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Genetic divergence in linseed (*Linum usitatissimum* L.) germplasm under late sown condition

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ABSTRACT

One hundred forty genotypes were studied for their genetic divergence in late sown condition through cluster analysis. The results revealed that there were significant differences among linseed germplasm for eight traits. Under late sown conditions, days to 50% flowering and number of capsules per plant are two important characters to be selected to increase seed yield. Intercrossing of selected genotypes from both the distant cluster IV and I would provide enough scope for recombination breeding programme.

1. Introduction

Linseed or flax (*Linum usitatissimum* L.), is popularly known as *Atasi*, *Pesi*, *Phesi* or *Tisi* in Odiya. In Odisha, linseed is cultivated in 0.264 lakh hectares with an annual production of 0.119 lakh tonnes and the productivity level is 451kg / ha. (Anonymous*,* 2011). The low productivity of linseed is mainly due to low yield potential of the existing cultivars with poor crop husbandry. The important linseed growing districts are Mayurbhanj, Kalahandi, Nawapara, Nowrangpur, Keonjhar and Puri.

Though linseed is an important *rabi* oilseed crop of Mayurbhanj district, a significant number of farmers are forced to sow linseed about one month late due to excess moisture in the field (Dash *et al.,* 2011*)*. Now a days, farmers of Mayurbhanj district are sowing linseed one month later than the recommended schedule of the crop i.e. mid October. So an experiment was laid out to study genetic diversity of linseed genotypes in late sown condition, which will help to identify genetically diverse parents for recombination breeding programme.

2. Materials and methods

The crop was sown one month late during November i.e. on 22.11.2006 and 22.11.2007. The field trial was laid out in a Randomized Complete Block Design (RCBD) with two replications. Each genotype was sown in a single row of 3m length with a spacing of 30cm X 5cm between and within the row, respectively. The fertilizers were applied as basal and weedings were done at the right stage following recommended package of practices. Ten randomly selected competitive plants were used to record biometric observations of plant height (cm), number of primary branches / plant, number of capsules / plant, number of seeds / capsule and seed yield / plant (g). But days to 50% flowering, days to maturity, 1000 seed weight (g), reaction to *Alternaria* blight and reaction to wilt were recorded on whole row basis.

3. Results and discussion

Analysis of variance revealed highly significant differences among the genotypes for all the eight characters. 140 linseed genotypes were tested for genetic divergence to ascertain the nature of genetic variability existing among the genotypes. Classification using multivariate analysis of

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genetic divergence aims at grouping the genotypes precisely and objectively into various clusters by adopting different methods. In the present investigation simultaneous variations in all the eight characters of 140 genotypes of linseed were tested for assessing the nature of genetic divergence among them following Mahalanobis (1928) D^2 statistics as described by Rao (1952) and group constellation was done following Tocher's method (Singh and Chaudhary, 1977).

Following the cluster analysis, by Tocher's method 140 linseed genotypes were grouped into 11 groups or clusters consisting of 2 to 68 genotypes. Cluster XI retained the highest number (68 genotypes) followed by cluster VI (27 genotypes). Cluster VIII contained 14 genotypes followed by cluster I, VII, and X contained 10, 6 and 5 genotypes respectively. Cluster II, III, IV, V and IX which had only 2 genotypes in each are presented in Table 1.

In the past, eco-geographical diversity has been largely relied as an index of genetic diversity. This criterion being only inferential, obviously, cannot be used for discrimination among the populations of same or similar geographical region. Published results are highly conflicting with regard to geographical distribution and genetic diversity. A number of workers indicated somewhat close relationship between the two (Sinha *et al*., 2001). On the other hand, a large number of crop plants including linseed with different breeding systems showed no parallelism between genetic diversity and eco-geographical distribution (Murthy and Arunachalam, 1966; Verma, 1996; Singh *et al*., 1999; Datta and Mani, 2003).

In the present study, all the eleven clusters contained genotypes from different locations. The clustering pattern revealed that the tendency of genotypes from diverse geographic regions to group together in one cluster might be due to similarity in requirements and selection approaches followed under domestic cultivation (Arunachalam and Ram, 1967). It was also observed that the genotypes belonging to the same state were distributed in different clusters indicating wide genetic diversity among genotypes

Table 1
Clustering pattern of 140 Linseed genotypes pooled over two years.

Cluster	No.of Genotypes	Genotypes
I	10	OL 3-1, OL 98-12-1,OL98-2-5, OL98-1-4, ACC.NO.442, 1052/RLC-27, RL-771, OLC-61, LCK-9814., LMH-78.
II	02	LIN-99289, PCA-12.
III	02	RLC-28, OL98-2-4.
IV	02	BAULK-2, JRF-4.
V	02	LCK-241, LMC-926.
VI	27	OL93418-2-2, OL98-11-4, LCK-14, RL-87, LMH-42, OL98-8-1, LC-1038, OL98-18-4, LC-54, LHCK-10, OL98-8-8, OL-4-1, RL-17, OL98-7-5, 1216/JRF-5, OL2-4, OL2-7, MLH-12, LMH16-5, RLC-3, OL98-2-2, LCK-206, OL98-3-I, BAUL-4-4, RLC-1, P650, OLC-22.
VII	6	JLT-32, Mayurbhanj Local, RLC-41, OL98-2-1, LC-1009, LCK-8901.
VIII	14	NML-4, LCK10-10, ACNO-1396, OL98-2-3, OL98-9-4, NL-129, LC-1049, OL98-1-2, GS-234,OL98-1-4, JRF-3, NL-9, OL98-17-6, RL-1011.
IX	02	OL98-18-3, OL98-7-2.
X	05	OL98-8-3, RLC-29, RLC-6, PCA-8, LCM-1020.
XI	68	OLC-58, LIN-2, LCK-3707, PLP-1, OL93418-1, PCA-18, LW36-3, POLF-19, RLC-27, OL92-16-3, LCK-119, OL98-16-7, LHCK-82, LCK-9733, RLA-71, SLS-27, JRF-5, RRL-1, LCK-216, SPS72-23-10, LIN-12, OL98-5-3, CI-1466, PCA-89, OL2-5, LCK-233-1, RLC-42, OL98-18-5, EC-41563, BAULK-1, LCK-9436, NL-142, NDL8804, OL98-11-2, PCA-7, LCK-8523, BAU-4708, LHCK-176, OL98-3-2, OL1-3RLC-44, OL7-7, OL3-2, LCK8132, CHIPILIMA-6, LMH-43, PKDL-8, NL-97, OL98-17-6, CHIPILIMA-3, SLS-26, 1396, LCK9816, LMH-16-5, OLC-37, OL98-5-1, LCK875, LMH-90-7, OL98-5-6, EC-1392, KL49-47, A95-13, LS-2323, PCA-9, BAULK-8, Padmimi, OLC-11, RLC-2.

