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RESEARCH ARTICLE

Selection Strategy and Estimation of Interrelationships for Improvement of Seed Yield and Other Related Traits in Linseed (*Linum usitatissimum* L.)

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Thirty five genotypes of linseed (*Linum usitatissimum* L.) were evaluated to determine the selection strategy and interrelationships of seed yield and yield related traits, during *rabi* 2013-14. Analysis of variance revealed significant differences among all the genotypes for all the traits under study. Sufficient genetic variability was observed in the present material selected for the study, through various genetic variability parameters, indicating the scope for selection of suitable initial breeding material for crop improvement. The genotypic and phenotypic correlation coefficient between different traits was similar in direction, whereas, in magnitude, genotypic correlation was higher than the corresponding phenotypic correlations. Seed yield per plant had significant and positive association with primary and secondary branches per plant. Secondary branches per plant exhibited the higher and positive direct effect on seed yield per plant indicating that selection for this character would lead to increase in the yield. Primary branches per plant contributed indirectly through biological yield per plant. The principal component analysis showed that primary branches per plant, secondary branches per plant and seed yield per plant had the maximum contributions, interpreting almost all the variation of traits. For the development of high yielding linseed varieties, breeding strategies should focus on secondary branches per plant prior to the primary branches per plant.

Key Words: Biplot, Correlation, Interrelationship, Linseed, Principal component analysis

Introduction

Linseed (*Linum usitatissimum* L.; n = 15), belongs to genus *Linum*, the largest genus of family Linaceae with about 200 species displaying great diversity in Karyotype. Linnaeus in 1857 was first to give a botanical name *L. usitatissimum* to the cultivated species. Linseed is an annual, self pollinating and non-edible oil crop. It is the sole species of agricultural importance within the family Linaceae and belongs to group of founder crops that initiated agriculture in "old world" (Zohary, 1999). The somatic chromosome number in other species of the genus *Linum* is reported to vary from 16 to 80 (Darlington and Wylie, 1956; Gill, 1966; Harris, 1968). Almost every part of the linseed plant is utilized commercially either directly or after processing. Linseed oil and meal are the two products provided by the seeds on account of its quick drying properties. Linseed oil is extensively used in industry for the manufacturing of high quality paints and varnishes. The oil content of the seed generally varies from 33 to 45%. About 20% of the total linseed oil is used for edible and domestic purposes and 80% goes for industrial utilization. The oil is also utilized for manufacturing paints, varnishes, oilcloth, linoleum, pad-ink, printers ink, soap etc. Across the globe it covers 2270.35 thousand hectare area with production of 2238.94 thousand tons having productivity of 986.16 kg/ha, where as in India its area is limited to 338 thousand hectares and production 147 thousand tons with the productivity of 434.91 kg/ha, (Anonymous, 2013). In spite of being an important oilseed crop, its average productivity in India is very low, because of various factors *viz*., narrow genetic base, raising of crop by the resource poor farmers in marginal and sub-marginal areas, non-availability of high yielding varieties and susceptibility to biotic and abiotic stresses, etc.

Selection is an integral part of a breeding programme by which genotypes with high productivity in a given environment can be developed. Yield per unit area is the end product of components of several characters, which are polygenic in inheritance and are thus highly influenced by environment. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. The measurement of genetic variation and mode of inheritance of quantitative and qualitative

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traits are of prime importance in planning the breeding programme efficiently and effectively (Shah *et al.*, 2015). Selection for yield has many complexities because it is end product of various yield components, which are naturally polygenic inherited and maximally influenced by environment. Therefore, only little progress could be made over a long span of time through direct selection for yield. Indirect selection through yield components has been proved more effective (Ford, 1964). Proper understanding of association of different traits, provide more reliable selection criteria to achieve high seed yield (Akbar *et al.*, 2001). This selection criteria takes into account the information on interrelationships among agronomic characters, their relationship with seed yield as well as direct influence on seed yield. However, selection for yield via highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis (Dewey and Lu, 1959). So path coefficient analysis technique is a statistical approach which is based on multiple regression and is useful for revealing the direct and indirect effects of characters in a network of factors like agro/morpho/physio/biochemical traits which is able to separate correlation coefficients into their components of direct and indirect effects (Dewey and Lu, 1959; Wright, 1960). However, information on the extent and nature of interrelationship among characters helps in formulating efficient scheme of multiple traits selection. The present study was conducted to study the selection strategy and interrelationships for the improvement of seed yield and other related traits in linseed.

