ASSESSMENT OF GENETIC DIVERSITY OF LINSEED (*Linum usitatissimum* L.) GERMPLASM

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ABSTRACT

One hundred and nine genotypes were evaluated for genetic divergence to identify potential parents for linseed programme aimed for yield improvement. Mahalanobis D^2 statistics for thirteen characters *viz.*, days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant[-1], number of capsule plant[-1], capsule size (mm), seed yield plant[-1] (g), seed size (mm), 1000 seed weight (g), seed yield plot[-1] in (kg ha^{-1}), % budfly infestation, % alternaria blight infestation, flower size (mm), were used in this study for computing genetic divergence. The analysis of dispersion for thirteen characters using Wilk's criterion, revealed highly significant difference between genotypes for all thirteen characters. The one hundred nine genotypes were grouped into eight clusters by Tocher's method. The maximum inter cluster distance was recorded between cluster II and VIII (D^2=31.70), whereas minimum inter cluster distance was found in between cluster I and cluster VI (D^2=15.11) and in between cluster V and cluster IX (D^2=7.60). The canonical analysis revealed that differentiation for thirteen characters among one hundred nine genotypes was completed in five phases indicated the importance of flower size, seed size, number of capsule plant[-1], days to 50% flowering for selecting parents. The canonical analysis and cluster means studied together revealed the importance of days to 50% flowering, capsule size, plant height, days to maturity of as important contributors towards the total divergence. The parents GS 52, Meera, GS 105, EC 99001, EX 16, EC 1534, Padmini, ES 1463, ES 14600, EC 1474, Indira Alsi 2, GS 49, ES 1463 can be used for further hybridization programme. These genotypes on hybridization with existing check varieties may also be used for their improvement.

(Keywords: Genetic divergence, linseed, clusters)

INTRODUCTION

Linseed is one of the most important oilseed crops for industrial as well as food, feed, and fiber purposes. It is an annual, self-pollinating, autogamous diploid (2n=2x=30) oilseed crop, belonging to the family *Linaceae* having 14 genera and over 200 species. The study of genetic diversity plays significant role by providing basis in making selection of parents for hybridization programme in crop improvement programme. Mahalanobis D^2 statistics is a powerful tool to measure the degree of divergence among group genotypes based on multiple characters and for selecting efficient parents for hybridization programme in out-breeding and self-pollinated crops.(Rao, 1952; Murty and Arunachalam, 1966).

MATERIALS AND METHODS

The experiment consisting of one hundred and nine genotypes of linseed was laid at AICRP on linseed and mustard farm, College of Agriculture, Nagpur in Randomized Block Design (RBD) with two replications. Each genotype was sown in a single row having spacing of 30 cm × 5 cm. Recommended agronomical practices and plant protection measures were adopted to raise the good crop. Five plants were taken randomly from each plot for recording the observations. Observations for thirteen quantitative characters *viz.,* days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant[-1], number of capsule plant[-1], capsule size (mm), seed yield plant[-1] (g), seed size (mm), 1000 seed weight (g), seed yield plot[-1] in (kg ha^{-1}), % budfly infestation, % alternaria blight infestation, flower size (mm) were used in this study for computing genetic divergence. D^2 analysis was carried out as per Mahalanobis (1936).

RESULTS AND DISCUSSION

The data on mean squares due to the genotypes were highly significant for all thirteen characters studied *i.e.* flower size (mm), days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant[-1], number of capsule plant[-1],

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capsule size (mm), seed yield plant^{-1} (g), seed size (mm), 1000 seed weight (g), seed yield plot^{-1} in (kg ha^{-1}), bud fly infestation (%), alternaria blight infestation (%) indicating the presence of considerable genetic variation among the genotypes for the characters studied. Paul *et al*. (2017) and Shah *et al*. (2021) observed highly significant differences among the genotypes for all the characters indicating sufficient variability in the material (Table 1) of linseed.

The analysis of dispersion to test significant differences in the mean values based on the Wilk's criterion revealed highly significant differences among genotypes for thirteen characters (Table 2). Diversity analysis was also carried out in linseed by Pali and Mehta (2015), Paul *et al*. (2017) and Sharma *et al*. (2017) also reported significant divergence among the genotypes for all the characters studied in linseed.

Data revealed that the contribution of plant height was maximum (36.07)% followed by capsule size(25.31%), flower size (18.82%), 1000 seed weight(g) (5.73%),seed size (5.33%),seed yield plant^{-1} (3.70%), days to 50% flowering (3.48%),number of primary branches plant^{-1} (0.48%),days to maturity (0.36%),% alternaria blight infestation (0.27%), seed yield plot^{-1}(0.24%),number of capsule plant^{-1} (0.17%) and % budfly infestation (0.03%) This indicates that the characters like plant height, capsule size, flowersize were important traits contributing towards genetic divergence (Table 3).

