each genotype was subjected to statistical analysis. Harvest index in per cent was calculated by dividing the seed yield per plant in grams by the biological yield per plant in grams. The data were subjected to statistical analysis to work out mean range as per standard methods. The genetic divergence was studied by employing and non–hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973).

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RESULTS AND DISCUSSIONS

Yield and Yield attributes of linseed genotypes

The mean performance of 63 genotypes and three checks for 10 characters is presented in table 1. Very wide range of variation in mean performance of genotypes was observed for all the characters under study. The comparison of high mean performance of 66 linseed entries for quantitative traits using least significant differences revealed existences of very high level of variability in germplasm collection. The genotype Gewargi 1-2 produced highest seed yield per plant (10.09g) and also showed highest mean performance for number of capsules/plant, harvest index and number of primary branches per plant.

The second highest yielding genotypes GS-415 (9.21g) was also present in significant groups of number secondary branches /plant. The third highest yielding genotypes H-660 (8.12g) was present in significant group for biological yield per plant. The line No. 1439 (7.21g) ranked fourth for seed yield per plant and showed significant group for test weight and biological yield per plant. The fifth highest yielding genotypes NDL 2011-08 (7.00g) present in significant group for number of primary branches branches per plant and showed moderate mean performance for remaining characters. In addition to it, the genotype L48, Holden, and N 36 also showed high mean performance for seed yield and some other characters may be recommended for use in breeding programme as donor or recurrent parent for developing superior genotypes. Sharma *et al.* (2017), Paul *et al.* (2016) and Kant *et al.* (2011) also reported desirable genotypes for seed yield and its components in flax.

Table1: Yield and Yield attributes of linseed genotypes

Characters	Range		Mean value	Range of parameters			
	Min.	Max.		LSD$_1$ 5%	LSD$_2$ 5%	LSD$_3$ 5%	LSD$_4$ 5%
Days to 50% flowering	59.97	94.97	79.41	1.66	2.88	3.3	2.71
Plant height (cm)	43.06	89.60	63.37	7.73	13.38	15.46	12.62
Number of primary branches plant $^{-1}$	3.37	10.17	5.10	1.19	2.06	2.39	1.95
Number of secondary branches plant $^{-1}$	16.93	100.40	50.25	22.56	39.07	45.12	36.84
Number of capsules plant $^{-1}$	28.13	94.66	65.02	10.36	17.95	20.73	16.92
Number of seed capsules $^{-1}$	4.51	8.97	6.55	1.41	2.47	2.86	2.33
Test weight (1000 seed weight g)	4.62	8.13	6.85	1.20	1.35	1.45	1.40
Seed yield plant^{-1}	3.30	10.09	6.69	0.09	0.85	0.87	0.80
Biological yield plant^{-1}	10.62	28.62	19.65	0.28	0.48	0.56	0.46
Harvest index (%)	31.00	35.25	31.12	0.43	0.83	0.96	0.78

LSD$_1$=Least significant difference between two check means.
LSD$_2$ = Least significant difference between adjusted mean of two genotypes in same block.
LSD$_3$ = Least significant difference between adjusted mean of two genotypes in different block.
LSD$_{4=}$ Least significant difference between adjusted mean of genotypes and check mean.

Clustering pattern of linseed genotypes

Sixty three genotypes of linseed were grouped in to nine distinct non over lapping clusters which is in agreement with earlier reports indicating substantial diversity in linseed materials (Kant *et al.* 2011, Pali and Mehta, 2015 and Paul *et al.* (2016). The nine clusters a formed in divergence analysis

Table 2: Clustering pattern of 66 linseed genotypes on the basis of non–hierarchical Euclidean cluster analysis for 10 characters

No. of cluster	No. of genotypes	Genotypes
1	6	L9, No-314, H-660, LCK-87042, NDL-205-22, 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, NP-26(SR) SK, No-1439, LW-81, H-49, NL-145, GS-436, NO-3*RR485, 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, JAISHI-1—3, NDL-2005-15, HIRA.
9	8	N-49, NDL-2005-09, NP-36, GS-361, L-107, NDL-2011-02,T-397.

