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DELINEATING MULTIVARIATE DIVERGENCE, HERITABILITY, TRAIT ASSOCIATION AND IDENTIFICATION OF SUPERIOR OMEGA-3-FATTY ACID SPECIFIC GENOTYPES IN LINSEED (*Linum usitatissimum* L.)

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Present investigation was undertaken to evaluate 50 linseed genotypes for three consecutive years for seed yield, oil content and agro-morphological traits using multivariate approach. Higher range, large value of Shannon-weaver diversity index for both traits and genotypes and large differences in mean values for most of the characters showed that a wide and significant variation existed among the genotypes and traits. Pooled analysis of variance revealed highly significant differences ($p<0.001$) among the genotypes for all the characters studied. The magnitude of the phenotypic coefficient of variation was somewhat higher than the genotypic coefficient of variation, indicating that the environment had little impact on the expression of these traits. Cluster analysis for yield and agro-morphological traits using unweighted pair group method of arithmetic averages (UPGMA) grouped the genotypes into nine clusters with varied number. Clustering of linseed genotypes from different geographical locations or source/origin into same cluster has confirmed that they are genetically related, and possibly from the same progenitor. The principal component analysis (PCA) revealed that most of the

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variation (76.41%) was accounted by first four PCA and indicated role of traits that contributed significantly towards a wide variation among the genotypes. The positive associations of seed yield per plant and oil content with component trait implies that improving one or more component traits could result in genetic enhancement of seed yield and oil content in linseed. The significant negative association of seed yield per plant and oil content with days to flowering and days to maturity has great advantages in breeding short duration linseed cultivars for hot and water stress climatic conditions of semi-arid regions. Trait specific genotypes namely, Shival, Sharda, IC54970, Mukta, IC56363, T-397, IC53281 and RLC-92 were identified for the development of short duration and dwarf cultivars with higher omega-3-fatty acid content.

Keyword: Multivariate approach, phenotypic diversity, linseed, omega-3-fatty acid

INTRODUCTION

Linseed or flax (*Linum usitatissimum* L. 2n= 30, x=15) an important oilseed crop belonging to the family Linaceae and the tribe Lineae which comprises of approximately 230 species, is the only species of this family with economic importance (TADESSE *et al*., 2010). Flax and linseed are two different morphotypes of cultivated linseed documented. Flax type plants are generally taller and have smaller number of branches while linseed types are often shorter, have more branches and produce more seeds. The flax types are commercially grown for the extraction of fibres, whereas the linseed is meant for the extraction of oil from seeds (DIEDERICHSEN and ULRICH, 2009). It has two separate centres of origin, linseed type originated in southwest Asia while fibre type originated in Mediterranean region (VAVILOV, 1951). It is largely grown in temperate regions and to some extent on subtropical and tropical highlands under favorable growing conditions of warm moist climate and well-drained medium heavy soils (WORKU *et al*., 2015). Approximately 20% of the total linseed oil produced is used as edible oil and the remaining 80% for industrial purpose. Linseed oil is an excellent drying oil used in manufacturing paints, inks, varnishes and other wood treatments, waterproof fabrics, oil cloth, soap, linoleum, putty and pharmaceuticals *etc***.** So, the crop is grown for fibre, oil or both seed and oil**,** but recently it has gained a new interest in the emerging market of functional food due to higher content of digestible proteins and lignans in seeds and high content of alpha linolenic acid (ALA), an essential omega-3-fatty acid in its oil which constitute up to 61% of the total fatty acid (REDDY *et al.*, 2013). Its medicinal and nutraceutical properties have paved the way for its diversified uses and value addition in various forms. Recent advances in neuro-biology have established it as the best herbal source of omega-3-fatty acids, which helps in regulating the nervous system (ANONYMOUS, 2017).

India ranks second in the world after Canada with respect to area and third in production. In India linseed is mostly grown as oilseed crop on approximate area of 3.2 lakh ha with production of 1.74 lakh metric tons (FAO STAT, 2018). It is cultivated in the temperate and sub-tropical environments as rainfed crop in the states of Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Maharashtra, Rajasthan, Bihar, Odisha, Jharkhand, Karnataka and Assam that account for more than 97 per cent of the total linseed area. The average yield of India recorded to be 533 kg/ha was found very low compared to world average yield of 927 kg/ha and highest average yield of 1497 kg/ha in Canada (FAO STAT, 2018). So, low productivity in India might be

associated with the narrow genetic base and non-availability of high yielding varieties, cultivation in marginal lands and vulnerability to biotic and abiotic stresses. Hence, with increased demand there is an urgent need of varieties with high yield potential. Development of high yielding varieties requires the assessment of existing genetic variability for yield and its component characters before planning for an appropriate breeding strategy for genetic improvement. There is need of diverse genotypes so that genetic improvement over existing linseed varieties can be achieved.

For boosting up the yield potential of any crop it is important to identify cultivars with improved yield and other desirable yield contributing characters (KUMAR *et al*., 2012). Genetic variation is the basis of crop improvement programme and provides a great array of genotypes that can be used in breeding high yielding cultivars (CHANDRAWATI *et al*., 2016). Further, to plan efficient breeding programme reliable estimates of extent of heritability, genetic advance and the magnitude and direction of genetic correlations among yield and morphological traits is required (KHAN *et al.*, 1998; AKBAR *et al.*, 2001, 2003; REDDY *et al.*, 2013; TYAGI *et al.*, 2014; AHMAD *et al.*, 2014, CHANDRAWATI *et al*., 2016; UPADHYAY *et al*., 2019). Heritability and genetic advance would be valuable tools in predicting the genetic improvement through selection (CHANDRAWATI *et al*., 2016). The pattern of genetic relationships between and within accessions can be studied by multivariate analysis methods (KAUR *et al*., 2018). Principal component analysis (PCA) and clustering are the two useful multivariate statistical tools for studying the relationship among the related genotypes (KAUR *et al*., 2018). Cluster analysis is used to study the association between landraces while relationships between traits are statistically analyzed using PCA (KUMAR *et al*., 2018). Therefore, the present experiment was conducted to analyze multivariate genetic diversity, genetic variation, heritability and association studies in 50 linseed genotypes for three consecutive years (2016-17, 2017-18 and 2018-19) to select the promising genotypes and to identify the most important characters for breeding programme. First time we have evaluated linseed in semi-arid conditions of Gujarat, India as an irrigated crop for yield, various morphological and quality traits. Further, considering the multiple health benefits of omega-3-fatty acids, genotypes were also subjected to fatty acid analysis using gas chromatography to identify the genotypes rich in omega-3-fatty acids.

MATERIALS AND METHODS

Experimental materials and location

Fifty linseed genotypes were sown during winter season for three consecutive years 2016-17, 2017-18 and 2018-19 at the Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, S.K.Nagar, Gujarat, India. Genotypes with their pedigree/parentage, source/origin and characteristics features are given in Table 1. Experimental site is located at 24º19'26" North latitude and 72º18'53" East longitude with an altitude of 172.00 meters above the mean sea level (Arabian Sea). The soil of experimental sight was loamy sand in texture with a pH of 7.5 and climatic condition falls under the category of semi-arid, characterized by less than 400 mm of annual average rainfall.

