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GENETIC DIVERSITY AND HERITABILITY ANALYSIS OF LINSEED (*LINUM USITATISSIMUM* L.)

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ABSTRACT

The experiment was carried out for 20 genotypes were subjected to diversity analysis, cluster analysis, heritability, correlation and path analysis. High PCV and GCV for the secondary branches (SB), followed by plant stand per plot (PSP), further trialed by yield per hectare (YH) and trialed by number of capsules per plant was greater than > 20% .High broad sense heritability was found for days to 50% flowering (DTF), followed by height (H), pursued by number of capsules per plant (NOCP), (98.49%), tailed by secondary branches (95.54%) and further monitored by plant stand per plot (88.89) and ensued by yield per hectare (91.23). Also, high heritability is governed by additive gene action for these characters. Characters with moderate heritability with low genetic advance as percentage of mean are governed by non-additive gene action and direct selection may not be possible because most of the variation in attributes due to the environmental effects. The high genetic mean advance for height (H), followed by primary branches (PB), pursued by secondary branches (SB), further followed by number of seeds per capsules (NOSC), trailed by plant stand per plot (PSP), yield per hectare (YH) and number of capsules per plant (NOCP). In the present study, days to 50% flowering (DTF) were correlated, significantly to the days to 75% maturity (DTF) (0.7991, 0.5391) and secondary branches (SB) (0.4511, 0.4181) significantly. Also, days to 75% maturity (DTM) positively and significantly correlated to height (H), secondary branches, number of seeds per capsule (NOSC) and 1000- seed weight (SW). Similarly, number of capsules were positively and significantly correlated to primary branches (PB) (0.6960, 0.5854) and yield per hectare (YH) (0.4977, 0.4912). Also, days to 75% maturity (DTM) were negatively and significantly to number of capsules per plant (NOCP), primary branches (PB) and 1000 seed weight (SW). Number of capsules per plant (NOCP) negatively correlated to secondary branches (SB) and number of seeds per capsule (NOSC). It showed positive and significant direct effect for primary branches (PB) *i.e.*, 0.5882, number of seeds per capsule (NOCP) i.e 0.4784 and plant stand per plot (PSP) 0.7529 and non-significantly positive for number of capsules per plant (NOCP), secondary branches (SB) and seed yield per hectare (YH). The genotypic correlations difference was higher than the corresponding phenotypic correlation for all traits, indicating that environment plays a small role in the expression of the traits, which suggests an inheritance between these traits at the genetic level. Cluster analysis displayed 10 clusters with diversity with 5 genotypes in cluster so they are related and four clusters have single genotype so they unrelated to any cluster.

Key words : Phenotypic coefficient of variation, Genotypic coefficient of variation and heritability, Cluster analysis.

Introduction

Linseed (*Linum usitatissimum* L. 2n=30) is one of the most important multiple-purpose winter (*rabi*) oilseed crop grown for oil and fibre content since ancient times. It is an annual, self-pollinated plant species belongs to the family Linaceae genus Linum commonly known as "Alsi" and is supposed to be originated in southwest Asia particularly in India (Vavilov, 1935 and Richharia, 1962). In India, it is cultivated in states of Rajasthan, West Bengal, Karnataka, Orissa, Bihar, Chhattisgarh, Madhya Pradesh, Uttar Pradesh, Maharashtra and Punjab. In Punjab, it is grown in foothills of Himalayas in the districts of Gurdaspur, Hoshiarpur and Rupnagar.

Linseed crop is grown for seed oil, stem fibre and to some extent for flour. Seed of this crop is also used preparing creams used in treatment of some challenging human and animal diseases. The oil is used for paints, inks, varnish and other wood treatments, like soap, linoleum, putty and pharmaceuticals. The fibre from flax/ linseed is used as raw material for textiles, thread/rope and packaging materials. Its straw and short fibre is used for producing pulp to make special papers for making cigarettes, currency notes and artwork. The wooden part serves as biomass energy or litter in cattle farming as addressed by Rowland (1998). Two morphologically different cultivated species of linseed are Flax and Linseed. The flax type is grown commercially for fibre, whereas the linseed is for oil from seeds and cake, as a by-product. Linseed has oil content from 36 to 48% rich in unsaturated fatty acids, especially alpha linolenic acid (ALA), an essential Omega-3 fatty acid and lignin oligomers which constitute about 57 % of total fatty acids in linseed (Reddy *et al*., 2012).

