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Morphological characterization and genetic divergence studies in linseed (*Linum usitatissimum* L.)

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Abstract

A study was conducted to assess the genetic variability, interrelationship among yield components and their direct and indirect effect on yield. Thirty genotypes of Linseed (*Linum usitatissimum* L.) were evaluated in Randomized Block Design with three replications during 2020-21 for twelve morphological characters to assess the genetic parameters of variability. The influence of environment on the manifestation of features was shown by larger phenotypic coefficient values than matching genotypic coefficient values. The highest GCV and PCV values were for leaf area per plant (LAP) and seed yield per plant (SYP). For the chlorophyll content index (CCI), oil content (OC), days to 50% flowering (DF), and 1000 seed weight (SW), higher magnitudes of heritability together with high to moderate genetic advance as a percentage of mean were observed. Number of capsules per plant (NCP), number of seeds per capsule (NSC), and 1000 Seed weight (SW) all demonstrated positive, statistically significant correlations with seed yield per plant. Path coefficient analysis revealed that number of capsules per plant has strong positive direct effect on seed yield per plant. Cluster analysis clearly differentiated 30 genotypes into five clusters with cluster I having 16 genotypes. Cluster IV and III had the greatest inter-cluster distance (26.00), followed by cluster III and II (25.91). Chlorophyll content index contributed the most to genetic difference among the twelve parameters examined (55.17%), followed by oil content (14.25%). The results attained could be applied to future breeding programmes.

Keywords: Morphological, characterization, divergence studies, *Linum usitatissimum* L.

Introduction

The genus *Linum* and family *Linaceae* include the linseed, *Linum usitatissimum* L. ($2n = 30$). One of the earliest plant species are cultivated for oil and fibre, it is a self-pollinated species sown during the *rabi* season (Lay and Dybing 1939). It was originated in the Mediterranean and southwest Asia (Vavilov, 1935). Linseed is grown on 3.26 million hectares around the world, producing 3.18 million tonnes at a productivity of 1011.20 kg/ha. With an area of 0.32 million ha, a production of 0.17 million tonnes, and a productivity of 543.8 kg/ha, India ranked sixth in the world (FAOSTAT 2018) for linseed cultivation.

The 'Linen' obtained from flax fibre is one of the best raw materials for textile. The best grades are used for linen fabrics such as damasks, lace and sheeting. Flax fibre is strong, non-lignified, soft, flexible, lustrous, shining, pale yellow colour and possesses high water absorbency quality. Flax contains 80-90% cellulose. The oil content of seed generally varies from 33 to 45 per cent (Gill, 1987) [28]. Linseed contains high amount of omega fatty acids. There are two groups of omega fats: omega-3 and omega-6 fatty acids. Linolenic acid, eicosapentaenoic acid (EPA) and docosahexanoic acid (DHA) are three types of omega-3 fatty acids and are nutritionally important.

Genetic variability is crucial in breeding or selection program of any crops. The low genetic variability observed in the crop necessitates strengthening of the breeding programmes through introduction of new germplasm, collection of local ecotypes and adopting interspecific hybridization. The magnitude of heritable variation in the traits studied has immense importance in understanding the potential of the genotype for further breeding programme.

Correlation is the mutual relationship between the variables, it aids in estimating the most effective procedures. A path coefficient is a standardized, partial regression coefficient that measures the direct influence of one trait upon another trait. To determine the direct and indirect effects of seed yield components on seed yield, it is essential to calculate correlations of the yield components among themselves and with seed yield.

Several workers give emphasis to the need of parental diversity in best possible magnitude to obtain superior genotypes in the segregating generations (Rama kant *et al.*, 2011; Srivastava *et al.*, 2009 and Tyagi *et al.*, 2015) [29-31]. Genetic diversity ascends due to different patterns of evolution. The present study was conducted with an objective to select the diverse parents for further use in linseed breeding programme.