Table 1. List of linseed genotypes, pedigree, source / origin, characteristic features and Shannon-weaver diversity index ($H^{'}$)

Sr. No.	Genotype	Pedigree/Parentage	Source/Origin	Growth habit	Lodging/ Non-lodging	Flower colour	Seed coat colour	Shannon-weaver Diversity Index($H^{'}$)
1	Padmini	EC-41628 x EC-77959 x DPL-20 x Neelum	CSAUAT, Kanpur (U.P.)	Semi-erect	Non - lodging	Blue	Brown	1.761386
2	Rashmi	Gaurav x Janki	CSAUAT, Kanpur (U.P.)	Erect	Non - lodging	Blue	Brown	1.726689
3	JLS-9	RL-102 x R-7/J-23	Jabalpur, M.P.	Semi-erect	Non - lodging	Blue	Brown	1.772403
4	Sheela	Gaurav x Janki	CSAUAT, Kanpur (U.P.)	Erect	Non - lodging	Pale blue	Brown	1.770653
5	Neela	Local selection of WB	West Bengal	Erect	Non - lodging	blue	Brown	1.753194
6	Sweta	Mukta x T-1206	CSAUAT, Kanpur (U.P.)	Erect	Non - lodging	blue	Yellow	1.720265
7	Surabhi	LC-216 × LC-185	Kangra Valley, Himachal Pradesh	Erect	Non - lodging	pale blue	Brown	1.752592
8	Neelum	T-1 x NP (RR)-9	CSAUAT, Kanpur (U.P.)	Semi-erect	Non - lodging	pale blue	Brown	1.764001
9	T-397	T-491 x T-1103-1	CSAUAT, Kanpur (U.P.)	Semi-erect	Non - lodging	blue	Brown	1.770388
10	Mukta	---	CSAUAT, Kanpur (U.P.)	Erect	Non - lodging	white	Brown	1.701442
11	Gaurav	Selection-3 x EC-1552	CSAUAT, Kanpur (U.P.)	Bushy	Lodging	blue	Yellow	1.751239
12	R-1 (J-1)	---	Jabalpur, M.P.	Bushy	Lodging	blue	Brown	1.717500
13	J-7	---	Jabalpur, M.P.	Semi-erect	Non - lodging	blue	Brown	1.723957
14	LC-185	---	Gurdaspur, Punjab	Bushy	Lodging	blue	Yellow	1.727496
15	Kartika	Kiran x LCK-88062	IGKV, Raipur	Erect	Non - lodging	blue	Brown	1.750330
16	LC-27	---	Gurdaspur, Punjab	Bushy	Lodging	blue	Brown	1.741187
17	Garima	T-126 x Neelum	CSAUAT, Kanpur (U.P.)	Erect	Non - lodging	blue	Brown	1.751295
18	Shekhar	Laxmi-27 x EC-1387	Kanpur, U.P.	Erect	Non - lodging	blue	Brown	1.760958
19	Parvati	EC-41628 x EC-77959 x (DPL-20 x Neelum x EC-216 x Hira) x (BR-1 x NP-440)	CSAUAT, Kanpur (U.P.)	Semi erect	Lodging	blue	Brown	1.756680
20	LC-54	K2 x Kangra local	Gurdaspur, Punjab	Semi erect	Lodging	white	Light brown	1.718911
21	Kiran	Afg-8 x R-11 x Afg-8	Raipur, CG	Semi erect	Lodging	blue	Brown	1.736568
22	Nagarkot	New River × LC-216	Himachal Pradesh	Semi erect	Lodging	blue	Brown	1.748436

23	Meera	RL-75-6-2 x RL-29-8 x LCK8528	Kota, Rajasthan	Erect	Non - lodging	blue	Brown	1.795007
24	Ruchi	---	CSAUAT, Kanpur (U.P.)	Semi-erect	Non - lodging	white	Brown	1.724748
25	Pusa-2	Selection from BS-12	New Delhi	Erect	Non - lodging	white	Brown	1.765293
26	Pusa-3	K2 x T-603	New Delhi	Erect	Lodging	white	Brown	1.741882
27	Baner	EC-21741 × LC-216	Himachal Pradesh	Semi erect	Lodging	white	Brown	1.767588
28	Kirtika	---	India	Erect	Lodging	Blue	Brown	1.743159
29	Shival	---	Nagpur, MH	Bushy	Lodging	white	Brown	1.782101
30	S-36	---	India	Semi erect	Lodging	Blue	Brown	1.727076
31	Suyog	Kiran x KL168 x Kiran	Sagar, MP	Erect	Non - lodging	white	Brown	1.740568
32	RLC-92	Jeevan x LCK-9209	IGKV, Raipur	Erect	Non - lodging	Pale blue	Brown	1.747124
33	Sharda	(Shubhra x J-1) x (J-1 x Kiran)	IGKV, Raipur	Erect	Non - lodging	white	Brown	1.711085
34	Deepika	Kiran x Ayogi	IGKV, Raipur	Erect	Lodging	Blue	Brown	1.759222
35	Janki	New River × LC-216	Himachal Pradesh	Erect	Non - lodging	Blue	Brown	1.759280
36	Shikha	Hira x CRISTA	CSAUAT, Kanpur (U.P.)	Semi erect	Lodging	Blue	Brown	1.752349
37	Pratap Alsi-1	ACC.750 x RL 29-8	Kota, Rajasthan	Erect	Non - lodging	white	Brown	1.737142
38	Hira	---	CSAUAT, Kanpur (U.P.)	Erect	Lodging	white	Brown	1.767075
39	Shubhra	Mukta x K-2	CSAUAT, Kanpur (U.P.)	Erect	Non - lodging	white	Brown	1.761253
40	NL-97	R-7 x RLC-4	Nagpur, Maharashtra	Erect	Non - lodging	Pale blue	Brown	1.750657
41	EC 41528	PONE-1005 / 65	Argentina	Erect	Non - lodging	Pale blue	Brown	1.780123
42	IC 53281	/P/619	Raigarh, M.P.	Erect	Non - lodging	Blue	Brown	1.726695
43	IC 54970	---	India	Erect	Non - lodging	Blue	Brown	1.814827
44	IC 56363	---	India	Erect	Non - lodging	Blue	Brown	1.779856
45	IC 56365	---	Akola, MH	Erect	Non - lodging	Pale blue	Brown	1.820885
46	IC 96491	---	India	Erect	Non - lodging	Pale blue	Brown	1.804344
47	IC 96473	---	India	Erect	Non - lodging	Blue	Brown	1.743442
48	IC 96461	---	India	Semi-erect	Non - lodging	Blue	Brown	1.821879
49	IC 96460	---	India	Erect	Non - lodging	Blue	Brown	1.778570
50	Subhra	---	India	Erect	Non - lodging	white	Brown	1.786063
	Average							1.755337

Field experiments and observations recorded

The genotypes were sown in randomized complete block design (RCBD) with 2 replications. Each genotype was represented by 2 rows of 2 m length with distance of 30 cm between rows and 10 cm between plants in a row. Thinning was performed after 21 days of germination to maintain plant geometry. From sowing till harvesting, all the recommended agronomic package of practices was followed to raise the good crops. Five plants were randomly selected and tagged for taking observations. The observations were recorded for quantitative traits such as days to 50% flower, days to maturity, plant height (cm), number of primary branches per plant, number of bolls per plant, number of seeds per boll, seed yield per plant (g) and oil content (%). Harvested seeds from five randomly tagged plants from each entry were stored separately in a cloth bag for determination of oil content. Oil content of each sample was determined through soxhlet extraction method (GARCIA-HERNANDEZ *et al*., 2017). The fatty acid composition of all the samples was determined by Gas chromatography method (LEWINSKA *et al*., 2015).

Statistical analysis

Genetic parameters

Genotypic and phenotypic coefficients of variation were computed according to the formula given by BURTON (1952):

$$Phenotypic coefficient of variation (PCV\%) = \frac{\sqrt{Phenotypic variance}}{Grand mean} x100$$

$$Genotypic coefficient of variation (GCV\%) = \frac{\sqrt{Genotypic variance}}{Grand mean} x100$$

The genotypic and phenotypic coefficient of variances (GCV and PCV, respectively) were categorized as low (0-10%), moderate (10-20%) and high (20% and above) as suggested by SIVASUBRAMANIAN and MADHAVAMENON (1973).

