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GENETIC DIVERSITY STUDIES FOR YIELD AND YIELD CONTRIBUTING TRAITS IN LINSEED

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ABSTRACT

Sixty-nine genotypes were evaluated for genetic divergence to identify potential parents for linseed programme aimed for yield improvement in *rabi* 2018-19. Mahalanobis D^2 statistics for thirteen characters viz., 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 capsules plant^{-1}, capsules 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 were used in this study for computing genetic divergence. The analysis of dispersion for thirteen characters correlated variables using Wilk's criterion, revealed highly significant difference between genotypes for all thirteen characters. The sixty nine genotypes were grouped into ten clusters by Tocher's method. The maximum inter cluster distance was recorded between cluster IV and IX (D^2=451.74), whereas minimum inter cluster distance was found in between cluster I and cluster V (D^2=97.59). The canonical analysis revealed that differentiation for thirteen characters among sixty nine genotypes was completed in five phases indicated the importance of days to 50% flowering, number of primary branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight, seed yield plant^{-1}, seed yield plot^{-1}, days to maturity and plant height for selecting parents respectively. The canonical analysis and cluster means study revealed the importance of days to 50% flowering, number of primary branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight, seed yield plant^{-1} and plant height as contributors to the total divergence. The parents NL 115, NL 394, NL 392, NL 409, NL 420, NL 414, NL 414, NL 418, NL 384, NL 375, NL 417 were significantly superior over the checks for number of capsules plant^{-1} and seed yield plant^{-1} and seed yield plot^{-1}. These genotypes on hybridization with existing check varieties may also be used for improvement of the check varieties.

(Key words: Genetic divergence, linseed, clusters)

INTRODUCTION

Linseed or flax (*Linum usitatissimum* L.) commonly known as Jawas alsi, tisi, mosina and arisi is a pristine crop. It is an annual, self- pollinating, autogamous diploid (2n=2x=30) oilseed crop, belonging to the family *Linaceae* and order Geraniale 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. The more diverse parents with in overall criterion of fitness are supposed to give higher amount of hybrid vigour and wide range of variability in segregating population. 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, became possible due to Mahalanobis D^2 statistics based on multivariate analysis of quantitative traits which is a powerful tool (Rao, 1952; Murty and Arunachalam, 1966).

MATERIALS AND METHODS

The experiment consisting of sixty- nine genotypes of linseed was conducted at AICRP on linseed and mustard farm, College of Agriculture, Nagpur is a Randomized Block Design (RBD) with two replications during *rabi* 2018-2019. The experiment was sown on 4th November, 2018. Each genotype was sown in a plot of 30 cm × 5 cm respectively. 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

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observations. Observations were recorded for thirteen quantitative characters viz. 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 capsules plant^{-1}, capsule size (mm), seed yield plant (g), seed size (mm), 1000 seed weight (g), seed yield plot^{-1} in (kg ha^{-1}), % bud fly infestation, % alternaria blight infestation were used in this study for computing genetic divergence. D^2 analysis has following important steps as per Mahalanobis (1936).

RESULTS AND DISCUSSION

The 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 capsules 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}), bud fly infestation (%), alternaria blight infestation (%) indicating the presence of considerable genetic variation among the genotypes for the characters studied. Choudhary *et al*. (2017) observed the analysis of variance due to genotypes for all the characters studied were found to be significant except number of seeds capsule^{-1} and number of primary branches plant^{-1} (Table 1).

The analysis of dispersion for the test of significance of difference in the mean values based on the Wilk's criterion revealed highly significant difference among genotypes for thirteen characters are presented in Table 2. Therefore, the data were further evaluated for D² and cluster analysis. Diversity analysis was also carried out in linseed by Pali and Mehta (2015) and Sharma *et al*. (2017),who also reported significant divergence among the genotypes for all the characters studied.

Contribution of capsule size was maximum (33.39%) followed by plant height (18.07), number of capsules plant^{-1} (17.05%), seed size (15.43%), number of primary branches^{-1} (10.10%), budfly (4.26%), days to maturity (3.58%), 1000 seed weight (1.36%), days to 50%flowering (0.80%), seed yield plot^{-1} (0.46%), alternaria blight (0.38%) and seed yield plant^{-1} (0.29%). This indicates that characters like capsule size, plant height, number of capsules plant^{-1} were important traits contributing towards genetic divergence (Table 3).