Table 1. List of linseed genotypes and their parentage/source used in the study

S. No.	Genotype	Source/pedigree
1	KL-241	Giza-7 × KLS-1
2	KL-242	Gaurav × KLS-1
3	KL-243	RL-904 × Exotic-2
4	KL-244	(RLC-29 × Jeevan) X RLC-29
5	KL-245	Jeevan × KLS-1
6	KL-246	Him Alsi-2 × RLC-29
7	KL-247	Neelam × Nagarkot
8	KL-248	Selection from KL-178
9	KL-249	–
10	KL-250	–
11	KL-251	–
12	KL-252	–
13	KL-253	Chambal × 89D-2B/5
14	KL-254	Him Alsi-2 × 8 9D-2B/5
15	KL-255	Binwa × Baner
16	KL-256	Binwa × Flak-1
17	KL-257	LC-2323 × KLS-1
18	KL-258	Janki × Surbhi
19	KL-259	KL-187 × Flak-1
20	KL-260	Binwa × KLS-1
21	KL-261	KL-233 × KLS-1
22	KL-262	Himalini × Flak-1
23	KL-263	Him Alsi-2 × Baner
24	KL-264	LC-2232 × KLS-1
25	KL-265	KL-168 × Baner
26	KL-266	LCK-9826 × 89D-2B/5
27	KL-267	Him Alsi-2 × Flak-1
28	KL-268	Early selection of Him Alsi-2
29	KL-269	Medium selection of Him Alsi-2
30	Bhagsu	RL-50-3 × Surbhi
31	Binwa	Flak-1 × SPS 47/ 7-10-3
32	Baner	EC 21741 × LC 216
33	Surbhi	LC-216 × LC-185
34	Nagarkot	New River × LC-216
35	American Flax	–

Materials and Methods

Experimental material consisted of 35 linseed genotypes (Table 1), evaluated at the Experimental Farm of the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh, India, situated at an elevation of 1300 m. above m.s.l with 3606’N latitude and 7603’E longitude, representing mid-hill zone of Himachal Pradesh, during *rabi* 2013-14. The experiment was laid out in a Randomized Block Design (RBD) with two replications. The plot size of each genotype consisted of three rows of 3 m with row to row and plant to plant spacing of 25 cm and 5 cm respectively. The experimental field was well prepared and recommended doses of fertilizers were applied @ 50 kg N, 40 kg, P_2O_5 and 20 kg K_2O per hectare. Half dose of N and full dose of P_2O_5 and K_2O were applied as basal and the remaining half nitrogen was top dressed after 45 days of sowing and regular weeding was done to keep the experimental field weed free. Data were recorded for plant height, primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule, 1000-seed weight and seed yield per plant for five randomly selected plants in each replication, whereas days to 50% flowering and days to 75% maturity were recorded on plot basis.

Statistical Analysis

The recorded data was subjected to analysis of variance (Panse and Sukhatme, 1985).

The genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV) and heritability

(H2) in broad sense were computed according to Burton and Devane (1953). Genetic advance (GA) was estimated following Johnson *et al.* (1955). The genotypic and phenotypic correlation coefficients were calculated as suggested by Al- Jibouri *et al.* (1958) and the path coefficient analysis was conducted as suggested by Dewey and Lu (1959).

Principal component analysis (PCA) analysis was performed using XLSTAT software to determine the best relationships among characters.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the traits (Table 2) indicating existence of sufficient variability in the material selected for the study and scope for selection of suitable breeding material for crop improvement.

The general mean and range of characters revealed a wide variability for seed yield per plant, 1000 seed weight, primary branches, secondary branches, plant height and capsules per plant indicating greater scope for selection. The PCV values were greater than the GCV values for all the traits studied. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. Higher estimates of PCV and GCV (>25%) were obtained for seed yield per plant Similar findings were also reported by Chandrashekhar *et al.* (1998); Pradhan *et al.* (1999); Rafiq *et al.* (2014). Moderate PCV and GCV (15-25%) was recorded for primary branches per plant, and 1000 seed weight. Whereas, moderate PCV and low GCV was recorded for secondary branches per plant. Low PCV and GCV (<15) were recorded for days to 50% flowering, days to 75% maturity, plant height, capsules per plant and seeds per suggested that the environment had little role and predominance of additive gene effects in the expression of these traits. All the characters studied in the present investigation expressed high heritability except seeds per capsule. High heritability indicates the scope of genetic improvement of these characters through selection. Similar results have been reported by Tewari (1999); Rai *et al.* (2000); Rama Kant *et al.* (2005); Pali and Mehta (2013); Rafiq *et al.* (2014).

Heritability estimates along with genetic advance are normally more helpful in predicting gain under selection than heritability estimates alone. The variability parameter for different characters are given in Table 3.