Broad-sense heritability was estimated by the formula suggested by FALCONER (1989):

$$H2 = \sigma^2 g / (\sigma^2 g + \sigma^2 e/r)$$

where, H^2= broad sense heritability, $\sigma^2 g$ = genotypic variance; $\sigma^2 e$ = residual variance and r = number of replications.

The Heritability was categorized as given by ROBINSON *et al*. (1949): Low = 0-30%, moderate = 30-60% and high = 60% and above.

Genetic advance (G.A.) was computed by the formula given by JOHNSON *et al*., (1955):

$$G.A. = H^2 k \sigma p$$

where, H^2 = heritability in broad sense, k = selection differential which is equal to 2.06 at 5% selection intensity and σp = phenotypic standard deviation

Genetic advance as per cent of the mean (G.A. % of mean) was estimated as per the formula suggested by JOHNSON *et al.* (1955).

$$G.A.(\%\ of mean) = \frac{G.A.}{X} x\ 100$$

Genetic advance as per cent of the mean was categorized as: Low = (< 10%), moderate = (10 - 20%) and high = (> 20%) according to FALCONER (1989).

The genetic parameters have been calculated using R statistical software, version 3.4.1 (R DEVELOPMENT CORE TEAM, 2017).

Cluster analysis

Hierarchical cluster analysis for oil content, seed yield and morphological characters was performed to produce dendrogram based on the average distance between genotypes. The intergenotypic divergence was calculated using the unweighted pair group method of arithmetic averages (UPGMA). Data of cluster analysis were analyzed using PAST software, version 3.25 (HAMMER, 2019).

Principal components analysis

Principal components analysis (PCA) is the data reduction technique applicable to quantitative type of data. PCA transforms multi-correlated variables into another set of uncorrelated variables for further study. These new set of variables are linear combinations of original variables. It is based on the development of eigen-values and mutually independent eigen-vectors (principal components) ranked in descending order of variance size. Such components give scatter plots of observations with optimal properties to study the underlying variability and correlation. Suppose $x_1, x_2, \ldots\ldots, x_n$ be the original data in a study, then principal components may be defined as:

$$\alpha'1x = \alpha 11x1 + \alpha 12x2 + \cdots + \alpha 1pxp = \sum_{j=1}^{p} \alpha 1jxj$$

Where, $\boldsymbol{\alpha}'_1 x$ is the linear function of the elements of **x** having maximum variance, and **α1** is a vector of p constants α11, α12,...,α1p, and ' denotes transpose, so that Next, look for a linear function $\boldsymbol{\alpha}'_2 x$, uncorrelated with $\boldsymbol{\alpha}'_1 x$ having maximum variance, and so on, so that at the k^{th} stage a linear function $\boldsymbol{\alpha}'_k x$ is found that has maximum variance subject to being uncorrelated with $\boldsymbol{\alpha}'_1 x$, $\boldsymbol{\alpha}'_2 x$.., $\boldsymbol{\alpha}'_{k-1} x$. The k^{th} derived variable, $\boldsymbol{\alpha}'_k x$ is the k^{th} PC (JOLLIFFE, 2002). The biplot based on two principal components were also generated to depict the two-dimensional view of

accession scores. Data of principal component analysis were analyzed using PAST software, version 3.25 (HAMMER, 2019).

Shannon-weaver diversity index

Shannon diversity index (H') was calculated to study diversity among the linseed genotypes with the formula given by SHANNON (1948):

$$_{i=1}^{N}H' = -\sum pi.lnpi$$

where p_i is the proportion of accessions in the i^{th} class of a n-class character and n is the number of phenotypic classes for a character and for quantitative traits 'n' equalled 8, based on Sturge's rule, n, the number of frequency classes = 1 + $Log_2(N)$, where, n = the observed number of genotypes. The indices are standardized by dividing each value of H' by $loge_n$ to keep the value in a range of 0 to 1 in order to estimate the importance of phenotypic diversity. The data were analyzed to calculate the diversity indices using R statistical software, version 3.4.1 (R DEVELOPMENT CORE TEAM, 2017)

Association analysis

Pearson correlation was used to measure the degree of relationship between linearly related variables. The following formula was used to calculate the Pearson r correlation:

$$r_{xy} = \frac{n\sum xiyi - \sum xi \sum yi}{\sqrt{n\sum xi2 - (\sum xi)2}\,\sqrt{n\sum yi2 - (\sum yi)2}}$$

where, r_{xy} = Pearson r correlation coefficient between x and y variables; n = number of observations; x_i = value of x for i^{th} observation and y_i = value of y for i^{th} observation. The data were analyzed for the Pearson correlation analysis using R statistical software, version 3.4.1 (R DEVELOPMENT CORE TEAM, 2017).

RESULTS

Genetic variations

Pooled analysis of variance revealed highly significant differences ($p<0.001$) among genotypes studied for all the characters studied (Table 2). The year variance showed non-significant differences for most traits except days to maturity, plant height, number of primary branches per plant and number of seeds per boll. The interaction variance between genotypes x year was found non-significant for all the traits except plant height ($p<0.001$) indicating consistence performance of the genotypes across the year.

Table 2. ANOVA (Analysis of variance) of eight quantitative traits in linseed

		Days to 50% flower				Days to maturity				Plant height			
Sources of variation	DOF	Sum of square	Mean sum of square	F value	Pr(>F)	Sum of square	Mean sum of square	F value	Pr(>F)	Sum of square	Mean sum of square	F value	Pr(>F)
Genotype	49	34	814.8	182.118	< 2e-16***	21790	444.7	41.221	< 2e-16***	21017	428.9	821.009	< 2e-16***
Replication	1	6	33.7	7.54	0.00659	216	216.1	20.028	1.28E-05	97	96.6	184.833	< 2e-16
Year	1	174	5.8	1.307	0.2543	82	81.7	7.57	0.00648**	49	49	93.804	< 2e-16***
Genotype: year	49	890	3.6	0.795	0.82752	175	3.6	0.332	0.99999	115	2.3	4.493	2.27E-14***
Residuals	199		4.5			2147	10.8			104	0.5		
		Number of primary branches per plant				Number of bolls per plant				Number of seeds per boll			
Genotype	49	1381.7	28.2	42.551	<2e-16***	99864	2038	288.673	<2e-16***	109.70	2.239	26.926	<2e-16***
Replication	1	1.3	1.25	1.893	0.17	2002	2002.1	283.581	<2e-16	16.90	16.898	203.235	<2e-16
Year	1	54.5	54.5	82.236	<2e-16***	3	3	0.429	0.513	0.53	0.53	6.38	0.0123*
Genotype: year	49	29.8	0.61	0.919	0.627	216	4.4	0.623	0.974	4.54	0.093	1.115	0.2975
Residuals	199	131.9	0.66			1405	7.1			16.55	0.083		
		Seed yield per plant				Oil content							
Genotype	49	832.3	16.986	92.63	< 2e-16***	1522.1	31.06	211.9	<2e-16***				
Replication	1	5.3	5.333	29.085	1.95E-07	102.1	102.08	696.5	<2e-16				
Year	1	0.3	0.264	1.437	0.232	0.0	0	0	1				
Genotype: year	49	10.4	0.213	1.162	0.235	0.0	0	0	1				
Residuals	199	36.5	0.183			29.2	0.15						

DOF: Degree of freedom, Significance codes: '***'=0.001, '**'=0.01, '*'=0.05

The mean performance, range, genotypic, phenotypic and environmental variance, phenotypic and genotypic coefficient of variation, broad sense heritability and genotypic advance as percentage of mean of genotypes studied for each trait are given in the Table 3. The wide range of variability was observed for most of the traits studied. The days to 50% flower ranged from 41.47 (Shival) to 88.53 (Sweta) and mean was found 61.92 days. Mean values for

days to 50% flower were recorded below average of 61.92 days for 24 genotypes. Mean value for days to maturity was observed 91.94 days with a range of 76.30 (Shival) - 111.30 (Sweta) days. Twenty-two genotypes (44%) showed days to maturity lower than average value. The genotype Sharda showed minimum plant height of 29.70 cm, maximum plant height taped in Neelum (71.70 cm) and 25 (50%) genotypes recorded minimum plant height. The mean values for other yield component traits like primary branches per plant ranged from 5.57 (Sharda) to 16.20 (IC54970), number of bolls per plant from 49.30 (Shubhra) to 149.07 (Mukta) and number of seeds per boll ranged from 5.8 (Pusa-3) to 8.70 (IC56363). The above average performance for primary branches per plant, number of bolls per plant and seeds per boll were recorded in 44%, 46% and 54% genotypes respectively. The mean value of seed yield per plant was 6.04 g with a range of 2.72-9.01 g. Minimum seed yield per plant (2.72 g) was observed in S-36 while, maximum (6.04 g) was found in T-397 and 31 genotypes (62%) recorded above mean seed yield per plant. The oil content ranged from 34.13% (Garima) to 41.39% (IC53281) with mean value of 37.88%.