The data regarding grouping of D² statistics into ten clusters are given inTable 4. The cluster II was largest comprising of 22 genotypes, followed by cluster I comprising of twenty genotypes, cluster III comprising of twelve genotypes, cluster IV comprising of nine genotypes, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX and cluster X each of comprising single genotypes. The checks LSL 93, Padmini, T 397 grouped into cluster II along with nineteen genotypes. While, the check PKV NL 260 grouped into cluster IV along with eight genotypes. This indicates that there are many germplasms which were highly diverse from the check and hence, offers good scope for improvement.

The value of first five canonical vectors and canonical roots are presented in Table 5a and 5b. The first five canonical roots accounted for 87.56 per cent of the observed variability in the material studied (λ_1= 33.21%, λ_2= 25.88%, λ_3= 11.51%, λ_4=10.36%, λ_5= 6.60%). The overall contributions of the five canonical roots to the total variability among 69 genotypes were 87.56 per cent suggesting the major portion of differentiation in first five phases. This indicates that differentiations for thirteen characters among 69 genotypes were completed in five phases. Further coefficient in first five canonical vectors that out of 13 characters seed size, seed yield plot^{-1}, number of primary branches plant^{-1}, days to maturity, number of capsules plant^{-1}, seed yield plant^{-1}, plant height contributed in vector I which accounted for 26.76% of total variation. Seed size, capsules size, 1000 seed weight, plant height, number of capsules plant^{-1}, flower size, days to 50% flowering and number of primary branches plant^{-1} were important characters in vector II which accounted for 22.69% of total variation. Number of capsules plant^{-1}, 1000 seed weight, days to 50% flowering, plant height, seed yield plot^{-1}, seed yield plant^{-1}, capsules size and number of primary branches plant^{-1} were important characters in vector III which accounted for 14.83% of total variation. The important characters in vector IV 1000 seed weight, plant height, seed size, days to maturity and number of primary branches plant^{-1} are accounted for 12.27% of total variation.The important characters in vector V are flower size, number of primary branches plant^{-1}, 1000 seed weight, days to 50% flowering, plant height, number of capsules plant^{-1} and flower size accounted for 9.30% of total variation. Plant height, days to 50% flowering, number of capsules plant^{-1}, days to maturity were important characters which accounted for 5.90% of total variation. This suggested that parent selected on the basis of days to 50% flowering, number of primary branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight, seed yield plant^{-1}, seed yield plot^{-1}, days to maturity and plant height may excepted to be genetically diverse.

Average intra and inter cluster statistical distance among thirteen characters are given in Table 6. The intra cluster distance ranged from 0.00 to 89.64. Cluster IV possessed highest intra cluster distance (D²=89.64) followed by cluster III (D²=87.77) and cluster II (D²=69.73). The average inter cluster distance was maximum between cluster IV and IX (D²=451.74), followed by cluster VI and cluster IX (D²=397.76), cluster VII and cluster VIII (D²=381.46) and cluster VI and cluster VIII (D²=364.01) 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 V (D²=97.59). These findings are in conformity with the finding of Chahande *et al*. (2016)

for average intra and inter cluster statistical distance among various characters.

Overall study for cluster mean considering all the thirteen characters indicated that cluster IV possessed the highest cluster mean for number of primary branches plant^{-1}, 1000 seed weight, seed size, seed yield plant^{-1}, seed yield plot^{-1}, number of capsules plant^{-1} and days to maturity. (Table. 7). Kanwar*et al.* (2013) also reported the importance for number of primary branches plant^{-1}, 1000 seed weight, seed size, seed yield plant^{-1}, seed yield plot^{-1}, number of capsules plant^{-1} and days to maturity for genetic divergence in linseed.

All possible cluster combinations beyond the mean statistical distance $\bar{D}$ = 81.5 have been arranged in descending order in Table 8. The data regarding clusters showing maximum inter cluster distance (303.03) was the cluster I and cluster IX , and the parents in cluster I showing highest mean significant superiority for seed yield plant^{-1} and number of capsules plant^{-1} are NL 392, NL 394, NL 409, NL 420, NL 414 and NL 418. Another cluster having inter cluster distance of 257.81 (cluster X and VI) also included only one parent each *i.e*. NL 115 and NL 384. Cluster I and VIII ($\bar{D}$ =211.76) consisted of parents NL 387, NL392, NL 394, NL 409, NL 420 and NL 414, whereas Cluster I and X ($\bar{D}$=171.63) included parents NL 392, NL 394, NL 409, NL 420, NL 414, which showed significant superiority for seed yield plant^{-1}, seed yield plot^{-1} and number of capsules plant^{-1}. Madke *et al.* (2020) were identified the genotypes belonging to distant cluster exhibiting high performance in desirable direction for plant height, seed yield plant^{-1} and number of pods plant^{-1} and were identified potential parents for hybridization programme.