In plant breeding gene action is measured in terms of genetic variance or combining ability and its effects. The gene action indicates additive genes action is requirement of gain under selection as it is only genetic variance responsible for selection. Thus, high genetic advance indicates additive gene action. Thus, variability and heritability in germplasm is very important for selection and designing future breeding program. Genetic variations present our existing germplasm and the heritability provides us all about how much traits are transmitted from parents to offspring. Estimates of heritability provides genetic advance, because without genetic advance the heritability is not much effective approach for selection (Raja Vardhan, 2000 and Kadir, 1996). The statistical measure of degree and association of traits the selection criteria for study of correlation between yield and yield related traits is of prime importance. Positive correlation between among characters helps the plant breeder to improve of traits simultaneously. On the other hand, negative correlation expressed between two desirable traits makes it impossible to achieve a significant improvement in both the traits. Though, simple correlation alone is not very effective approach to true biological relationship of these traits with yield. The path coefficient analysis developed by Wright (1921, 1960) and described by Dewey and Lu (1959) is a standardized partial regression analysis, allows partitioning of correlation coefficient into direct and indirect effects of various traits (independent variables) towards dependent variable (yield). Thus, helps in appraising the cause effect relationship as well as effective selection. The true relationship between yield and character correlation shows direct effect. So, selection can be given due importance on this character to improve seed yield. If the correlation is due to indirect effect of the character through another component trait, the selection would be based on later trait through which indirect effect is exerted. Phenotypic values of a character are partly determined by genotypes, which are heritable and partly affected by environment, which is non-heritable is basis of selection criteria. The present study was conducted to evaluate linseed genotypes for genetic variability, heritability, correlation and path coefficient analysis for their yield and yield contributing parameters with an objective to accumulate knowledge of this crop and to generate the selection strategies to enhance yield.

Materials and Methods

The experimental material consisted of twenty linseed genotypes Surbhi, Bhagsu, Himani-1, Nagarkot, Himalsi, Janki, Jeevan, Binwa, Baner, Himalsi-2, BAU-2012-1-8, BAU-06-03, LC2063, LC2023, LC54, T397, JRF-2, G-42, LCP-87 and Giza-8 belonging to different geographic regions. It was laid out in Randomized Block Design (RBD) in 9 square meter plot with three replications at P.A.U., Regional Research Station, Gurdaspur in 2020-2022. The experiment was carried to assess genetic variability, heritability, correlation and path analysis for seed yield and their associated traits. A seed rate of 15kg/ hectare was utilized with improved package practice inputs were used including two-hand weeding and fertilizer application.

Coefficients of variance: In 1964 Falconer gave formula to calculate the genotypic and phenotypic coefficients of variation as follows:

$$\text{Genotypic variation coefficient} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic variation coefficient} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Sivasubramanian and Madhavamenon (1973) proposed the range of variation as <10%: low, 10-20%: moderate and >20%: high

Heritability and genetic advance

Heritability : The heritability in broad sense refers to the proportion of genotypic variance to the total observed variance in total population. Allard (1960) proposed a formula to calculate heritability:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h^2 = heritability in broad sense

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance ($\sigma^2 g$) + ($\sigma^2 e$)

$\sigma^2 e$ = environmental variance

Heritability estimates were categorized by Johnson *et al*. 1955 (h^2) as: Low: 0-30%, Medium: 30-60% and high: above 60%.

Genetic advance : Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. Burton (1952) gave formula to estimate heritability to estimate the genetic advance as:

$GA = K. h^2 (b). \sigma p$

Where,

GA = expected genetic advance

K = Selection differential, the value of which is 2.06 at 5% selection intensity.

σp = phenotypic standard deviation

h^2 (b) = heritability in broad sense

The relative utility of genetic advance among the characters, genetic advance as percent for mean was computed to visualize the

$$\text{Genetic advance as percent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

The genotypic and phenotypic coefficients of correlation were calculated as described by formula given by Fisher (1918). Genotypic and phenotypic coefficients were calculated using the formula as used by Wright (1921), Burton and Devane (1952) and elaborated by Dewey and Lu (1959). Cluster analysis based of K mean.