A considerable variation existed among genotypes for the traits studied. Higher values of PCV: GCV were recorded for the seed yield per plant (48.49:47.97), number of primary branches per plant (44.50:43.47), number of bolls per plant (37.76:37.63), days to 50% flower (32.69:32.51) and plant height (30.84:30.80) (Table 3). The magnitude of phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the characters under study showing little influence of environment on the expression of these traits.

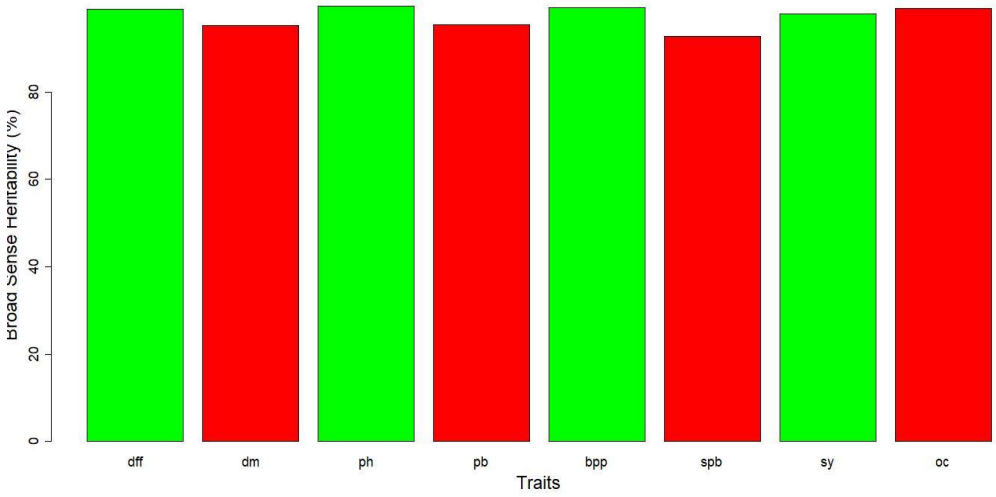

Fig. 1 Diagram showing heritability of eight quantitative traits in linseed

dff: Days to 50% flower, dm: Days to maturity, ph: Plant height, pb: Primary branches per plant, bpp: Bolls per plant, spb: Seeds per boll, sy: Seed yield per plant, oc: Oil content

Table 3. Mean, range, variance, coefficient of variations (phenotypic and genotypic), heritability, genetic advance as per cent of mean and Shannon-weaver diversity index of linseed

Characters	Mean	Range	PV	GV	EV	PCV	GCV	H^2	GAM	$H^{'}$
Days to 50% flower	61.92	41.47-88.53	409.66	405.19	4.47	32.69	32.51	98.91	66.61	3.894
Days to maturity	91.94	76.30-111.63	227.75	216.96	10.79	16.46	16.07	95.26	32.30	3.908
Plant height (cm)	47.51	29.70-71.70	214.72	214.19	0.52	30.84	30.80	99.76	63.38	3.897
Number of primary branches per plant	8.52	5.57-16.20	14.43	13.77	0.66	44.50	43.47	95.41	87.47	3.882
Number of bolls per plant	84.66	49.30-149.07	1022.55	1015.49	7.06	37.76	37.63	99.31	77.25	3.890
Number of seeds per boll	7.48	5.80-8.70	1.16	1.08	0.08	14.41	13.88	92.84	27.56	3.909
Seed yield per plant (g)	6.04	2.72-9.01	8.58	8.40	0.18	48.49	47.97	97.86	97.76	3.871
Oil content (%)	37.88	34.13-41.39	15.60	15.46	0.15	10.43	10.38	99.06	21.28	3.910
Mean										3.895

PV= Phenotypic variance, GV= Genotypic variance, EV= Environmental variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, H^2= Broad sense heritability, GAM= Genetic advance as per cent of mean, $H^{'}$ = Shannon-weaver diversity index

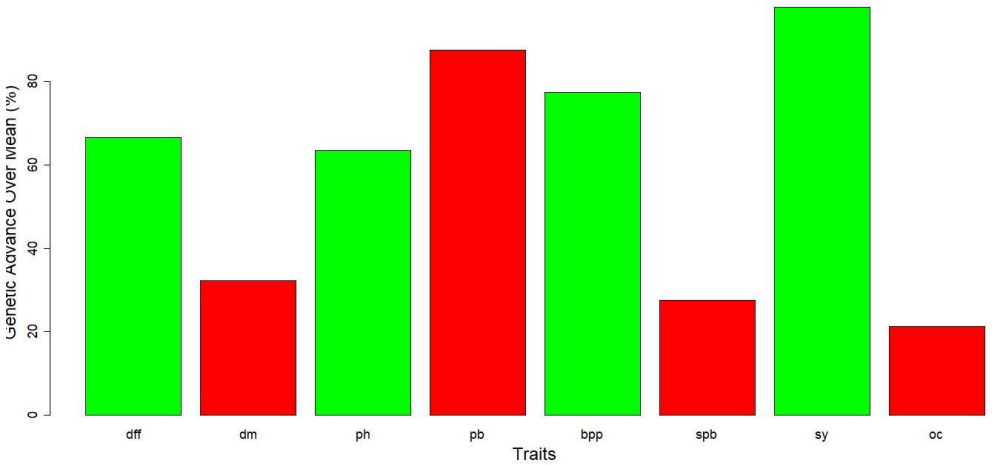

Fig. 2 Diagram showing genetic advance as per cent of mean of eight characters in linseed
dff: Days to 50% flower, dm: Days to maturity, ph: Plant height, pb: Primary branches per plant, bpp: Bolls per plant, spb: Seeds per boll, sy: Seed yield per plant, oc: Oil content

Highest estimate of heritability was observed for plant height (99.76%) followed by number of bolls per plant (99.31%), oil content (99.06%), days to 50% flower (98.91%), seed yield per plant (97.86%), number of primary branches per plant (95.41%), days to maturity (95.26%) and number of seeds per boll (92.84%) showed that these characters were governed by additive genes (Table 3 and Fig. 1). Maximum genetic advance as percent of mean was observed for seed yield (97.76%) followed by number of primary branches per plant (87.47%) and number of bolls per plant (77.25%) days to 50% flower (66.61%), plant height (63.38%), days to maturity (32.30%), number of seeds per boll (27.56%) and oil content (21.28%) indicating the presence of additive gene effects (Table 3 and Fig. 2).

Cluster analysis

The cluster analysis through the UPGMA method grouped the genotypes into nine clusters with varied number of genotypes (Fig. 3).