Table 1. Analysis of variance for thirteen characters

Sr. No.	Characters	Replication	Genotypes	Error
1	**d.f.**	1	68	68
2	**Plant height (cm)**	3.96	103.62**	2.57
3	**Days to 50% flowering**	15.33	77.09*	11.09
4	**Flower size(mm)**	30652.28	25.09*	22.46
5	**Capsule size (mm)**	0.29	1.39**	0.026
6	**Seed size (mm)**	0.0036	0.4642**	0.0150
7	**Seed yield plant $^{-1}$ (g)**	20.12	7.92*	3.67
8	**Number of primary branches plant^{-1}**	0.023	2.72**	0.14
9	**1000 seed weight (g)**	3.25	4.36*	0.71
10	**Seed yield plot^{-1} (kg ha^{-1})**	74374.5	35006.0*	8075.39
11	**Number of capsule plant^{-1}**	421.57	193.68**	6.78
12	**Days to maturity**	204.52	34.66**	3.75
13	**% Alternaria blight infestation**	16.28	22.41*	8.43
14	**% Budfly infestation**	1594.6	26.95*	14.17

Note: ** Significant at 1% level, * Significant at 5% level

Table 2. Analysis of dispersion

Sources of variation	df	Sum of squares	Mean sum of squares
Genotypes	68	1.8782E20	2.7621E18*
Error	67	4.6540E09	6.9463E07
Total	135	1.8782E20	1.3913E18

* Significant at 5 % level

Table 3. Contribution of different characters towards genetic divergence in linseed

Sr. No.	Characters	Time ranked 1st	Per cent contribution
1	Plant height (cm)	424	18.07
2	Days to 50% flowering	19	0.80
3	Flower size(mm)	0	0
4	Capsule size (mm)	760	33.39
5	Seed size (mm)	362	15.43
6	Seed yield plant $^{-1}$ (g)	7	0.29
7	Number of primary branches plant^{-1}	237	10.10
8	1000 seed weight (g)	32	1.36
9	Seed yield plot^{-1} (kg ha^{-1})	11	0.46
10	Number of capsule plant^{-1}	400	17.05
11	Days to maturity	84	3.58
12	% Alternaria blight infestation	9	0.38
13	% Budfly infestation	1	4.26
	Total	**2346**	
	Tocher cut off value	**181.71**	

Table 4. Grouping of genotypes into different clusters in linseed

Cluster	Number of genotypes	Name of the genotypes
I	20	NL 390, NL 392, NL 394, NL 409, NL 420, NL 413, NL 414, NL 399, NL 408, NL 418, NL 353, NL 385, NL 402, NL 400, NL 375, NL 411, NL 375, NL 417, NL 378, NL 425
II	22	NL 416, NL 423, NL 383, TL 24, TL 253, T 397, NL 404, NL 398, NL 401, NL 429, Padmini, NL 406, NL 422, NL 424, NL 428, TL 16, TL 189, NL 381, LSL 93, TL 89, NL 382, NL 397
III	12	NL 407, NL 427, NL 377, NL 379, NL 334, NL 389, NL 412, NL 396, NL 386, NL 388, NL 380, NL 405
IV	9	NL 391, NL 395, NL 374, NL 339, NL 419, PKV NL 260, NL 410, NL 403, NL 421
V	1	NL 415
VI	1	NL 384
VII	1	NL 376
VIII	1	NL 387
IX	1	NL 426
X	1	NL 115

Table 5 a. Values of first five vectors

Sr. No.	Characters	Vector I	Vector II	Vector III	Vector IV	Vector V
1	Plant height	0.0327	0.6560	0.3472	0.4765	0.1967
2	Days to 50% flowering	0.1295	0.1362	0.0649	0.0805	0.3243
3	Flower size	0.0310	-0.1145	-0.0197	-0.0606	0.0866
4	Capsule size	0.7964	0.1068	-0.3140	0.1428	-0.3225
5	Seed size	0.2770	-0.3219	0.8072	0.1056	-0.2355
6	Seed yield plant^{-1}	0.2355	-0.1020	-0.0280	-0.0372	-0.1772
7	Number of primary branches	0.3233	-0.0477	0.0875	-0.4467	0.6305
8	1000 seed weight	0.2357	0.0981	-0.0225	0.0670	0.3349
9	Seed yield plot^{-1} (kg ha^{-1})	-0.0207	-0.1437	0.1452	-0.1382	-0.0369
10	Number of capsule plant^{-1}	0.0571	0.5585	0.1729	-0.6798	-0.3092
11	Days to maturity	0.1711	-0.1569	-0.0419	0.1189	0.1618
12	% Alternaria blight infestation	0.1472	-0.1456	-0.0780	-0.0839	0.1228
13	% Budfly infestation	0.0113	-0.1491	0.2387	-0.1533	0.0995