Materials and Methods

The experimental materials comprised of thirty linseed genotypes collected from department of Genetics and Plant Breeding, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The experiment was laid out in a Randomized block design with three replications during Rabi 2020-21. Geographically, Sardarkrushinagar is situated at 24° 19' North latitude and 72° 19' East longitudes with an elevation of 154.52 meters above the mean sea level and situated in the North Gujarat Agro climatic Zone. The standard week wise meteorological data for the period of this investigation recorded at the Meteorological Observatory, Agronomy Instructional Farm, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The genotypes were obtained by phenotypic selection from the linseed germplasm pool. The entries were sown in one row each of 3m length with spacing of 30 cm between rows and 10 cm approximately between the plants. The observations were recorded for different quantitative characters in linseed (based on Catalogue on linseed germplasm, Project Coordinating Unit (Linseed), C.S.A.U.A. & T. campus, Kanpur, 2010.

The analysis of variance for individual characters and for the attributing characters respectively, were carried out using the mean values of each plot using the method given by Panse and Sukhatme (1985). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed, following Burton and Devane, (1953) [33] method. Broad sense heritability h^2 (broad sense) was calculated as a ratio of genotypic variance to phenotypic variance (Allard, 1960) [34]. The expected genetic advance under selection for the different characters was estimated as suggested by Johnson *et al.*, (1955) [35]. To determine the degree of association of various characters with yield and the yield components, the correlation coefficients are calculated. The correlation was calculated using the formula given by Fisher (1918) [36]. The direct and indirect effects were estimated using path coefficient analysis as suggested by Wright (1921) [37] and elaborated by Dewey and Lu (1959) [38].

Results and Discussion

Linseed (*Linum usitatissimum* L.) is an important Rabi oilseed crop grown in India and in other developing countries of the world. The purpose of the present investigation was to generate information on morphological traits, which can throw light on the chances of further improvement of these genotypes either through selection or through hybridization programme. Analysis of variance for yield and yield attributing traits in linseed is given in Table 1. The table indicated that the mean sum of squares due to genotypes was significant for all the traits showing the presence of variability among linseed genotypes for yield and its contributing traits and non-significant mean squares for replications for each

character is indicative of homogeneity of experimental plot.

Genetic variability

Results of genetic variability shows that in general, phenotypic coefficient of variation for all the traits under study was marginally higher to corresponding genotypic coefficient of variation indicating substantial influence of environment in the expression of characters (Table 2).

Table 1a: Analysis of variance (ANOVA) for seed yield and its contributing traits in linseed.

Mean sum of squares							
Sources of variation	Df	DF	DM	PH	NPB	NCP	SW
Replication	2	4.04	23.01	44.96	2.07	45.61	0.14
Genotypes	29	86.64**	128.45**	204.93**	9.85**	433.16**	5.16**
Error	58	3.493	11.241	16.660	0.752	35.536	0.264
Total	89						

*, **= Significant at 5% and 1% levels, respectively. Df = Degree of Freedom.

Table 1b: Analysis of variance (ANOVA) for seed yield and its contributing traits in linseed.

Mean sum of squares							
Sources of variation	Df	NSC	CL	LAP	CCI	OC	SYP
Replication	2	0.42	0.03	17013.47	7.57	5.34	0.82
Genotypes	29	3.41**	1.57**	137917.45**	789.03**	78.26**	5.11**
Error	58	0.218	0.199	10525.278	4.070	2.029	0.308
Total	89						

*, **= Significant at 5% and 1% levels, respectively. Df = Degree of Freedom.

Estimation of genetic variability parameters

The estimation of genotypic and phenotypic components of variation gives us an idea of relative range of heritable and non-heritable variation. The coefficient of variation measures the relative amount of variability available for characters in a population. When comparisons among different characters for presence of variability are to be made, it is not proper to compare magnitude of variances as such, because of different units of measurements involved as well as various characters; therefore coefficients of variation were calculated.