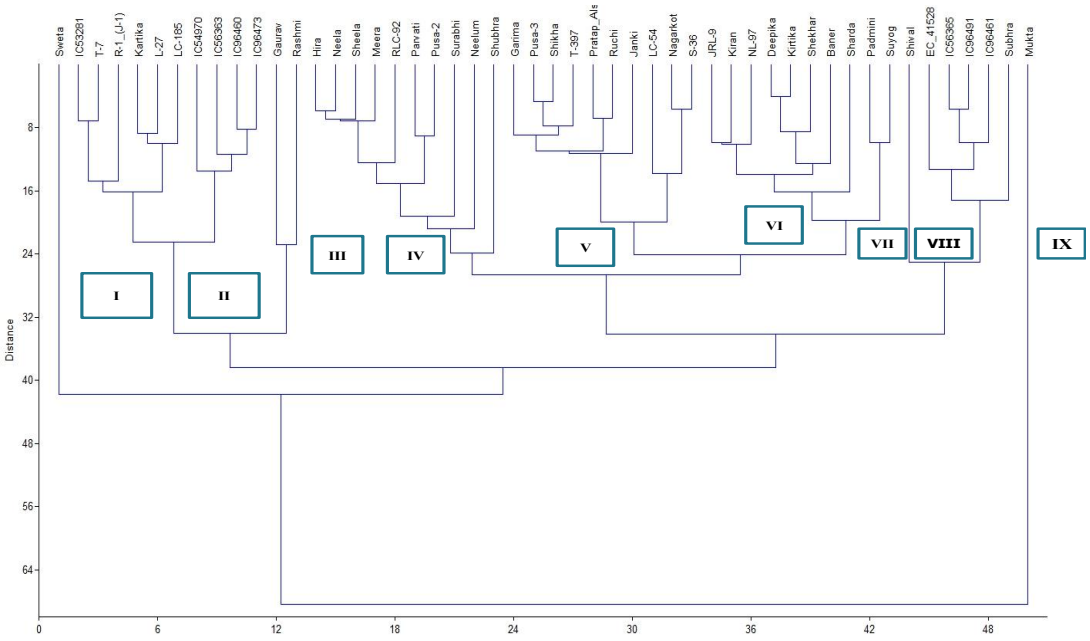

Fig. 3 Dendrogram showing 50 genotypes of linseed (Note: cut off point for making optimal number of clusters is 23)

Cluster I possessed single genotype Sweta having late flowering, late maturity, dwarf stature, a greater number of bolls per plant, a higher number of seeds per boll, high seed yield per plant and high oil content (%). Cluster II comprised 10 genotypes namely, IC53281, J-7, R-1(J-

1), Kartika, L-27, LC-185, IC54970, IC56363, IC96460 and IC96473 with early flowering and maturing habits, a greater number of bolls per plant, seeds per boll, seed yield per plant and high oil content (%). Cluster III was represented by two entries Gaurav and Rashmi which possessed a higher number of primary branches and bolls per plant. Hira, Neela, Sheela, Meera, RLC-92, Parvati, Pusa-2, Surabhi, Neelum and Subhra with a greater number of seeds per boll and seed yield per plant were grouped in the cluster IV. The similar grouping also happened in cluster V which possessed 10 genotypes with a higher number of seeds per boll and seed yield per plant. The genotypes in cluster VI *viz*., JLS-9, Kiran, NL-97, Deepika, Kirtika, Shekhar, Baner, Sharda, Padmini and Suyog had high cluster mean for number of seeds per boll, oil content, early flowering, maturity duration and dwarf height. The cluster VII was constituted of a single genotype, Shival, with shortest days to flowering, maturity duration and plant height among all the genotypes studied. The 5 genotypes were grouped on the basis of early flowering and maturity duration along with a greater number of primary branches per plant, seeds per boll, seed yield and oil content (%) in cluster VIII. The genotype Mukta showed more diversity and separated in cluster IX on the basis of highest number of bolls per plant, a highe rnumber of primary branches per plant, seeds per boll and seed yield per plant.

Principle component analysis

Eigen value greater than 1 are considered significant and only the first four principal components were used for the study and traits with loadings greater than ±0.3 were taken to represent the corresponding principal axis (HAIR *et al*., 1998). The first four principal components having eigen value greater than 1 were extracted from the mean of 8 traits and they explained 76.41% variance in linseed genotypes.

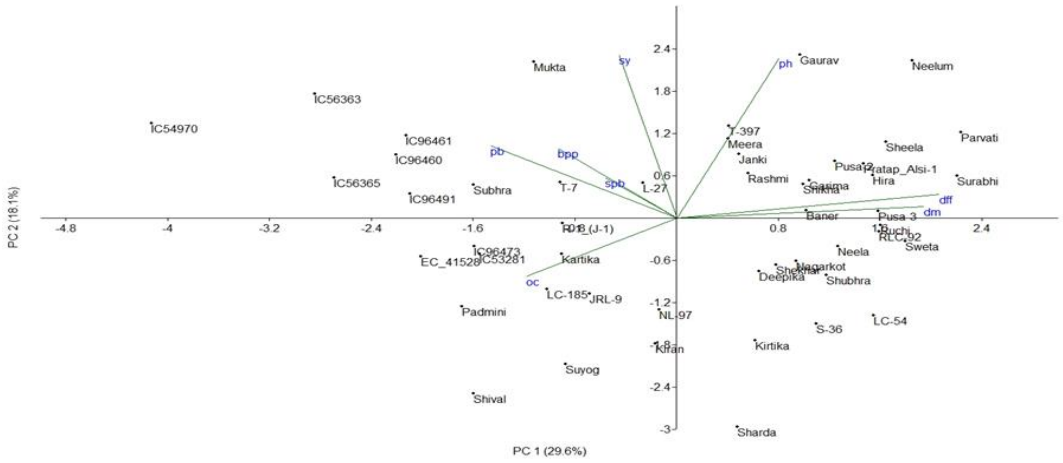

Fig. 4 PCA biplot showing eight quantitative traits and 50 genotypes of linseed

dff: Days to 50% flower, dm: Days to maturity, ph: Plant height, pb: Primary branches per plant, bpp: Bolls per plant, spb: Seeds per boll, sy: Seed yield per plant, oc: Oil content

The first principal component (PC1) was most important and accounted 29.63% of variation. The major contributors for variation observed in first principle component were days to 50% flower (0.86), days to maturity (0.81) and plant height (0.34). A variance of 18.14, 15.24 and 13.40 were derived from second, third and fourth principal components, respectively. The variation in PC2 was mainly due to plant height (0.74), primary braches per plant (0.33), bolls per plant (0.32) and seed yield per plant (0.75). PC3 imparted 15.24% variance mainly through days to 50% flower (0.41), days to maturity (0.51), primary braches per plant (0.38), bolls per plant (0.56), seeds per boll (0.31) and oil content (0.36). Likewise, major contributors to the variation observed in PC4 were bolls per plant (0.32), seeds per boll (0.35) and oil content (0.34) (Table 4). The Genotype-trait biplot based on two principal components were generated to represent the two-dimensional view of different genotypes of linseed and eight traits (Fig. 4).

Estimation of Shannon-weaver diversity index

Shannon-weaver diversity index revealed sufficient diversity for both genotypes and traits (Table 1 and Table 3 respectively). The linseed genotypes were diverse for all the quantitative traits and also diverse among themselves ($H^{'}$>0.5). Diversity index ranged from 1.701442 (Mukta) to 1.821879 (IC96461) among the genotypes. Average diversity index of 1.755337 and 3.895 for genotypes and traits respectively revealed that linseed genotypes were more diverse among themselves and for all the quantitative traits.