Table 5 b. Five canonical roots and their contribution expressed as per cent of the total variation

Root	Eigene value	Contribution in per cent
Y_1	1475.11	33.21
Y_2	1149.33	25.88
Y_3	511.05	11.51
Y_4	460.13	10.36
Y_5	293.02	6.60
Total	3888.64	87.56
Sum of all canonical roots		100
Residual		12.44

Table 6. Average intra and inter cluster distance D^2 values in linseed

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**59.61**	128.91	131.05	107.8	97.59	111.34	97.77	211.76	306.03	171.63
II		**69.73**	165.05	136.79	124.78	185.19	224.45	161.65	233.79	144.13
III			**87.77**	227.87	119.87	212.39	166.83	138.74	155.14	175.81
IV				**89.64**	197.14	189.11	205.06	251.54	451.74	226.59
V					**0.00**	177.90	106.36	220.96	144.07	137.19
VI						**0.00**	105.48	364.01	397.76	257.81
VII							**0.00**	381.46	357.50	188.03
VIII								**0.00**	179.29	243.52
IX									**0.00**	246.12
X										**0.00**

$\underline{D} = 81.5$ (Bold figures are average intra cluster distance)

Table 7. Cluster means for thirteen characters

Cluster	Plant height	Days to 50 % flowering	Flower size	Capsule size	Seed size	Seed yield plant^{-1}	No. of branches plant^{-1}	1000 seed weight	Seed yield plot^{-1}	No. of capsules plant^{-1}	Days to maturity	% Alternaria blight	% Bud fly
1	56.78	59.92	34.31	8.22	5.13	12.17	3.58	7.88	452.22	44.28	104.35	6.51	15.57
2	44.25	54.05	33.13	8.19	5.30	12.16	3.01	7.11	470.25	34.95	103.59	6.77	15.16
3	56.73	51.83	31.11	7.17	5.03	11.20	2.08	6.23	455.65	38.82	110.67	7.12	13.87
4	53.61	58.11	33.39	8.76	5.88	12.27	3.76	8.22	458.83	42.14	104.33	6.40	14.68
5	44.00	60.00	34.23	7.75	4.40	10.75	3.00	8.20	468.88	57.80	106.00	2.77	11.14
6	59.10	59.00	31.17	9.23	4.28	12.10	3.20	8.20	355.72	25.70	106.00	6.96	18.36
7	57.30	50.00	27.83	8.94	4.24	11.90	3.70	6.60	430.28	56.20	95.00	6.26	9.05
8	55.50	50.00	30.13	6.12	5.92	10.90	3.70	6.80	439.97	28.30	107.00	6.57	25.75
9	42.10	55.00	32.90	6.09	4.38	13.70	1.00	4.60	370.46	39.00	104.00	8.21	13.45
10	43.70	65.00	24.97	7.78	4.90	10.30	3.20	7.00	1116.04	44.40	89.00	21.74	8.11
SD	**6.87**	**4.93**	**3.01**	**1.09**	**0.63**	**0.98**	**0.87**	**1.14**	**219.43**	**10.42**	**6.30**	**5.05**	**5.02**
VAR	**47.19**	**24.35**	**9.05**	**1.19**	**0.39**	**0.97**	**0.76**	**1.29**	**48147.99**	**108.60**	**39.75**	**25.48**	**25.16**

Table 8. Selection of genotypes based on inter cluster distances and cluster means

Clusters	Distance between clusters	Recombinant lines (Selection based on seed yield plant^{-1}, seed yield plot^{-1} and number of capsules plant^{-1})
I & IX	303.03	NL 115 X NL 392, NL 115 X NL 394, NL 115 X NL 409, NL 115 X 420, NL 115 X NL 414 and NL 115 X NL 418
X & VI	257.81	NL 115 X NL 384
I & VIII	211.76	NL 387 X NL 392, NL 387 X NL 394, NL 387 X NL 409, NL 387 X NL 420 and NL 387 X NL 414
I & X	171.63	NL 115 X NL 392, NL 115 X NL 394, NL 115 X NL 409, NL 115 X NL 420 and NL 115 X NL 414

$\bar{D}$ = 81.5

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