Phenotypic and genotypic coefficient of variability

The GCV and PCV were highest for SYP (GCV= 31.05% and PCV= 33.914%) followed by LAP (GCV= 24.36% and PCV= 27.21%), CCI (GCV= 24.57% and PCV= 24.64%), NPB (GCV= 21.52% and PCV= 24.04%) and SW (GCV= 20.15% and PCV= 21.94%). These characters having high GCV and PCV in comparison to other characters indicate the presence of high variability in the population.

The magnitude of PCV was higher than the corresponding GCV for all the traits. This might be due to the interaction of the genotypes with the environment to some degree or environmental factor influencing the expression of these traits. Close correspondence between phenotypic and genotypic coefficient of variation were observed *i.e.* sufficient variability among the traits is present among the genotype. Hence, there is ample scope of improvement of these traits (Fig. 1).

Higher estimates of genotypic and phenotypic coefficients of variation means there is presence of good amount of variability among the genotypes for the traits *viz.*, SYP, LAP,

CCI, NPB and SW. Therefore, simple selection could be effective for bringing further improvement. All traits exhibited a relatively low magnitude of difference between

PCV and GCV indicating less environmental influence on these characters. Whereas, DF, DM and CL had lower estimates of GCV and PCV had little scope for selection.

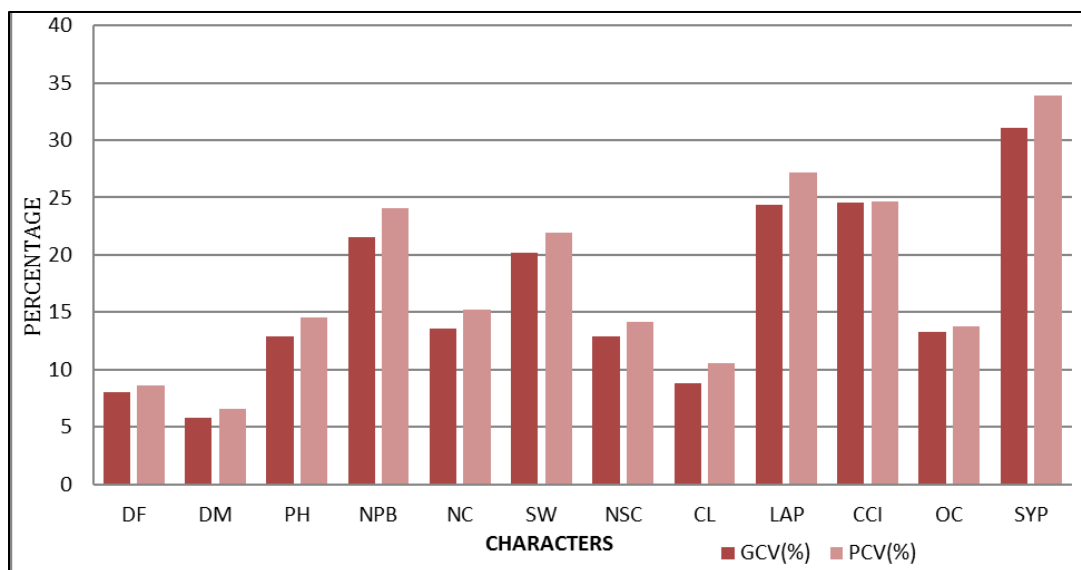


Fig 1: Genotypic and phenotypic coefficient of variation for 12 characters in linseed

Table 2: Estimated Variability parameters for yield and yield contributing traits in thirty linseed genotypes