Results and Discussion

The broad base of variation were indicated by range, mean, coefficient of variation phenotypic (PCV) and genotypic (GCV), broad sense heritability (h^2) and genetic advance as percentage of mean (GA %M) are genetic estimates of variability are presented in Table 1 were computed to have a better understanding of the nature of the gene action for various quantitative characters for an effective breeding programme. K- means analysis tells about diversity and distances is displayed in Tables 2, 3 and 4.

Range : The range among the 20 genotypes indicated a broad base of variation for all the characters primary branches (3.14-5.14), 1000 seed weight (5.00-8.36), days to 50% flowering was (103.44-122.00), height (69.23-102.29), number of capsules (55.86-188.55), primary branches (3.13-5.14), secondary branches (16.67-41.39), plant stand (1117.41-1634.00) and yield hectare^{-1}(370.00 -2248.89). The characters like number of seeds capsule^{-1} (NOSC) (5.00-8.36) and 1000- seed weight ranges (7.07-9.00) showed minimum variation. The findings were in line with Satapathi *et al*. (1987) and Rao (2007) reported a wide range of variation for all or almost all chacters *viz*. seeds/capsule, capsule/plant, seed weight/plant and yield these characters. Similarly, Kasana *et al*. (2018) conveyed high variability in following characters 50% flowering, size of corolla, primary branches, plant height, capsule size, number of capsules, number of seeds capsule^{-1}, 1000-seed weight, oil percentage and seed yield in eleven traits of 151 gentypes. However, Gupta *et al*. (1999), Sarkar (2005) and Rao (2007) revealed broad range for number of primary branches, capsules and seed yield.

The mean value for days to 50% flowering, days to maturity height, capsule amount, primary branches, secondary branches, number of seeds per capsules, plant stand, 1000-seed weight and yield is 112.44, 153.86, 90.28, 117.01, 4.03, 30.08, 6.98, 1339.63, 7.76 and 1608.72. The mean performance of 15 characters *i.e.* plant height, primary branches, secondary branches, leaf area, number of capsules, seeds in capsule, stem diameter, days to 50% flowering, maturity, biological yield per plant, grain yield per plant and harvest index disclosed high variability in thirty-one genotypes along with their means as reported by Tyagi *et al* (2014).

Coefficient of variation phenotypic and genotypic (PCV and GCV)

In the present study, the phenotypic coefficient of variation (PCV) ranged from 5.26 days to maturity (DTM) and 33.82 numbers of capsules per plant (NOCP) as in Table 1. The PCV estimates showed that the phenotypic variability was low (below 10%) days to 75% maturity (DTM), followed by days to 50% flowering (DTF) and 1000 seed weight (SW)(g). Moderate PCV is (10-20%) for height (H), followed by primary branches (PB) and further number of seeds per capsules (NOSC).

The high phenotypic coefficient of variation(> 20%) was estimated for the secondary branches (SB) is 26,68, followed by plant stand per plot (PSP)27.53, further trialed by yield per hectare (YH) 32.21 and pursued by number of capsules per plant (NOCP) 33.82 in Table 1. Tyagi *et al*. (2014) revealed high percentage of PCV for grain yield per plant, biological yield per plant, harvest index, capsules per plant, secondary branches, primary branches, grain yield per plot along with moderate PCV for biological yield per plot, 1000- seed weight, leaf area

Table 1 : Mean, Range, GCV (%). PCV (%), Heritability h^2 % (BS), Genetic advance GA% mean and coefficient of variance (CV%) among Linseed entries.

Character	G Mean	Range	PCV	GCV	H2	GAM	CV
DTF	112.44	103.44-122.00	6.54	6.31	92.90	12.53	1.74
DTM	153.86	144.45-165.66	5.26	4.02	58.59	6.35	3.38
H	90.28	69.23-102.09	13.08	12.44	90.50	24.38	4.03
NOCP	117.01	55.86-188.55	33.82	33.73	98.49	69.32	2.39
PB	4.03	3.13-5.14	17.18	14.33	69.58	24.63	9.47
SB	30.08	16.67-41.39	26.68	26.08	95.54	52.52	5.63
NOSC	6.98	5.00-8.36	18.80	16.79	79.79	30.90	8.45
PSP	1339.63	1117.411634.00	27.53	25.96	88.89	50.42	9.17
1000SW	7.76	7.07-9.00	9.13	7.62	69.69	13.11	5.02
YH	1608.72	370.00-2248.89	32.21	30.77	91.23	60.54	9.54

*Days to flowering (DTF), days to maturity (DTM), height (H), number of capsules per plant (NOCP), primary branches (PB), secondary branches (SB), number of seeds per capsule (NOSC), plant stand per plant (PSP), seed weight of 1000 seeds (SW), seed yield hectare (YH).