The entire genotypes were grouped on the basis of D^2 statistics into eight clusters. The cluster I was largest comprising of 41 genotypes, followed by cluster II comprising of thirty six genotypes, cluster III comprising of seventeen genotypes, cluster IV comprising of eleven genotypes, cluster V, cluster VI, cluster VII, cluster VIII each of comprising single genotypes. The check PKV NL 260 was grouped into cluster IV along with sixteen genotypes. This indicates that there are many germplasms which were highly diverse from the check and hence offers good scope for improvement (Table 4).

Data of the first five canonical vectors and canonical roots are presented in Table 5 and Table 6. The first five canonical roots accounted for 88.37 per cent of the observed variability in the material studied (ë1= 37.74%, ë2=20.61 %, ë3=15.72 %, ë4=8.39%, ë5=5.91 %).The overall contributions of the five canonical roots to the total variability among 109 genotypes were 88.37 per cent suggesting the major portion of differentiation in first five phases. This indicates that differentiations for thirteen characters among 109 genotypes were completed in five phases. Further coefficient in first five canonical vectors shows that out of 13 characters plant height, flower size,alternaria blight infestation, capsule size, seed yield plant^{-1}, seed size contributed in vector I accounting for 37.74% of total variation. Capsule size, days to 50% flowering, seed size, seed yield plot^{-1}, flower size, were important characters in vector II which accounted for 20.61 % of total variation. Flower size, seed size, number of primary branches, number of capsule plant^{-1}, capsule size were important characters in vector III which accounted for 15.72 % of total variation. The important characters in vector IV seed yield plant^{-1},1000 seed weight, flower size, number of capsule plant^{-1}are accounted for 8.39% of total variation. The important characters in vector V were capsule size, flower size, 1000 seed weight, number of primary branches accounted for 5.91 % of total variation. This suggested that the parents selected on the basis of flower size , seed size,number of capsule plant^{-1}, days to 50% flowering , may expected to be genetically diverse.

Data regarding inter cluster distance showed that in most of the cases under cluster distances were higher than the intra cluster distance. The intra cluster distance ranged from 0.00 to 17.57. Cluster IV possessed highest intra cluster distance (D^2=17.57) followed by cluster III (D^2=13.56) and cluster II (D^2=12.80). The average inter cluster distance was maximum between cluster II and VIII (D^2=31.70), followed by cluster V and cluster VII (D^2=31.39), cluster III and cluster VIII (D^2=31.25) and cluster VII and cluster VIII (D^2=27.60) suggesting more variability in genetic makeup of genotypes included in these clusters. The inter cluster distance was found to be minimum between cluster I and cluster VI (D^2=15.11) (Table 7).

Data of cluster mean for all the thirteen characters revealed highest cluster mean for plant height, days to 50% flowering, days to maturity, % alternaria blight infestation, capsule size, seed yield plant^{-1}(Table 8).

All possible cluster combinations beyond the mean statistical distance D = 9.24 have been arranged in descending order. From the data clusters showing maximum inter cluster distance (31.25) was the cluster III and cluster VIII, and the parents in clusters showing highest mean significant superiority for seed yield plant^{-1} and % bud fly infestation were parents Meera, GS 52 and GS 105, another clusters having inter cluster distance of 24.65 (cluster III and IV) also included parents GS 52, EC 99001, ES 16, EC 1534, Padmini, ES 1463, ES 14600, EC 1474 and GS 105. Cluster III and V (D=23.43) consisted of parents GS 52, Indira Alsi 2 and GS 105, whereas Cluster IV and VII (D=21.43) included parents PKV NL 260 and GS 49. Cluster IV and VII (D=21.28) which included parents PKV NL 260 and Meera which was followed by cluster IV and V (D=21.12) included parents *viz*.,PKV NL 260 and Indira Alsi 2 followed by cluster III and VII (D=20.79) which included parents *viz*., GS 52, GS 49 and GS 105 all of these parents were significantly superior for seed yield plant^{-1} with resistance in % bud fly infestation over other parentsand these were identified potential parents for further hybridization programme (Table 9).