Sr. No.	Characters	Genetic parameters										Genetic advance as a percent mean (GAM)
		Mean	Variance components		Range		Critical Difference	Coefficient of variation		h ² (%)	GA	
			σ ² p	σ ² g	Maximum	Minimum		GCV (%)	PCV (%)			
1	DF	65.1778	28.87	27.71	77.66	53.33	4.06	8.07	8.57	88.80	10.22	15.68
2	DM	107.6222	42.81	39.07	126.00	98.00	7.29	5.80	6.59	77.65	11.34	10.54
3	PH	61.3350	68.30	62.75	74.60	45.53	8.87	12.91	14.52	79.02	14.50	23.65
4	NPB	8.0910	3.28	3.03	14.00	5.683	1.88	21.52	24.04	80.13	3.21	39.69
5	NCP	85.0414	144.38	132.54	103.13	52.78	12.96	13.53	15.24	78.85	21.06	24.76
6	SW	6.2001	1.72	1.63	8.66	3.83	1.11	20.15	21.94	84.35	2.35	38.13
7	NSC	8.0142	1.13	1.06	9.68	6.44	1.01	12.87	14.13	83.02	1.93	24.17
8	CL	7.6460	0.52	0.45	8.97	6.15	0.96	8.79	10.59	68.92	1.15	15.03
9	LAP	845.8434	45972	42464	1281.17	483.64	223.09	24.36	27.21	80.13	380.01	44.92
10	CCI	65.8133	263.01	261.65	99.9	43.93	4.38	24.57	24.64	98.46	33.06	50.24
11	OC	38.0541	26.08	25.41	50.40	31.08	3.09	13.24	13.76	92.60	9.99	26.26
12	SYP	4.0738	1.70	1.60	5.58	1.33	1.20	31.05	33.91	83.84	2.38	58.58

Heritability and Genetic Advance as percent mean

An important factor that determines the scope of any crop species is the type and degree of intrinsic capacity of a genotype for a feature. Heritability estimates provide some insight into the gene activity responsible for the expression of many polygenic characteristics. If the estimated variance resulting from additive genes continues to be very useful in studies of the inheritance of quantitative traits, then selection should be successful. % of the mean was used to calculate genetic gain. The main contributors to the increase in mean genotypic value of chosen plants relative to the parental population are genetic advancement and heredity. Genetic progress is dependent on genetic variability, heritability and selection intensity.

The highest heritability estimate was observed for CCI (98.47%) followed by OC (92.61%), DF (88.80%), 1000 SW (84.35%), NSC (83.02%) and LAP (80.14%) indicating predominance of additive gene action in the expression of these traits. This being fixable in nature considerable progress is expected through appropriate selection scheme to be

adopted.

In the present study, moderate heritability coupled with low genetic advance was obtained for capsule length. Thus this trait is not suitable for effective selection of desirable plants due to these traits predominantly under non additive genetic control. On the contrary high heritability coupled with low genetic advance was observed for DF, NPB, SW, NSC, OC and SYP.

These results were in accordance with the findings of Malik and Singh (1995) [11], Mirza *et al.* (1996) [13], Popescu *et al.* (1998) [17], Pradhan *et al.* (1999) [18], Akbar *et al.* (2003) [2], Jain and Rao (2003) [8], Awasthi and Rao (2005) [3], Gauraha *et al.* (2011a) [6], Reddy *et al.* (2013) [20], Ahmad *et al.* (2014) [1], Kanwar *et al.* (2014) [9], Hussain *et al.* (2015) [7], Paul *et al.* (2015) [15], Singh *et al.* (2015) [23], Choudhary *et al.* (2016) [4], Sahu *et al.* (2016) [21], Siddique *et al.* (2016), Upadhyay *et al.* (2019) [25] and Meena *et al.* (2020) [12].

Genotypic and phenotypic correlation coefficients

Correlation coefficient analysis revealed that seed yield per

plant exhibited significant and positive correlation both at genotypic and phenotypic level with NC, NSC and 1000 SW. Hence, direct selection for these traits would therefore be most effective in the improvement of linseed genotypes (Table 3).

In the present study high correlation was observed between number of capsules per plant and seed yield per plant at both genotypic and phenotypic levels, respectively, which specifies that the number of capsules per plant may be reliable yield indicator. Such significant association of number of capsules per plant with seed yield has also been observed by Tariq *et al.* (2014) [24], Rajanna *et al.* (2014) [19], Singh *et al.* (2015) [23], Mohit *et al.* (2016) [14], Dash *et al.* (2016) [5], Siddique *et al.* (2016) and Paul *et al.* (2017) [16], Meena *et al.* (2020) [12].