Table 2 : Cluster and its Membership.

Cluster No	Number of genotypes	Members
1	5	1, 2, 3, 11, 18
2	2	4, 8
3	1	12
4	1	20
5	1	5
6	2	6, 10
7	2	7, 17
8	2	15, 16
9	3	9, 14, 19
10	1	13

and plant height and low PCV for stem diameter, seeds per capsule, oil content and days to 50% flowering maturity.

Similar pattern of genotypic coefficient of variation (GCV) demonstrated by all the ten characters and ranged from 4.02 to 33.73. It was highest for number of capsules per plant (NOCP) followed by yield per hectare (YH), trialed by plant stand per plot followed by secondary branches (SB) greater 20%. Moderate GCV (10-20%) was for the number of seeds per capsules (NOSC), followed by primary branches (PB) further ensued by height (H). The low GCV less than 10% for days to flowering (DTF) followed by primary branches (PB) and further pursued by 1000 -seed weight. Tyagi *et al* (2014) reported moderate GCV for 1000-seed weight (22.50%) and grain yield per plot (22.15%). However, all other characters have minimal GCV (below 10%) with the lowest value for days to flowering.

Bibi *et al.* (2013) also showed high potential for effective selection of seed yield per hectare in linseed based on PCV and GCV. GCV with the moderate range for stem diameter (12.08%), whereas lowest GCV <10% is for seeds per capsule (5.92%), days to 50% flowering (3.44%) and the oil content (4.30%) also high GCV was observed for the grain yield per plant, harvest index, secondary branches per plant and primary branches per *a* stated by Tyagi *et al.* (2014). High PCV and GCV (above 20%) were for secondary branches (SB) (26.68, 26.08), plant stand per plot PSP (27.53, 25.96), further trialed by yield per hectare YH (32.71, 30.77) and number of capsules per plant NOCP (33.82, 33.73). These findings were like Paul *et al.* (2017), who also observed that the PCV values were greater than the GCV values for all the traits studied. Previous studies by Basavaraj *et al.* (2011) and Asgarinia *et al.* (2014) stated high PCV and GCV for number of capsules per plant, number of seeds per capsule and yield per plant. Hence, selection for number of primary branches, number of capsules per plant and seed yield per plant are influenced by environmental effects from difference between the PCV and GCV was high could be due to the heterogeneity in soil fertility status and other unpredictable factors (Reddy *et al.*, 2012). Scientists previously also observed similar results (Khan *et al.*, 2007 and Manggoel *et al.*, 2012). Similar pattern of difference between PCV and GCV were reported by several workers for all or most of these characters (Satapathi *et al.*, 1987 and Rao, 2007).

Heritability

The current study of heritability in broad sense (H) ranges from (58.59%) for days to 75% maturity (DTM) to number of capsules per plant (NOCP) (98.49%) in (Table 1). Medium heritability estimates ranged from (30-60%). Moderate heritability for days to 75% maturity

Table 3 : Maximum variable values of each cluster of Linseed genotype.

Cluster No	Maximum Variable Values of each cluster									
	1	2	3	4	5	6	7	8	9	10
Character	Days to 50% flowering	Days to 75% maturity	Height	Number of capsules /plant	Primary branches	Secondary branches	Number of seed/ capsule	Plant Stand	1000-seed weight	Seed yield (kg/ha)
1	108.202	151.756	89.540	137.774	4.028	22.156	6.294	1,407.842	7.926	1,305.600
2	106.665	148.890	92.015	167.390	4.640	22.085	6.400	1,144.415	7.530	1,613.630
3	109.330	154.670	84.070	82.000	3.530	32.110	8.370	1,276.000	7.800	339.260
4	110.670	153.330	69.230	110.870	4.530	33.110	8.530	779.330	9.000	2,148.890
5	105.440	149.330	84.410	129.110	4.420	25.930	6.510	1,781.520	7.080	1,997.140
6	105.945	149.835	88.725	137.780	4.455	35.930	5.915	1,402.150	7.435	1,565.980
7	107.225	150.780	97.085	103.155	3.760	30.590	6.790	1,664.740	7.180	1,572.070
8	119.665	163.500	93.035	95.065	4.300	25.530	7.635	132.165	7.735	376.110
9	110.557	155.793	90.903	112.237	4.177	35.300	6.777	1,446.370	8.057	1,789.087
10	108.330	153.000	72.530	76.970	3.600	41.390	7.800	1,290.330	6.730	2,194.070

Table 4 : Intra and Inter-Cluster Distances between different clusters.