Table 4. Principal components of eight quantitative traits in linseed

Principal Components	PC1	PC2	PC3	PC4
Eigen Value	2.37	1.45	1.22	1.07
% Variance	29.63	18.14	15.24	13.40
		Loadings		
Days to 50% flower	0.86	0.11	0.41	0.05
Days to maturity	0.81	0.05	0.51	0.06
Plant height	0.34	0.74	-0.28	-0.10
Primary branches per plant	-0.61	0.33	0.38	-0.18
Number of bolls per plant	-0.39	0.32	0.56	0.32
Number of seeds per boll	-0.24	0.19	0.31	-0.82
Seed yield per plant	-0.19	0.75	-0.17	0.35
Oil content	-0.49	-0.27	0.36	0.34

PC1, PC2, PC3 and PC4= Principal component 1, Principal component 2, Principal component 3 and Principal component 4 respectively

Twenty-three genotypes (46%) exhibited above average diversity indices. Genotypes, IC96461 (1.821879), IC56365 (1.820885), IC54970 (1.814827), IC96491 (1.804344), Meera (1.795007), Subhra (1.786063), Shival (1.782101), EC41528 (1.780123), IC56363 (1.779856) and IC96460 (1.778570) were major contributors for diversity among the genotypes studied (Table 1). However, the Shannon-weaver diversity indices for all the traits together revealed that

oil content (3.910), number of seeds per boll (3.909), days to maturity (3.908) and plant height (3.897) contributed more for diversity among the genotypes (Table 3).

Association studies

Conclusively, association studies among various traits revealed that days to 50% flower showed significant positive correlation with days to maturity (0.87) and plant height (0.21); days to maturity with plant height (0.15); primary branches per plant with number of bolls per plant (0.35) and number of seeds per boll (0.29). Seed yield per plant had significant positive correlation with plant height (0.34), number of bolls per plant (0.18) and primary branches per plant (0.19). Oil content was positively and significantly correlated with number of primary branches per plant (0.19) and number of balls per plant (0.20) (Fig. 5). Further, seed yield per plant showed significant negative correlation with days to 50% flower (-0.11) and days to maturity (-0.12). Days to maturity had significant negative association with number of primary branches per plant (-0.27). Oil content was also negatively and significantly correlated with days to 50% flower (-0.28), days to maturity (-0.15) and plant height (-0.31). Further, days to 50% flower showed significant negative association with number of primary branches per plant (-0.30), number of bolls per plant (-0.10) and number of seeds per boll (-0.11) (Fig. 5).

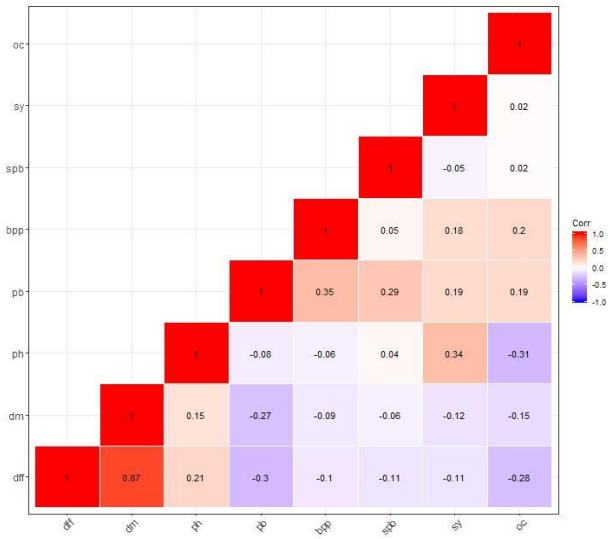

Fig. 5 Pearson's correlation among eight quantitative traits in linseed, red color represents highest positive correlation (r=+1.0), whereas blue color represents highest negative correlation (r=-1.0) and the white color represents no correlation ((r=0.0)

dff: Days to 50% flower, dm: Days to maturity, ph: Plant height, pb: Primary branches per plant, bpp: Bolls per plant, spb: Seeds per boll, sy: Seed yield per plant, oc: Oil content

Fatty acid composition

Thirty-two genotypes with good plant type (mostly erect or semi-erect growth habit), lodging resistance, early to mid-maturity duration, bold seed, high seed yield and oil content were selected. Seeds of selected linseed genotypes were analyzed for various saturated (palmitic and stearic acid) and unsaturated (oleic, linoleic and linolenic acid) fatty acids (Table 5).

Table 5.Fatty acid composition of 32 selected genotypes in linseed (p<0.001)

Sr.No.	Genotype	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Linolenic acid
1	Padmini	5.89	6.15	24.86	11.26	51.85
2	JLS-9	6.03	6.52	24.50	12.21	50.73
3	Sheela	5.96	5.01	25.09	12.08	51.86
4	Neela	6.16	7.10	25.89	10.85	50.00
5	Surabhi	5.51	7.29	21.91	10.38	54.92
6	Neelum	5.63	7.12	23.78	10.02	53.45
7	T-397	5.44	5.21	25.72	12.74	50.89
8	Mukta	5.26	7.24	20.87	10.75	55.87
9	J-7	6.18	7.29	28.40	10.22	47.90
10	Kartika	5.76	5.84	25.69	12.42	50.28
11	Garima	5.98	7.51	19.51	11.68	55.32
12	Shekhar	5.64	7.31	20.28	11.02	55.76
13	Meera	5.05	6.75	22.11	11.81	54.28
14	Ruchi	5.75	7.03	25.21	8.63	53.38
15	Pusa-2	6.10	6.75	24.84	8.35	53.97
16	Shival	5.55	5.16	24.20	10.61	54.49
17	Suyog	5.48	6.62	24.53	9.33	54.04
18	RLC-92	5.52	5.52	16.75	13.51	58.71
19	Sharda	5.59	6.56	26.56	12.45	48.84
20	Janki	5.35	5.56	21.13	10.52	57.45
21	Pratap Alsi-1	5.52	8.68	29.20	9.91	46.68
22	NL-97	5.78	6.21	26.97	12.94	48.10
23	EC 41528	5.94	6.40	23.10	11.93	52.64
24	IC53281	5.78	6.92	24.73	10.47	52.11
25	IC54970	5.50	7.46	24.89	11.85	50.30
26	IC56363	5.83	6.87	23.79	10.12	53.39
27	IC56365	6.03	6.77	23.74	11.61	51.84
28	IC96491	5.32	7.52	25.69	13.23	48.25
29	IC96473	5.27	6.03	22.72	9.45	56.53
30	IC96461	5.27	6.92	22.31	10.36	55.14
31	IC96460	5.36	7.40	23.55	10.86	52.84
32	R-1-J-1	5.50	7.06	22.13	12.53	52.79

The palmitic acid ranged from 5.05 (Meera) to 6.18% (J-7) with mean value of 5.65 and stearic acid ranged from 5.01 (Sheela) to 8.68% (Pratap Alsi-1) with mean value of 6.68%. Oleic, linoleic and linolenic acids ranged from 16.75 (RLC-92) to 29.20% (Pratap Alsi-1), 8.35 (Pusa-2) to 13.51% (RLC-92) and 46.68 (Pratap Alsi-1) to 58.71% (RLC-92) with means of

23.90, 11.13 and 52.64% respectively. 17 out of 32 genotypes recorded higher and above average $\boldsymbol{\alpha}$-linolenic acid content. As per the linseed descriptor of WORKU *et al*., 2015 Mukta (55.87%), Garima (55.32%), Shekhar (55.76%), IC96473 (56.53%) and IC96461 (55.14%) were registered for medium category and RLC-92 (58.71%) and Janki (57.45%) for high linolenic acid content (Figs. 6a and 6b).

