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Correlation and genetic diversity of linseed (*Linum usitatissimum* L.) genotypes based on principal component analysis in Mid-Hills of North-West Himalayas

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Abstract
Sixteen linseed genotypes were subjected to study the correlation and genetic diversity at the Experimental Farm of the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, during *rabi* 2015-2016. Correlation coefficient revealed that seed yield had maximum genotypic and phenotypic correlation with plant height, capsules per plant and seeds per capsule so direct selection of plants based on these three would be effective to increase seed yield. Path analysis showed that plant height had maximum direct effect on seed yield per plant followed by seeds per capsule and capsules per plant at both genotypic and phenotypic levels. Principal component analysis (PCA) indicated that five components (PC1 to PC3) accounted for about 72% of the total variation among traits in linseed genotypes. Out of total principal components retained PC1, PC2 and PC3 with values of 39.7%, 18.5% and 13.9% respectively contributed more to the total variation. The first principal component had positive loading for 7 traits out of 8 viz. days to 50% flowering, days to 75% maturity, primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule and seed yield per plant which contributed more to the diversity. The result of present study could be exploited in planning and execution of future breeding programme in linseed.

Keywords: *Linum usitatissimum* L., Genetic diversity, Principal component analysis, Correlation, Path analysis.

Introduction
Linseed (*Linum usitatissimum* L.; n=15) belongs to family Linaceae having about 14 genera and over 200 species, which are widely spread in temperate and subtropical areas of the world [1]. Out of all the species *Linum usitatissimum* L. is the only cultivated both for oil and fibre. Linseed is used in treatment of some inflammatory human and animal diseases and its oil is mainly utilized in the preparation of printing ink, paint and several innumerable by-products. Linseed is important due to its oils composition having 51.9 to 55.2% α-linoleinic acids used for cardiovascular diseases and lowering cholesterol [2, 3]. Due to the excellent palatability of linseed cake it is better quality supplement for cattle. It contains 3% oil and 36% protein and serves as nutritious feed for cattle. It is also a good source of phosphorus (370 mg/100g), manganese, calcium (170 mg/100g), potassium [2]. There is consistent need to increase genetic seed yield potential to increase the demand of linseed. Recombination of favorable genes is one of the way to increase seed yield potential and related traits. One of the important approaches to linseed breeding is hybridization and subsequent selection. Choice of parents' is the first step in plant breeding program through hybridization. Genetic distance between parents is necessary to benefit transgressive segregation [4]. Higher the genetic distance between parents, the higher heterosis in progeny can be observed [5].
Estimation of genetic distance and correlation is one of appropriate tools for parental selection in linseed hybridization programs. Appropriate selection of the parents is essential to be used in crossing to enhance the genetic recombination for potential yield increase [6]. Some appropriate methods, factor analysis, cluster analysis and PCA, for parental selection and genetic diversity identification [7]. Principal component analysis helps researchers to distinguish significant relationship between traits. The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only [8]. The main objective of this study was to assess the potential genetic diversity and correlation by using cluster analysis-PCA-based methods for selection of parents in hybridization programme to obtain desirable segregants in advanced generation.

Materials and Methods

The linseed germplasm consisted of thirteen genotypes viz., KL-285, KL-288, KL-289, KL-290, KL-293, KL-294, KL-295, KL-296, KL-297, KL-299, KL-300, KL-301 and KL-302 with three checks namely Nagarkot, Baner and Himani evaluated to estimate genetic diversity and correlation during *rabi* 2015-16 at Experimental Farm of the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India (32°8′ N, 76°3′ E) which represents humid sub-temperate climate zone with an annual rainfall of 2500mm and acidic soil having pH of 5.0 to 5.6. The experiment was conducted in complete randomized block design having three replications. Each replication consisted of three rows of each genotype with the distance of 30 cm and 10 cm for row to row and plant to plant respectively and maintained by thinning. Normal cultural practices were carried out as recommended for linseed. Data was recorded for all the characters except for days to 50 per cent flowering and days to maturity which was recorded on plot basis.

Statistical analysis: The recorded data was subjected to analysis of genotypic and phenotypic correlation coefficients as per the standard formula [9] and the path coefficient analysis was conducted as per the standard formula [10].

PCA: Principal component analysis (PCA) analysis was performed using XLSTAT software.

Results and Discussion

The increase of seed yield is the primary target of crop improvement and it requires understanding the correlation between various yield contributing traits and genetic diversity in the germplasm. The correlation coefficients between different characters are given in Table 1. The results of experiment revealed that the traits plant height, capsules per plant and seeds per capsule had the positive association with seed yield per plant at both genotypic and phenotypic levels. Whereas, days to 50% flowering, primary branches per plant and secondary branches per plant exhibited positive but non-significant associations with seed yield per plant. The genotypic and phenotypic correlation coefficient were similar in directions, while in magnitude, genotypic correlations were higher than corresponding phenotypic correlations for most of the traits. Similar findings were reported by [11, 12]. Thus the low phenotypic correlation could be due to the masking and modifying effect of environment on the association of characters at genotypic level. On the basis of present studies, it can be concluded that the selection based on traits *viz.,* plant height, capsules per plant and seeds per capsule can provide better result for improvement of seed yield per plant in linseed, as earlier reported by Tariq [13] for plant height, number of capsules per plant, number of seeds per capsule, Yadav [14] for number of capsules per plant and number of seeds per capsule.