Cluster No	1	2	3	4	5	6	7	8	9	10
1	0.000	406.412	976.959	1,052.348	786.125	260.825	371.930	1,579.057	485.894	898.638
2		0.000	1,284.069	650.898	744.663	264.157	526.017	1,600.542	353.897	605.932
3			0.000	**1,876.833**	**1,733.904**	1,234.482	1,292.896	1,144.638	1,460.137	**1,854.933**
4				0.000	1,013.942	853.724	1,057.137	**1,887.494**	758.213	514.201
5					0.000	574.470	441.796	**2,312.952**	395.089	532.139
6						0.000	265.126	1,740.972	229.014	641.102
7							0.000	**1,944.102**	308.158	726.966
8								0.000	**1,929.812**	**2,155.821**
9									0.000	435.884
10										0.000

(DTM) is 58.9 is given in Table 1. However, moderate estimate of heritability for plant height was reported by Khan and Gupta (1995) and also by Tadesse *et al.* (2010). Nevertheless, others (Tefra and Gumuru 2020) reported moderate heritability for plant height (36.23), primary branches (40.0) per plant and secondary branches per plant (30.12). Other workers also conveyed information for moderate heritability for similar characters by Ramakant *et al*. (2005) and Kumar *et al*. (2016) as heritability is a good index of transmission of characters from parents to its progeny.

High broad sense heritability is >60%. High broad sense heritability was found for days to 50% flowering (DTF) is 92.90%, followed by height (H) 90.50%, pursued by number of capsules per plant (NOCP) (98.49%), tailed by secondary branches (95.54%) and further monitored by plant stand per plot (88.89%) and ensued by yield per hectare (91.23%). The selection of these characters with more than 90% of heritability were useful as it is controlled by additive genes which act as component for crop improvement according to Kumar *et al*. (2012). Correspondingly, earlier workers like; Gupta and Godawat (1981), Satapathi *et al*. (1987), Rao (2007), Pali and Meheta (2013) reported that high heritability of seed weight. Bibi *et al*. (2013) found high heritability for days to flower initiation, days to flower completion, days to maturity, 1000-grain weight, capsules per plant and harvest index. The heritability estimates suggest extent of variation observed in traits are influenced by genetic factors, which plays crucial role for breeding program.

Genetic advance as percent of mean

It was characterized by Johnson *et al*. (1955) that genetic advance as percent mean was estimated as low < 10%, moderate (10–20%) and high > 20%. In the present study, the GA % M ranged from 6.35% for days to 75% maturity (DTM) to 69.32% number of capsules

per plant (NOCP) in (Table 1). The low genetic advance in mean percent (below 10%) for days to 75% maturity (DTM) is 6.35%.Low estimates of genetic advance were observed by Tadesse *et al*. (2010) for days to maturity (7.1%), plant height (5.0%) and percent oil content (2.9%) also it was expected low GCV and PCV. The low genetic advance in percent over the years indicated that genetic improvement for plant height, number of bolls per plant, 1000-seed weight and seed yield can be achieved through selection up to the level within the perspective of tested materials portrayed by Mirza *et al*. (2011). Similarly, Muduli and Patnaik (1993), Naik and Satapathy (2002) observed low genetic advance for seed weight, plant height and days to 50% flowering. The moderate genetic advance % was between (10-20%). It was found to be for days to 50% flowering (DTF) and 1000 -seed weight. Moderate genetic advances (>17%) were revealed for lodging and days to maturate reported by Tefra and Gurmu (2020) and were contrary to our studies. Similarly, moderate genetic advance was observed by capsules per plant and yield.