In the present study, genotypic and phenotypic correlations among 12 characters of linseed were computed. For majority

of the cases, the genotypic and phenotypic correlations showed very close values. In all the cases, the range of difference between phenotypic and genotypic correlations was very narrow. This indicates that the environmental effect pertaining to the expression of such characters was very less.

Path coefficient analysis at genotypic and phenotypic levels: The characters which were found to have significant positive correlation with seed yield were NC, SW and NSC both at genotypic and phenotypic levels, while negative significant correlation exhibited by DM at genotypic level and LAP exhibited negative significant correlation at both genotypic and phenotypic levels. The characters like DF, PH, CL, and OC showed negative non-significant correlation with seed yield per plant whereas positive non-significant correlation was shown by CCI (Table 4).

Table 3: Correlation coefficients of thirty linseed genotypes

Sr. No.	Character	DF	DM	PH	NPB	NC	SW	NSC	CL	LAP	CCI	OC	SYP	
1	DF	r _g	1.000	-0.032 NS	0.143 NS	-0.106 NS	-0.181 NS	0.464**	-0.105 NS	0.185 NS	0.125 NS	0.075 NS	0.082 NS	-0.100 NS
		r _p	1.000	0.028 NS	0.109 NS	-0.101 NS	-0.199 NS	0.393**	-0.100 NS	0.158 NS	0.066 NS	0.068 NS	0.092 NS	-0.105 NS
2	DM	r _g		1.000	0.073 NS	-0.240*	-0.506**	-0.281**	0.335**	0.342**	0.131 NS	0.346**	-0.086 NS	-0.222*
		r _p		1.000	0.113 NS	-0.178 NS	-0.395**	-0.227*	0.275**	0.233*	0.102 NS	0.304**	-0.059 NS	-0.183 NS
3	PH	r _g			1.000	0.049 NS	-0.076 NS	0.265*	0.144 NS	0.012 NS	-0.037 NS	-0.068 NS	0.085 NS	-0.060 NS
		r _p			1.000	0.036 NS	-0.009 NS	0.252*	0.111 NS	-0.010 NS	-0.037 NS	-0.057 NS	0.082 NS	-0.046 NS
4	NPB	r _g				1.000	0.347	-0.079 NS	0.296**	0.041 NS	0.001 NS	0.322**	0.026 NS	0.035 NS
		r _p				1.000	0.275**	-0.026 NS	0.214*	0.052 NS	0.014 NS	0.286**	0.005 NS	0.012 NS
5	NC	r _g					1.000	0.067 NS	0.073 NS	-0.232*	-0.112 NS	-0.018 NS	-0.003 NS	0.558**
		r _p					1.000	0.074 NS	0.145 NS	-0.176 NS	-0.074 NS	-0.005 NS	-0.014 NS	0.579**
6	SW	r _g						1.000	0.003 NS	-0.158 NS	-0.153 NS	-0.087 NS	0.007 NS	0.262*
		r _p						1.000	-0.005 NS	-0.107 NS	-0.124 NS	-0.075 NS	0.003 NS	0.253*
7	NSC	r _g							1.000	0.527**	-0.185 NS	0.114 NS	0.082 NS	0.303**
		r _p							1.000	0.409**	-0.134 NS	0.102 NS	0.073 NS	0.362**
8	CL	r _g								1.000	0.038 NS	0.149 NS	0.031 NS	-0.049 NS
		r _p								1.000	-0.007 NS	0.122 NS	0.026 NS	-0.029 NS
9	LAP	r _g									1.000	-0.089 NS	0.339**	-0.412**
		r _p									1.000	-0.074 NS	0.259*	-0.326**
10	CCI	r _g										1.000	-0.281**	0.099 NS
		r _p										1.000	-0.269*	0.095 NS
11	OC	r _g											1.000	-0.008 NS
		r _p											1.000	-0.009 NS
12	SYP	r _g												1.000
		r _p												1.000