Table 2
Estimates of average intra and inter cluster distances for 11 clusters involving 140 genotypes of linseed.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	4.999	4.814	4.834	4.332	4.436	5.149	5.189	5.32	5.643	4.932	5.169
II		1.016	2.643	2.701	1.628	4.315	3.668	4.39	2.289	4.22	3.907
III			1.033	2.861	2.4	4.429	4.527	4.559	3.677	4.422	4.058
IV				1.106	2.784	4.319	4.177	4.393	3.617	3.954	3.831
V					1.127	3.944	3.529	4.204	2.896	3.886	3.723
VI						5.221	5.058	5.327	5.18	5.036	5.081
VII							4.652	5.419	4.073	5.087	4.910
VIII								5.45	5.311	5.003	5.206
IX									1.438	4.907	4.613
X										5.051	4.897
XI											4.874

originating from the same geographic regions. The clustering pattern, thus, revealed lack of strict correspondence between genetic divergence and geographic distribution. This could be due to genetic drift and selection in different environments which caused greater diversity than geographic distances. Previous research work also observed non parallelism between genetic diversity and geographic distribution of the genotypes in linseed (Murthy and Arunachalam, 1966; Jeswani *et al.,* 1970; Asthana and Pandey, 1980; Sarkar, 2005).

The estimates of average intra and inter cluster distances among the 140 genotypes have been presented in Table 2. Using Mahalanobis D^2 statistics the highest intra-cluster distance was noticed in cluster VIII (5.45) followed by cluster VI (5.221). The least intra-cluster distance was reported in cluster II (1.016). The spectrum of intra cluster distance revealed that Cluster VIII contained 14 genotypes, but showed maximum intra cluster distance (5.45), which would be due to heterogeneous nature of the genotypes included in the cluster i.e some genetic divergence still existed among the genotypes.

The spectrum of intercluster distance ranges from 1.628 (Cluster II and V) to 5.643 (Cluster I and IX). The highest inter cluster distance of 5.643 was obserced between cluster IX and cluster I followed by 5.419 (Cluster VII and VIII) and 5.327 (Cluster VI and VIII). This indicated that the genotypes of cluster IX were distantly related to those of clusters I, and those of VIII to VII and VI. On the other hand, minimum intercluster distance was observed between cluster V and cluster II (1.628) indicating less divergence between the genotypes.

As regards the inter-cluster distance cluster IX showed maximum genetic distance from cluster I suggesting wide diversity between these groups. Crosses involving genotypes from these clusters are likely to produce wider and desirable recombinants and this could help in producing wider variable progeny. It has been pointed that selection of parent for hybridization should be done from two clusters having wider inter cluster distance to get maximum variability in segregating generations (Mahto, 1995; Singh *et al*., 1995; Mahto and Singh, 1997; Payasi, 2000; Sarkar, 2005; Naik, 2008).

The intra cluster means of eight yield parameters for different clusters revealed that Cluster I had maximum values in number of primary branches per plant (0.702), number of capsules per plant (18.382), and seed yield per plant (0.697g). Cluster II had minimum days to 50% flowering (68.38). Cluster III was characterized with minimum values in plant height (50.775 cm), number of seeds per capsule (6.813) and seed yield per plant (0.411g). Cluster IV had maximum days to 50% flowering (72.25) and minimum values in 1000 seed weight (4.887g). Cluster V showed maximum days to maturity (119.38) and plant height (54.975 cm) Cluster VII had maximum number of seeds per capsule (8.058). Cluster IX was characterized with minimum days to maturity (116.88), number of primary branches per plant (0.100) and number of capsules per plant (11.400) and maximum 1000 seed weight (6.913).

Under late sown conditions, days to 50% flowering and number of capsules per plant are two important criteria for selection to increase seed yield. Cluster IV and I had highest cluster means for days to 50% flowering and number of capsules per plant, respectively. Two genotypes,*viz.* BAULK- 2 and JRF- 4, whose mean number of capsules per

plant are 16.30 and 16.50 respectively were selected for days to 50% flowering from cluster IV. Similarly, four genotypes,*viz* OL3-1, OL98-2-5, OL98-1-4 and RL-771, whose mean for days to 50% flowering are 80.25, 74.75, 73.00 and 71.00 were selected for number of capsules per plant from cluster I , keeping the score of days to 50% flowering above the grand mean of 70.25. Inter crossing of selected genotypes from both the distant clusters IV and I would provide enough scope for recombination breeding programme to have varieties with higher days to 50% flowering and number of capsules per plant for improving seed yield in late sown conditions.

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