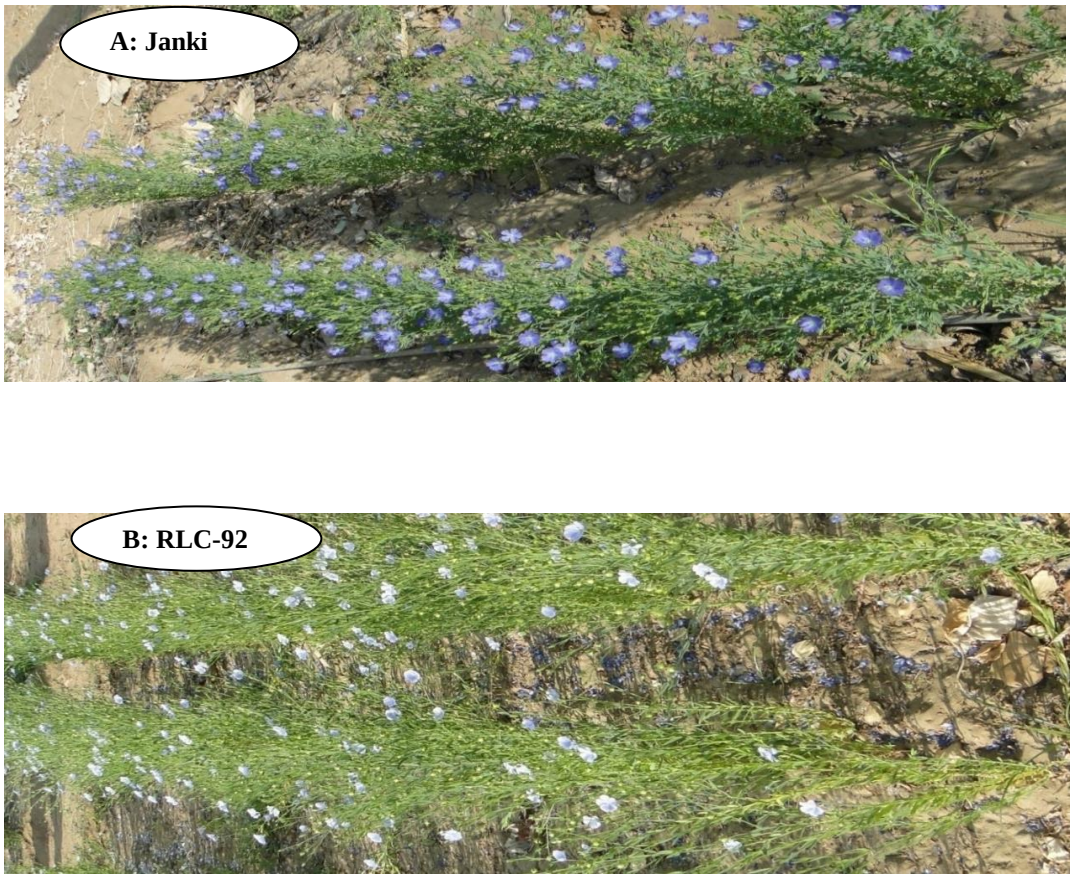

Fig. 6 Diagram showing high omega-3-fatty acid identified genotypes a. Janki and b. RLC-92 of linseed

DISCUSSION

Assessment of genetic diversity based on morphological differences is useful for plant breeders (KUMAR *et al*., 2012). The most of the genotypes having lower value of days to flower and maturity than average value could be used in breeding programme for development of early

duration linseed varieties. The 50 per cent genotypes recorded dwarf stature can be used for development of lodging resistant cultivars. Maximum genotypes (31 out of 50) registered seed yield above the mean value can be further used for the development of high yielding varieties in linseed (DIEDERICHSEN and FU, 2008; NIZAR and MULANI, 2015; REDDY *et al.,* 2013; SIVARAJ *et al*., 2012). Multivariate genetic diversity among 50 linseed genotypes representing nine major states of India and Argentina revealed a considerable variability for seed yield, oil content and morphological traits (KAUR *et al*., 2018; TADESSE *et al.,* 2010; TYAGI *et al*., 2014; YOU *et al*., 2017). Higher range, more diversity index and large differences in mean values for most of the characters revealed that sufficient diversity existed among the genotypes and traits (DIKSHIT and SIVARAJ, 2015). The analysis of variance revealed significant differences among the genotypes being evaluated and ample scope of improvement by selection. The similar range of variability for seed yield, oil content and morphological traits were reported by ADUGNA and LABUSCHAGNE, 2002; AKBAR *et al*., 2003; CHANDRAWATI *et al*., 2016; DHIRHI and MEHTA, 2019.

Success of any crop improvement programme lies in exploiting genetic variability and partitioning of total genetic variability into genetic and non-genetic components is also necessary for effective breeding approaches. High PCV and GCV for seed yield per plant, number of primary branches per plant, number of bolls per plant, days to 50% flower and plant height indicated genetic variation for these traits and scope for genetic improvement through selection. Earlier, TADESSE *et al.*, 2010; MIRZA *et al.*, 2011; SIVARAJ *et al*., 2012; REDDY *et al.,* 2013; TYAGI *et al*., 2014; DIKSHIT and SIVARAJ, 2015; NIZAR and MULANI, 2015; CHANDRAWATI *et al*., 2016; YOU *et al*., 2017; KAUR *et al*., 2018; DHIRHI and MEHTA, 2019 have also reported similar variations for these characters in linseed.

High heritability coupled with high genetic advance for all the traits studied revealed that studied characters were predominantly governed by additive gene action and phenotypic selection for these characters will be effective for genetic improvement. High heritability coupled with high genetic advance for yield and related traits were reported in linseed by AKBAR *et al*., 2003; TADESSE *et al.*, 2010; MIRZA *et al.*, 2011; KUMAR *et al*., 2012; SIVARAJ *et al*., 2012; DIKSHIT and SIVARAJ, 2015; CHANDRAWATI *et al*., 2016; YOU *et al*., 2017; KAUR *et al*., 2018; DHIRHI and MEHTA, 2019.

Grouping of genotypes into few numbers of homogenous clusters facilitates the selection of diverse lines for the hybridization purpose. It permits precise comparison among all the possible pairs of genotypes and provides an opportunity for bringing together gene constellations and yielding transgressive segregants from crossing between diverse lines (KUMAR *et al*., 2020). The distribution of 50 linseed genotypes into nine different clusters revealed considerable differences among linseed genotypes for yield and various morphological characters. The clustering of genotypes enables identification of potential parents from different clusters for hybridization programme to generate desirable recombinants in segregating generations. So, cluster analysis based on morphological data is easy cost-effective and can be considered as a universal approach for evaluating genetic diversity among genotypes. Similar, grouping of linseed genotypes based on quantitative data was reported by ADUGNA *et al.,* 2006; BEGUM *et al*., 2007; FULKAR *et al.,* 2007; SRIVASTAVA *et al.,* 2009; KANDIL *et al.,* 2011; KHAN *et al*., 2013; DIKSHIT and SHIVARAJ, 2015; NIZAR and MULANI, 2015; CHAUDHARY *et al*., 2016; CHANDRAWATI *et al*., 2016; KAUR *et al*., 2018; PATIAL *et al*., 2019. Further, genotypes from

different source/origin were grouped in the same cluster, so grouping did not happen on the basis of origin or geographical location. DIKSHIT and SHIVARAJ (2015) and KAUR *et al*. (2018) also reported that linseed accessions did not necessarily assemble into the same cluster based on their geographical origins. Clustering of linseed accessions together regardless of their source supports the possibility of a common progenitor but separation by geographical or ecological isolation mechanisms as reported by KUMAR *et al*. (2020) in pearl millet. The genotypes from the different geographical location falls under different clusters didn't rules out the pollen-mediated gene flow in linseed (JHALA *et al*., 2011) and ryegrass (MAITY *et al*., 2021). So in the present study weak patterns among geographical regions/origins were observed but, more importantly, germplasm with specific characteristics was identified and clustered (YOU *et al*., 2017). Therefore, for any hybridization programs in linseed the choice of suitable diverse parents based on genetic divergence analysis would be more rewarding than the choice based on the geographical distances.