*, ** = Significant at 5% and 1% levels, respectively

Table 4: Path Analysis of thirty linseed genotypes

Sr. No.	Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of capsules	Seed weight	Number of seeds per capsule	Capsule length	Leaf area per plant	Chlorophyll content index	Oil content	Correlation values	
1	Days to 50% flowering	G	-0.0708	0.0022	-0.0101	0.0075	0.0128	-0.0322	0.0075	-0.0130	-0.0089	-0.0053	-0.0058	-0.1000 NS
		P	-0.0709	0.0006	-0.0092	0.0074	0.0133	-0.0306	0.0073	-0.0123	-0.0073	-0.0051	-0.0061	-0.1019 NS
2	Days to maturity	G	0.0051	-0.1604	-0.0117	0.0385	0.0811	0.0463	-0.0538	-0.0551	-0.0210	-0.0555	0.0137	-0.2224*
		P	0.0010	-0.1072	-0.0095	0.0232	0.0496	0.0290	-0.0335	-0.0322	-0.0128	-0.0354	0.0081	-0.2072 NS
3	Plant height	G	-0.0118	-0.0060	-0.0825	-0.0041	0.0063	-0.0214	-0.0119	-0.0004	0.0031	0.0056	-0.0070	-0.0603 NS
		P	-0.0125	-0.0085	-0.0962	-0.0043	0.0048	-0.0245	-0.0127	0.0002	0.0036	0.0061	-0.0081	-0.0549 NS
4	Number of primary branches per plant	G	0.0403	0.0909	-0.0186	-0.3781	-0.1312	0.0269	-0.1119	-0.0079	-0.0004	-0.1219	-0.0097	0.0350 NS
		P	0.0334	0.0691	-0.0142	-0.3200	-0.1021	0.0172	-0.0847	-0.0091	-0.0019	-0.0988	-0.0058	0.0262 NS
5	Number of capsules	G	-0.0933	-0.2602	-0.0391	0.1785	0.5146	0.0307	0.0375	-0.1241	-0.0579	-0.0093	-0.0016	0.5575**
		P	-0.0983	-0.2421	-0.0261	0.1670	0.5234	0.0335	0.0526	-0.1143	-0.0511	-0.0070	-0.0038	0.5657**
6	Seed weight	G	0.0801	-0.0509	0.0458	-0.0125	0.0105	0.1764	-0.0043	-0.0276	-0.0241	-0.0178	0.0041	0.2345*
		P	0.0867	-0.0543	0.0511	-0.0108	0.0129	0.2008	-0.0036	-0.0267	-0.0254	-0.0193	0.0043	0.2353*
7	Number of seeds per capsule	G	-0.0400	0.1272	0.0547	0.1122	0.0277	-0.0093	0.3792	0.1981	-0.0700	0.0431	0.0313	0.3025**
		P	-0.0357	0.1078	0.0455	0.0914	0.0347	-0.0063	0.3454	0.1640	-0.0571	0.0378	0.0273	0.3250**
8	Capsule length	G	-0.0101	-0.0189	-0.0003	-0.0011	0.0132	0.0086	-0.0287	-0.0549	-0.0026	-0.0076	-0.0017	-0.0536 NS

9	Leaf area per plant	P	-0.0076	-0.0131	0.0001	-0.0012	0.0095	0.0058	-0.0208	-0.0437	-0.0012	-0.0056	-0.0012	-0.0472	NS
		G	-0.0313	-0.0326	0.0093	-0.0003	0.0280	0.0341	0.0460	-0.0117	-0.2494	0.0221	-0.0845	-0.0845	-0.4116
10	Chlorophyll content index	P	-0.0249	-0.0289	0.0090	-0.0015	0.0236	0.0306	0.0400	-0.0068	-0.2418	0.0202	-0.0748	-0.3790	**
		G	0.0211	0.0976	-0.0191	0.0909	-0.0051	-0.0285	0.0321	0.0391	-0.0250	0.2822	-0.0793	0.0985	NS
11	Oil content	P	0.0171	0.0780	-0.0150	0.0730	-0.0032	-0.0227	0.0258	0.0305	-0.0197	0.2363	-0.0654	0.0972	NS
		G	0.0108	-0.0113	0.0112	0.0034	-0.0004	0.0030	0.0109	0.0040	0.0446	-0.0370	0.1316	-0.0089	NS
		P	0.0099	-0.0087	0.0097	0.0021	-0.0008	0.0025	0.0091	0.0032	0.0357	-0.320	0.1155	-0.0099	NS