Path coefficient analysis permits the separation of the correlation coefficients into components of direct and indirect effects. Keeping seed yield per plant as resultant variable and other traits as causal variables, the following results were obtained. The direct and indirect effects of genotypic path coefficients were mostly higher in magnitude than the corresponding phenotypic path coefficients (Table 2). As earlier reported by [15, 16] with respect to path coefficients in linseed. Plant height exerted maximum direct effect on seed yield per plant followed by seeds per capsule and capsules per plant at both genotypic and phenotypic levels.

Table 1: Estimates of genotypic (G) and phenotypic (P) correlation coefficients among different traits of linseed

		Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Capsules per plant	Seeds per capsule	Seed yield per plant (gm)
Days to 50% flowering	P	.0738	.2197	-.0270	.0211	.0605	.0635	.0374
	G	.0501	.2513	-.0473	.0217	.0503	.0877	.0566
Days to 75% maturity	P		-.0184	.3209*	.3706**	.2480	.2983*	-.0931
	G		-.0221	.4092**	.4544**	.2712	.3351*	-.1890
Plant height (cm)	P			-.3348*	-.2281	-.1788	-.0610	.3364*
	G			-.3708**	-.2859	-.1897	-.0549	.3920**
Primary branches per plant	P				.8937**	.6513**	.3857**	.0392
	G				.9751**	.7388**	.5844**	.0542
Secondary branches per plant	P					.6914**	.4083**	.1579
	G					.8206**	.6377**	.1846
Capsules per plant	P						.1440	.2887*
	G						.1963	.2877*
Seeds per capsule	P							.3364*
	G							.3107*

* P≤0.005and ** P≤0.001

Table 2: Estimates of genotypic (G) and phenotypic (P) direct and indirect effects of different traits on seed yield in linseed

		Days to 50% flowering	Days to 75% maturity	Plant height	Primary branches per plant	Secondary branches per plant	Capsules per plant	Seeds per capsule	Seed yield per plant (gm)
Days to 50% flowering	P	-.0575	-.0065	.0131	.0103	.0082	.0851	-.0154	.0374
	G	.4122	.1004	.1934	-1.2346	-.9488	.7380	.7959	.0566
Days to 75% maturity	P	-.0042	-.2089	-.0071	-.0975	.1809	.0538	-.0100	-.0931
	G	.0206	-.2107	-.0170	-.1065	.01971	.06359	.0413	-.1890
Plant height (cm)	P	-.0126	.0038	.3874	.1017	-.1113	-.0388	.0062	.3364*
	G	.1036	-.0443	.7698	-.1989	-. 1012	-.2787	.0405	.3920**
Primary branches per	P	.0016	-.0670	-.1297	-.3039	.4362	.1414	-.0393	.0392

plant	G	-.0195	.8211	-.2854	-.2666	-.4258	.1835	0.0469	.0542
Secondary branches per plant	P	-.0012	-.0774	-.0884	-.2716	.4880	.1501	-.0416	.1579
	G	.0089	.9119	-.2201	-.2579	-.4345	.1726	.0037	.1846
Capsules per plant	P	-.0035	-.0518	-.0693	-.1979	.3374	.2171	.0567	.2887*
	G	.0207	.5441	-.1460	-.1962	-.3535	.2430	.1756	.2877*
Seeds per capsule	P	-.0037	-.0205	-.0236	-.1172	.1993	.0313	.2708	.3364*
	G	.0361	-.1957	-.0423	-.1584	-.2796	.2781	.6725	.3107*

* P≤0.005and ** P≤0.001

Where days to 50% flowering showed positive direct effect at genotypic level and secondary branches per plant at phenotypic level. Days to 75% maturity and primary showed negative direct effects on seed yield per plant at both (genotypic and phenotypic) levels. Seed yield had maximum genotypic and phenotypic correlation with plant height, capsules per plant and seeds per capsule so direct selection of plants based on these three would be effective to increase seed yield.