Table 1. Analysis of variance for thirteen characters

Sr. No	Characters	Replication	Genotypes	Error
1	**d.f**	1	108	108
2	Days to 50% flowering	5.62	66.75**	6.09
3	Days to maturity	2.69	41.66**	10.04
4	Plant height (cm)	0.39	133.38**	1.82
5	Number of primary branches plant^{-1}	0.1763	0.3465**	0.0848
6	Number of capsule plant^{-1}	23119.38	115.12**	29.36
7	Seed yield plant $^{-1}$ (g)	0.0505	0.2198**	0.0143
8	Seed yield plot^{-1} (kg ha^{-1})	4.30	60643.01**	19772.07
9	1000 seed weight (g)	1	5.50**	0.51
10	% Budfly infestation	226.28	47.34*	27.46
11	% Alternaria blight infestation	8.88	42.90*	29.38
12	Flower size(mm)	0.66	9.36**	0.22
13	Capsule size (mm)	0.0001	0.7215**	0.0147
14	Seed size (mm)	0.0412	0.1704**	0.0110

* significant at 5% level** significant at 1% level

Table 2. Analysis of dispersion

Sources of variation	df	Sum of squares	Mean sum of squares
Genotypes	108	4.1518E15	3.8443E13*
Error	107	2.6966E02	2.5202E00
Total	215	4.1518E15	1.9311E13

* significant at 5% level

Table 3. Contribution of different characters towards divergence in linseed

Sr.No.	Characters	Time ranked 1st	Percent Contribution
1	Days to 50% flowering	205	3.48 %
2	Days to maturity	21	0.36%
3	Plant height (cm)	2123	36.07%
4	Number of primary branches plant^{-1}	28	0.48%
5	Number of capsule plant^{-1}	10	0.17%
6	Seed yield plant $^{-1}$ (g)	218	3.70%
7	Seed yield plot^{-1} (kg ha^{-1})	14	0.24 %
8	1000 seed weight (g)	337	5.73 %
9	% Budfly infestation	2	0.03%
10	% Alternaria blight infestation	16	0.27%
11	Flower size(mm)	1108	18.82%
12	Capsule size (mm)	1490	25.31%
13	Seed size (mm)	314	5.33%
	Total	**5886**	
	Tocher cut off value	**189.45**	

Table 4. Grouping of genotypes into different clusters in linseed

Cluster	Number of genotypes	Name of the genotypes
I	41	CI 2260,FR 11,GS 109,EC 1066,ES 14230,GS 69,GS 20,GS 42,NL 356,GS 1 28,Gewargi 1-2,ES 165-36,EC 41741,JSL 95,GS 410,GS 100,GS 145,BAU 14-19,A 429, GS 111,EC 41623,GS 139,GS 85,GS 54,R552,Kiran,GS 129,Parvati,EC 11588,GS 121,ES 15890,GLC 11-1,FRW 6,FR 11,ES 1444,EC 14539,EC 41659,EX 313-23,ES 1531,FLAX 16,GS 187.
II	36	EC 1645,EC 41628,GS 108,RAC 6,CI 1924,CI 2006, Fatehpur,Mutant 2,GLC 1-1,GS 55,GS 40,Mutant-5,Priyam,GS 82,GS 36,UPN 15,Binwa,EC 98994,GS 27, Mutant-4,GS 30,GF 3-3-NO-3,ES 1456,ES 1440,EC 1628,E20X NATURAL, EC 51904,Indira-Alsi-32,GS 15,EC 1424,GF 3-3,OL 10-15,RLC-159,Shekhar,GS 134,FX 16.
III	17	GIF White,Divya,GS 130,T 397,EX 3,GS 43,GS 4,GS 61,GS 51,EX 53-98,GS 41,GS 64,GS 148pp,GS 52,EC 1386,GS 105,ES 15889.
IV	11	EC 99001,EX 16,ES 1534,NL 97,PKV NL 260,Padmini,FRW 12,TL 99,ES 1463,ES 14600,EC 1474.
V	1	Indira Alsi 2
VI	1	EI 5611
VII	1	GS 49
VIII	1	Meera