The PCA based on correlation was used to study interrelationships among the different traits and genotypes (KUMAR *et al*., 2020). The first four principal components accounted for 76.41% of the total variance. The major contributors for variation observed in PC1, PC2, PC3 and PC4 were days to 50% flower, maturity; plant height, primary braches per plant, bolls per plant and seed yield per plant; days to 50% flower, days to maturity, primary braches per plant, bolls per plant, seeds per boll and oil content; bolls per plant, seeds per boll and oil content respectively. The PCA analysis indicated the role of traits (specific to each PC) which contributed more towards genetic divergence in discriminating the genotypes of linseed. The present study was in agreement with the PCA traits analysis of WORKU *et al*. (2015); CHAUDHARY *et al*. (2016); CHANDRAWATI *et al*. (2016); PAUL *et al.* (2017); YOU *et al*. (2017); KAUR *et al*. (2018), PATIAL *et al*. (2019) in linseed.

Diversity index is a quantitative measure that reflects the distribution pattern of genetic diversity and phylogenetic relationship among the individuals in a population. Twenty three genotypes (46%) exhibited above average Shannon-weaver diversity indices which indicated sufficient diversity existed among the genotypes studied. Mukta contributed minimum and IC96461 contributed maximum towards the diversity among the genotypes. However, the Shannon-weaver diversity index for all the traits together revealed that oil content, number of seeds per boll, days to maturity and plant height had significant contribution towards the diversity. The similar trait specific indices was calculated by DIKSHIT and SHIVARAJ (2015) for qualitative traits in linseed germplasm accessions, KUMARI *et al*. (2016) for both qualitative and quantitative traits and KUMAR *et al*. (2020) for quantitative traits in pearl millet for deciphering phenotypic diversity.

Significant positive associations among various traits gives an insight on simultaneous improvement of characters and their direct or indirect effects on seed yield will lead to concurrent augmentation in yield (KUMAR *et al*., 2020). The positive association of seed yield per plant with plant height, number of bolls per plant and primary branches per plant and oil content with number of primary branches per plant and number of balls per plant implies that improving one or more components traits could result in enhancement in seed yield and oil content in linseed. These results were supported by ADUGNA and LABUSCHAGNE (2004); GAURAHA and RAO (2011); RAHIMI *et al.* (2011); DIKSHIT and SIVARAJ (2015); KAUR *et al*. (2018) in linseed. Further,

seed yield per plant showed significant negative correlation with days to 50% flower and days to maturity. Early duration maturity is a preferred trait for its cultivation as crop escape terminal heat and water stress allows linseed cultivation in semi-arid environments and permits multiple cropping systems.

The present study also elucidated trait specific superior linseed genotypes, which may be used in further breeding program. A white flowered, brown seed coat colour and dwarf stature genotype Shival, was identified as early flowering (41 days to 50% flower) and early maturing (76 days for maturity) genotype which is significantly earlier under semi-arid conditions of Gujarat, India. Another genotype with blue flower and brown seed colour T-397 was recorded as high seed yielding type whereas white flowered genotype, Mukta possessed large number of bolls per plant. Local collections namely, IC54970, IC56363 and IC53281 with blue flower and brown seed coat colour were identified for more number of primary branches per plant, seeds per boll and oil content respectively, whereas Mukta, IC53281, IC54970 and IC56363 were found potential genotypes with multiple traits. Exotic collection, EC41528 was also identified as a candidate genotype for multiple traits except number of seeds per boll. In India, average productivity is very low as compared to world average due to cultivation of linseed on marginal land with less input, therefore identified genotypes may play a crucial role in developing high yielding varieties suited to new niche areas in semi-arid climatic conditions. RLC-92 and Janki possessed high omega-3- fatty acid, alpha linolenic acid (>57%) while, Mukta, Garima, Shekhar, IC96473 and IC96461 were identified with 55-57% alpha linolenic acid. The similar genotypes have also been identified earlier with desirable fatty acid composition in linseed (WORKU *et al*., 2015; YOU *et al*., 2017; MHIRET, 2019) and in soybean for water use efficiency (KUMAR and LAL, 2015).

CONCLUSIONS

Higher range, more diversity index and large differences in mean values for most of the characters found in this study established that considerable phenotypic diversity existed among the linseed genotypes in the present study. High heritability accompanied with high genetic advance was observed for all the traits suggesting that they can be improved through direct selection due to presence of predominant additive variation. Clustering of the genotypes independent of the geographical location or source/origin for various yield and agro-morphological characters suggested that hybridizing the genetically diverse parents belonging to different clusters could provide an opportunity for bringing desirable genes of diverse nature together. Further, clustering of linseed genotypes from different source/origin into same cluster has confirmed that they are genetically related, and possibly from the same parent or pollen-mediated gene flow. It might be due to genotypes separated by geographical/ecological isolation or and a free exchange of breeding materials over locations. Principal component biplot supported the results of cluster analysis which further validated the diversity pattern in the linseed accessions. The genotypes Shival, Sharda, IC54970, Mukta, IC56363, T-397, IC53281 and RLC-92 were found to be promising for the characters like early duration, dwarf stature, a greater number of primary branches, number of bolls, seeds per boll, seed yield, oil content and omega-3-fatty acid and can be used for hybridization or selection process in subsequent generations.

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DELINEACIJA MULTIVARIJANTNE DIVERGENTNOSTI, HERITABILNOST, POVEZANOST SVOJSTAVA I IDENTIFIKACIJA SUPERIORNIH GENOTIPOVA LANA (*Linum usitatissimum* L.) ZA OMEGA-3-MASNE KISELINE

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Izvod

Sadašnje istraživanje je sprovedeno radi procene 50 genotipova lana tokom tri uzastopne godine za prinos semena, sadržaj ulja i agromorfološka svojstva primenom multivarijcijskog pristupa. Veći opseg, velika vrednost indeksa diverziteta (*Shannon-weaver*) i za osobine i za genotipove i velike razlike u srednjim vrednostima za većinu osobina pokazale su da postoji široka i značajna varijacija među genotipovima i osobinama. Objedinjena analiza varijanse otkrila je izuzetno značajne razlike ($p < 0,001$) među genotipovima za sve proučavane osobine. Viši fenotipski koeficijent varijacije (*PCV*) u poređenju sa genotipskim koeficijentom varijacije (*GCV*) označavao je mali uticaj okoline na ekspresiju svih proučavanih osobina. Klaster analiza prinosa i agro-morfoloških svojstava primenom aritmetičkih proseka (UPGMA) grupisala je genotipove u devet klastera. Grupisanje genotipova lana sa različitih geografskih lokacija ili izvora / porekla u isti klaster potvrdilo je da su genetski povezani, a možda i od istog pretka. Analiza glavnih komponenata (PCA) otkrila je da je većina varijacija (76,41%) pripala glavnim komponentama i ukazala je na ulogu osobina koje su značajno doprinele velikim varijacijama među genotipovima. Pozitivna povezanost prinosa semena po biljci i sadržaju ulja sa osobinama komponenti implicira da bi poboljšanje jedne ili više osobina komponenata moglo rezultirati genetskim povećanjem prinosa semena i sadržaja ulja u semenu lana. Značajna negativna povezanost prinosa semena po biljci i sadržaja ulja sa danima do cvetanja i danima do sazrevanja ima velike prednosti u oplemenjivanju sorti lana kratke vegetacije, za tople i sušne klimatske uslove polusušnih regiona. Specifični genotipovi, kao što su Shival, Sharda, IC54970, Mukta, IC56363, T-397, IC53281 i RLC-92 identifikovani su za razvoj sorti krače vegetacije i patuljastog rasta sa višim sadržajem omega-3-masnih kiselina.

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