The high genetic mean advance was observed for height (H), followed by primary branches (PB), pursued by secondary branches (SB), further followed by number of seeds per capsules(NOSC), trailed by plant stand per plot (PSP), yield per hectare (YH) and number of capsules per plant (NOCP). Similar results for number of capsules per plant and yield were reported by Kumar *et al*. (2012), for branches per plant, capsules per plant, yield per plant and seed weight were reported by Gupta and Godawat (1981) and also for number of primary branches portrayed by Naik and Satapathy (2002).Genetic advance as a percentage of mean was found to be highest for the number of capsules per plant (56.67%) followed by SYP (53.11%), BM (48.71%) and NSB (46.99%) was accounted by Hussain *et al*. (2022).

Heritability coupled with genetic advance

The study shed light on heritability coupled with genetic advance of various traits in linseed genotypes. High heritability coupled along with high genetic advance for height (H), number of capsules per plant (NOCP), number of seeds per capsule (NOSC), primary branches (PB), secondary branches (SB), plant stand per plot (PSP) and yield per hectare (YH). It portrays additive gene action and selection for improvement was shown by characters with high heritability coupled with high genetic advance. However, Tefra and Gumuru (2020) studied high heritability coupled with high genetic advance as percentage of mean (>50) for lodging percentage, number of capsules per branch, seed yield per hectare and harvest index, indicated predominance of additive gene action for these characters and showed that selection for improvement of traits. High heritability along with genetic advance for plant height, bolls m^{-2} and seed yield reported by Popescue *et al.* (1998), for number of bolls per plant Mishra and Yadav (1999), seed yield by Payasi *et al*. (2000) and for 1000-seed weight reported by Vardhan and Rao (2012. The additive gene action controls all the above characters and are good enough for selection based on phenotypes. The traits with high heritability coupled with high values of GA% were under control of additive genes and are helpful for selection on basis of phenotypic performance as illustrated by Mirza *et al.* (2011). Also, the high heritability along with high genetic advance for plant height (cm), seeds per capsule, capsules per plant, number of primary branches per plant and number of secondary branches per plant were observed by Chauhan *et al*. (2012), for number of seeds per plant were observed by Belete and Yohannes (2013), for two characters *viz.* capsules per plant and seed yield per plant (Tewari *et al*., 2012). Kadir *et al*. (1996) advised that the high heritability is not considered as mark of high genetic gain, but should be accompanied by high GA% when describing the genetic parameters in any crop.

High heritability coupled with moderate genetic advance for days to flowering DTF (92.90,12.53) and 1000 seed weight SW (69.69,13.11). Contradictory to above results moderate heritability coupled with moderate genetic advance observed for number of primary branches $plant^{-1}$ (36.72%, 36.02%), number of capsules $plant^{-1}$ (35.48%, 66.59%) were accounted by Dhiri and Mehata *et al*. (2019). Likewise, high heritability coupled with moderate genetic advance for number of capsules per plant indicates that this character is heritable and can be improved by selection. Pali and Mehta (2013) also reported high heritability with moderate genetic advance for oil content and all other fatty acid components.

On conflicting side, high heritability with low genetic advance for days to 50% flowering and days to maturity were reported by Bibi *et al.* (2013). Moderate heritability (58.58) with low GA%M (6.35%) was observed for days to 75% maturity (Table 1). Alike, outcome for moderate heritability with low genetic advance as percentage of mean was revealed for plant height and days to 50% flowering reported by Dash *et al*. (2016). The important genetic parameters of heritability and genetic advance are for selecting a genotype that permits greater effectiveness of selection by separating out environmental influence the total variance. Both are normally more helpful in predicting gain under selection than heritability estimates alone. However, traits with high heritability but

low genetic advance, or those with low heritability, may not respond as well to selection.

Clustering pattern of genotypes

Genetic diversity plays important role in parental selection for hybridization showed diversified groups especially in quantitative characters. The present study showed 20 genotypes grouped in 10 distinct clusters based on K2 value is presented in Table 2 . The highest number of genotypes appeared in cluster I considered to be populus with 5 genotypes, followed by 3 genotypes in cluster IX and erstwhile having 2 genotypes in cluster II, VI and VII, respectively. Also, cluster III, IV, V and X contained 1 genotype, while Cluster III, VI and VII had three genotypes.