Table 5. Values of first five vectors

Sr. No.	Characters	Vector I	Vector II	Vector III	Vector IV	Vector V
1	Days to 50% flowering	0.06773	0.26725	-0.01948	0.02720	-0.6882
2	Days to maturity	-0.0351	0.00434	-0.06500	-0.0027	-0.3288
3	Plant height	0.80534	0.12165	-0.33179	0.02270	-0.2030
4	Number of primary branches	0.08134	0.02579	0.20446	0.07506	0.04711
5	Number of capsule plant^{-1}	-0.1289	-0.08233	0.17690	0.10001	-0.1631
6	Seed yield plant^{-1}	0.04856	-0.01020	-0.20124	0.67036	-0.1198
7	Seed yield plot^{-1}	-0.2033	0.18560	0.00799	0.05287	-0.1469
8	1000 seed weight	-0.2891	0.02401	-0.26630	0.58542	0.06352
9	% Budfly infestation	-0.0699	-0.09940	-0.06560	0.06319	-0.1381
10	% Alternaria blight infestation	0.28018	-0.04581	-0.07010	0.09593	0.05155
11	Flower size	0.29620	0.03777	0.77927	0.39827	0.07547
12	Capsule size	0.14768	0.87544	0.15536	0.02121	0.32352
13	Seed size	0.04636	0.30231	0.24517	-0.1263	-0.4198

Table6. Five canonical roots and their contribution expressed as per cent of the total variation

Root	Eigen value	Contribution in percent
λ_1	5873.08	37.74
λ_2	3208.29	20.61
λ_3	2446.94	15.72
λ_4	1305.85	8.39
λ_5	920.23	5.91
Total	13754.39	88.37
Sum of all canonical roots		100
Residual		11.63

Table 7. Average intra and inter cluster distance D² values in linseed

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**12.00**	16.85	16.99	17.46	19.71	15.11	16.85	21.56
II		**12.80**	16.64	21.62	23.88	21.38	19.93	31.70
III			**13.56**	24.65	23.43	19.17	20.79	31.25
IV				**17.57**	21.12	22.23	21.45	21.28
V					**0.00**	25.10	31.39	22.27
VI						**0.00**	16.59	21.76
VII							**0.00**	27.60
VIII								**0.00**

=9.24 Bold figures are average intra cluster distance

Table 8. Cluster means for thirteen characters

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches	No. of capsules	Seed yield plant^{-1} (g)	Seed yield plot^{-1} (kg ha^{-1})	1000 seed weight (g)	% Bud fly	% Alternaria blight	Flower size (mm)	Capsule size (mm)	Seed size (mm)
1	57.12	112.80	50.80	2.81	43.12	1.24	823.63	7.72	23.52	16.14	14.91	7.17	4.49
2	57.65	112.32	38.90	2.72	46.65	1.14	838.06	7.24	26.00	13.74	14.37	7.74	4.69
3	55.56	112.12	39.93	2.65	42.47	1.30	851.62	7.73	24.15	14.14	14.37	6.64	4.43
4	56.23	112.64	53.67	2.87	48.75	1.49	877.77	8.63	23.16	14.70	17.39	7.90	4.75
5	50.00	108.00	46.10	3.60	52.70	0.92	718.50	5.20	17.35	19.05	19.60	6.71	5.11
6	61.50	106.50	60.20	3.00	55.40	1.33	1130.00	9.55	26.10	16.85	11.10	6.34	4.92
7	61.00	110.00	53.30	2.60	42.30	2.16	863.50	11.10	25.90	20.35	12.40	7.69	4.12
8	62.50	119.00	71.20	3.30	52.60	1.22	817.50	8.00	24.70	22.35	17.40	6.80	4.69
SD	**4.05**	**3.77**	**10.65**	**0.35**	**5.17**	**0.37**	**117.55**	**1.72**	**2.87**	**3.13**	**2.81**	**0.59**	**0.31**
VAR	**16.39**	**14.22**	**113.35**	**0.12**	**26.75**	**0.13**	**13817.86**	**2.97**	**8.22**	**9.81**	**7.87**	**0.35**	**0.09**

Table 9.Selection of genotypes based on inter cluster distances and cluster means

Clusters	Distance between clusters	Selection based on seed yield plant^{-1} and % bud fly infestation
III &VIII	31.25	GS 52 X Meera, GS 105 X Meera
III & IV	24.65	GS 52 X EC 99001, GS 52 X EX 16, GS 52 X EC 1534, GS 52 X Padmini, GS 52X ES 1463, GS 52 X ES 14600, GS 52 X EC 1474, GS 105 X EC 99001, GS 105 X EX 16, GS 105 X EC 1534, GS 105 X Padmini, GS 105X ES 1463, GS 105 X ES 14600, GS 105 X EC 1474
III & V	23.43	GS 52 X Indira Alsi 2, GS 105 X Indira Alsi 2
IV & VII	21.45	PKV NL 260 X GS 49
IV & VIII	21.28	PKV NL 260 X Meera
IV &V	21.12	PKV NL 260 X Indira ALSI 2
III & VII	20.79	GS 52 X GS 49, GS 105 X GS 49

$\bar{D}$=9.24

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