*, ** = Significant at 5% and 1% levels, respectively

Genetic divergence through D² Analysis

To improve a complex trait like yield, knowledge of the extent of genetic variation and variability is essential. As a result, selecting parents with a large number of characters of divergence is crucial for increasing crop yield, as demonstrated by Mahalanobis D² statistics (1936).

On the basis of D² statistics five clusters were formed from 30 genotypes of Linseed. The composition of clusters is given in the Table 6. The cluster I was the largest having 16 genotypes followed by cluster III (9 genotypes), cluster II (3 genotypes), cluster IV (1 genotype) and cluster V (1 genotype).

Intra cluster average D² values ranged from 11.18 to 14.93. Among the clusters, cluster III showed maximum intra-cluster distance (D² = 14.93), followed by cluster I (D² = 12.18), while the minimum intra-cluster distance was observed for cluster II (D² = 11.18). The zero intra-cluster distance was observed for clusters IV and V (D² = 0). These two clusters was a solitary cluster (Table 5).

Inter cluster distances were higher than intra-cluster distances

which indicated the existence of substantial diversity among the genotypes. Wider ranges of mean values among the clusters were recorded for different traits. The cluster I had the highest mean values and desirable mean score for NC (88.81) and seed yield per plant (4.35 g). Cluster II had a desirable mean score for PH (cm), CL (7.95mm) and OC (49.18%). The cluster IV had the highest mean values for the DM (110.96), NPB (8.81), NSC (8.44), CL (7.95) and CCI (86.46). The cluster V showed desirable rating for LAP (963.38 cm²) (Table 7).

Table 5: Average Intra-cluster and Inter-cluster distances of thirty genotypes of linseed

Clusters	I	II	III	IV	V
I	12.18	15.35	19.91	14.98	14.40
II		11.18	25.91	16.48	16.39
III			14.93	26.00	23.75
IV				0.00	18.18
V					0.00

Table 6: Distribution of 30 genotypes of linseed to different clusters on the basis of D² statistics

Sr. No.	Cluster	Number of genotypes	Name of genotypes
1	I	16	Surabhi, EC41528, Suyog, Padmini, Hira, IC56363, Shubhra, Pusa-3, Neela, Rashmi, Pusa-2, Kartika, T397, IC96473, IC56365, JRL 9
2	II	3	Neelum, L27, LC185
3	III	9	Subhra, Mukta, Sikha, Sharda, Nagarkot, Parvati, T7, Sweta, Gaurav
4	IV	1	IC53281
5	V	1	Deepika

Table 7: Cluster Means of different characters in linseed

Cluster Number	(DF)	(DM)	(PH)	(NPB)	(NCP)	(SW)	(NSC)	(CL) (mm)	(LAP) (cm ²)	(CCI)	(OC) (%)	(SYP)
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
I	64.50	106.10	58.10	7.89	88.81	6.01	7.94	7.49	876.04	59.58	37.86	4.35
II	69.56	107.33	68.80	7.28	76.87	7.23	7.85	7.95	949.63	49.70	49.18	3.30
III	65.48	110.96	63.78	8.81	83.76	6.31	8.44	7.95	766.23	86.46	35.36	4.26
IV	72.00	103.33	65.63	7.98	87.74	7.62	7.54	7.68	650.43	44.60	31.16	3.06
V	53.33	107.00	64.47	7.40	58.13	3.83	6.44	6.43	963.38	49.33	38.96	1.33

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