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation [17]. In this analysis the first factor retains the information contained in 3.179 of the original variables. PCA for the first three principal components of these data are given in table 3. Three principal components PC 1 to PC 3, which extracted from the original data and having latent roots greater than one, accounting nearly 72% of the total variation. Suggesting these principal component scores might be used to summarize the original eight variables in any further analysis of the data. Out of the total principal components retained, PC1, PC2 and PC3 with values of 39.7%, 18.5% (Fig. 1) and 13.9% respectively contributed more to the total variation. According to [18], traits with lower absolute value closer to zero influence the clustering less than those with largest absolute value closer to unity within the first principal component. The present study revealed differentiation of the genotypes into different clusters was because of relatively high contribution of few traits rather than small contribution from each trait. Accordingly, the first principal component had positive component loading from days to 50% flowering, days to 75% maturity, primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule, seed yield per plant and negative loading from plant height. The traits which load positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters. Hence, the major contributing traits for the diversity in the second principal component (PC 2) were seed yield per plant followed by plant height and days to 50% flowering; days to 50% flowering followed by days to 75% maturity and seeds per capsule in principal component three (PC 3). Usually it is customary to choose one variable from these identified groups. Hence, for the first group secondary branches per plant is best choice, which had the largest loading from component ones, seed yield per plant for the second and days to 50% flowering for the third group.

Table 3: Eigenvectors and eigenvalues of 3 principal components for 8 characters of 16 linseed genotypes

	Days to 50% flowering	Days to 75% maturity	Plant height	Primary branches per plant	Secondary branches per plant	Capsules per plant	Seeds per capsule	Seed yield per plant	Eigenvalue	Variability (%)	Cumulative %
PC 1	0.007	0.285	-0.187	0.533	0.546	0.445	0.318	0.041	3.179	39.738	39.738
PC 2	0.383	-0.067	0.627	-0.042	0.083	0.159	0.040	0.648	1.486	18.579	58.318
PC 3	0.586	0.451	0.199	-0.083	-0.066	-0.255	0.368	-0.450	1.113	13.912	72.229

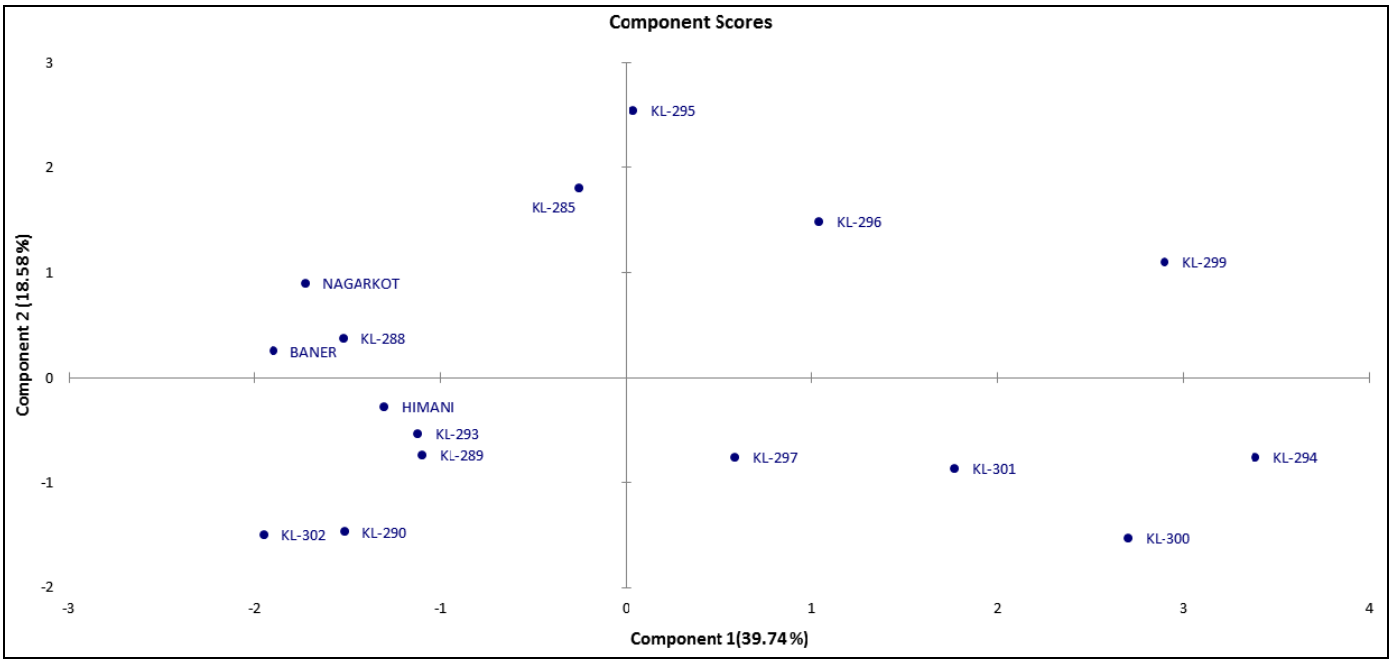

Fig 1: Score plot of 16 genotypes of *Linum usitatissimum* L.

These findings revealed that seed yield had maximum genotypic and phenotypic correlation with plant height, capsules per plant and seeds per capsule so direct selection of plants based on these three would be effective to increase seed yield. First three principal components were related to various traits in linseed mostly associated with high seed yielding genotypes and also these traits can identify the diverse genotypes which could be employed in hybridization programme for improvement of linseed.

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