In clustering pattern no parallelism was found in geographical distribution of genotype sindicating a lack of correlation between geographical and genetic diversity in the examined material. This observation contrasts with studies by six clusters were evaluated while analyzing 35 genotypes reported by Kumar *et al*. (2017). Kasana *et al*. (2018) reported different genetic background and the free exchange of materials among regions contributed to divergent clustering patterns. Some earlier workers *viz*. Kandil *et al*. (2011) and Patial *et al*. (2019) reported different clustering patterns in linseed.

The diversity present due to variation among the germplasm in cluster is supported by an appreciable amount of means for different traits was also reported earlier by Kumar *et al*. (2021) and Patial *et al*. (2019). The use of Tocher's method in Mahalanobis D^2 statistics by Pali and Mehta (2017) in 48 flax genotypes revealed five clusters based on morphological divergence. Nizar and Mulani (2015) identified 12 clusters in germplasm, with Cluster I was the largest with 23 accessions, cluster XII was smaller with two accessions and clusters V, VI, VIII, X and XI, respectively were the smallest with one accession with Mahalonobis' D^2 distance. A large and diverse clustering pattern gave an indication of presence of significant amount of variability and diversity in the germplasm.

Mean values of clusters

Table 3 depicts maximum means of variation in the cluster for 10 quantitative characters. The maximum mean for days to 50% flowering (DTF) is in 119.665 in cluster VIII. Days to maturity (DTM) showed maximum mean in cluster VIII (163.500 days) followed by cluster IX (155.793 days). Also, for plant height (H) maximum mean were observed in cluster VII (97.085) followed by cluster VIII (93.350 cm). In terms of the number of capsules per plant (NOCP) cluster II exhibit highest mean 167.390, followed cluster VI with value of 137.780. The number of primary branches per plant (PB) exhibited maximum mean in cluster VI (4.640) followed by cluster V (4.455). Similarly, primary branches (PB) in cluster II have presented maximum mean with 4.550 followed by 4.420 in cluster V. Furthermore, cluster maximum mean for secondary branches (SB) is depicted by cluster VI with value of 35.930. Cluster III presented maximum mean value for number of seeds per capsule (NOSC) is 8.530 followed by cluster II with value 8.370. The maximum mean for plant stand (PS) for cluster V with value of 1,781.520 and minimum mean was 132.165 for cluster VIII. Similarly, maximum mean of 1000- seed weight in cluster IV with 9.000gms and followed by cluster IX with weight 8.057 gms. Seed weight (SW) have maximum mean 2194.070 in cluster X and minimum mean value was 339.260 for cluster III. These findings were similar observations by other researchers, including Fulkar *et al*. (2007), Kumari and Rao (2008), Ranjana et al. (2019), Kumar and Kumar (2021), who reported comparable variations in characters within different clusters.

Intercluster and intracluster distance

The maximum intercluster distance between different clusters is different in Table 4. The maximum intercluster distance between cluster V and cluster VIII with value of 2312.952 followed by interdistance cluster X and Cluster VIII 2155.821. Similarly, Cluster VIII and Cluster VII have intercluster distance of 1929.812 in Table 4. Similarly, cluster VI and cluster II has minimum intercluster distance 260.825. Similar, findings were also reported by Pal *et al*. (2000) and Meshram *et al*. (2008). In clusters III to X genotypes were genetically more distant among themselves as well as from the other collections for they formed the most different single genotyped cluster II. So, they can be bused for the crossing programmes to develop more productive genotypes. No similarity between the geographical origins and genetic diversity was found among genotypes. The variability observed among these genotypes of linseed for different characters indicated for genetic improvement of the crop through selection and cross breeding.

Conclusion

In conclusion the results of the present investigation show the presence of adequate genetic variability within and among the genotypes, which suggests scope for further genetic improvement in linseed. Traits with high PCV and GCV values indicate effective selection possibilities, supported by high heritability and genetic advance indicates prevalence for additive gene action.

Genetic variability is crucial for breeding, allowing diverse parent selection in hybridization. Positive correlations among traits, like for number of capsules per plant (NOCP), primary branches (PB), secondary branches (SB), plant stand (PS) and 1000-seed weight (SW) for seed yield per hectare (SY) suggest effective hybridization selection. Future breeding should focus on varietal and hybrid development. Genotypes in clusters III to X, genetically distant are suitable for crossing programs. No correlation between geographic origins and genetic diversity emphasizes.

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