Table 3: Cluster mean of 9clusters 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 (g)	Harvest Index (%)	Test weight (g)	Seed yield /plant (g)
I	84.174	63.950	4.982	51.962	64.450	6.786	17.595	34.400	6.783	6.945
II	68.097	51.744	4.615	44.410	60.056	6.010	18.352	35.475	7.850	5.713
III	77.982	65.945	4.588	29.073	44.648	6.764	21.039	31.596	6.200	6.075
IV	85.278	67.658	6.149	72.567	83.621	6.511	16.179	35.870	6.654	6.898
V	77.611	68.667	4.878	42.0678	73.033	6.911	17.941	32.257	6.467	6.108
VI	89.644	56.067	3.778	16.933	31.067*	6.711	16.982	31.436	7.077	5.251
VII	81.778	74.600	5.511	100.400	93.400*	5.578	17.556	32.552	6.673	7.744
VIII	87.378	89.600	6.111	27.800	48.800	8.978	16.176*	31.292	6.133	6.594
IX	62.578	46.533	3.511*	29.467	39.133	4.511	16.552	32.882	6.090	5.334

contained genotypes of heterogeneous origin there by indicating no parallelism between genetic and geographic diversity.

Cluster mean of 9 clusters for different characters in linseed

The cluster I having 6 genotypes possessed moderate cluster mean for all the traits except number of secondary branches /plant and number of seeds /capsule which showed lowest cluster means (Table 2 and 3). The cluster II having6 entries possessed moderate cluster mean for all the traits except days to flowering which showed highest cluster means. The 11 genotypes falling in cluster 3rd resulted in highest cluster means for number of secondary branches /plant and test weight which lowest cluster mean for rest of the traits. The cluster IV comprising 7 genotypes had moderate means performance for all the characters. Cluster V having 4 genotypes had highest cluster mean for days to 50 % flowering and number of primary /plant while remaining characters showed highest mean for capsules/plant. Cluster VII comprising 9 genotypes exhibited highest cluster mean for seeds / capsule and lowest cluster mean for test weight while remaining characters showed moderate cluster mean. Cluster IX represented by 8 genotypes which showed lowest cluster mean for the plant-height, number of primary branches / plant and capsule/plant.

Inter - Cluster distances for the 9 clusters in linseed

An examination of the estimates of within and between cluster diversity presented by intra and inter cluster D^2 values revealed that genotypes of the some cluster had little divergence from each other with respect to aggregate effect of 10 characters under study (Table 4). The crosses between the number of clusters separated by high inter cluster distance are likely throw desirable segregates. In this content cluster VI had very high intercluster distance between clusters from remaining 8 clusters. Based on the high inter cluster distance between cluster VI and I, hybridization between genotypes of these the cluster VI (ICAR Sel-1) and Cluster I (L-9, No-314, H660, LCK 87042, NDL 2005-22, GS 335) may produce promising genotypes in segregating genotypes. Pali and Mehta (2015), Sinha and Wagh (2013), Tyagi *et al.* (2014) and Chauhan *et al.* 2013 also suggested the crossing between those clusters with high mean value and high inter cluster distance would help to accumulate favourable and desirable alleles for further improvement in seed yield and its components in flax.

Table 4: Estimate of average intra and inter - Cluster distances for the 9 clusters in linseed

	I	II	III	IV	V	VI	VII	VII	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	23273
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

CONCLUSION

Genetic diversity is essential for crop genetic improvement as it help breeder in selecting parent for hybridization programmes. Among the diverse clusters, genotypes ICAR Selection 1, L 9, No. 314, H660, LCK 87042, NDL 2005-22, GS 335 may be crossed to obtain wider variation for seed yield and other important yield attributes in segregating population.

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