Table 2. Analysis of variance for various traits in linseed

S. No.	Traits	Replication df = 1	Genotypes df = 34	Error df = 34	CV (%)
1	Days to 50% flowering	25.14	11.53**	1.85	1.08
2	Days to 75% maturity	4.48	13.60**	2.46	0.86
3	Plant height (cm)	37.05	115.47**	5.22	3.83
4	Primary branches per plant	0.34	1.34**	0.22	10.05
5	Secondary branches per plant	0.06	0.66**	0.06	6.12
6	Capsules per plant	2.53	19.79**	4.95	7.13
7	Seeds per capsule	1.03	0.69**	0.20	5.73
8	1000 Seed weight (g)	0.99	3.59**	0.13	4.81
9	Seed yield per plant (g)	0.01	0.05**	0.01	19.57

* P≤0.005and ** P≤0.001

Table 3. Genetic parameters of variability for different agro-morphological traits of linseed

S. No.	Traits	Mean ± S.E.(m)	Range	PCV (%)	GCV (%)	h^{2}bs (%)	GA (%)	GAM
1	Days to 50% flowering	126.00±0.96	121-130	2.05	1.75	72.36	3.86	3.06
2	Days to 75% maturity	183.29±1.11	179-189	1.55	1.29	69.39	4.05	2.21
3	Plant Height (cm)	59.69±1.62	47.70-75.20	13.01	12.44	91.35	14.62	24.49
4	Primary branches per plant	4.62±0.33	2.80-7.00	19.11	16.25	72.35	1.32	28.48
5	Secondary branches per plant	3.83±0.17	2.50-5.50	15.63	14.38	84.66	1.04	27.26
6	Capsules per plant	31.22±1.57	25.75-44.90	11.26	8.72	59.99	4.35	13.92
7	Seeds per capsule	7.81±0.32	6.50-9.30	8.54	6.33	54.96	0.76	9.67
8	1000 Seed weight (g)	7.42±0.25	4.78-9.99	18.37	17.73	93.16	2.61	35.26
9	Seed yield per plant (g)	0.41±0.07	0.15-0.79	42.52	36.64	74.27	.27	65.05

The present study revealed that all the traits under study showed low genetic advance (<15), coupled with high heritability except seeds per capsule. High heritability coupled with low genetic advance indicates non-additive gene action. The heritability exhibited due to favourable influence of environment rather than genotypes and selection for such traits may not be rewarding. High heritability coupled with high genetic advance as percentage of mean (GAM) were also more useful than heritability alone in predicting the resultant effect during selection of best individual genotype. Genetic advance is the measure of genetic gain under selection and expression in percentage of mean (Johnson *et al.*, 1955). In the present experiment high heritability and GAM (>30) was recorded for 1000 seed weight and seed yield per plant. Simple selection based on phenotypic performance of these traits would be more effective. High heritability and moderate GAM (15-30), were observed for the traits, plant height, primary branches per plant and secondary branches per plant. These traits could be exploited through manifestation of dominance and epistatic components through heterosis. Other traits except seeds per capsule showed high heritability along with low GAM (<15) indicating the presence of non-additive gene action. Hence selection can be postponed for these characters or these characters can be improved by intermating of superior genotypes of segregating population from recombination breeding.

Correlation Coefficient Analysis

The possible enhancements of high yield through yield attributes, as primary target of crop improvement, requires understanding the amount of correlations among various yield contributing characters or in fact, yield components. The correlation coefficients between different characters are given in Table 4. The primary and secondary branches per plant had positive correlation with seed yield per plant at both genotypic and phenotypic levels, whereas, days to 50% flowering showed negative significant correlation with seed yield per plant. Seed yield per plant had negative and non-significant correlation with days to 75% maturity but a positive and non-significant correlation with plant height, capsules per plant, seeds per capsule and 1000 seed. The genotypic and phenotypic correlation coefficients were similar in directions, in magnitude, genotypic correlations were mostly higher for most of the traits than corresponding phenotypic correlations. Similar findings were reported by Sohan *et al.* (2004); Joshi (2004). Thus the low phenotypic correlation could results due to the masking and modifying effects of environment on the association of characters at genotypic level. On the basis of correlation analysis studies, it can be concluded that the selection based on traits *viz.*, primary and secondary branches per plant can provide better results for improvement of seed yield per plant in linseed, as reported by most of the workers in linseed (Mishra and Yadav, 1999; Savita *et al.,* 2011).

Table 4. Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different traits of linseed

		DTM	PH	PB	SB	CPP	SPC	SW	SYP
DTF	P	0.2466*	0.0276	0.0473**	-0.1600	0.2699*	-0.0333	0.0134	-0.2532*
	G	0.3233**	-0.0062	0.1200	-0.1655	0.3922**	-0.0241	0.0202	-0.3377**
DTM	P		0.3253**	0.2215	0.0855	0.1023	-0.1347	0.2285	-0.1287
	G		0.3928**	0.3944**	0.1514	0.4850**	-0.1786	0.3310**	-0.0939
PH	P			0.3722**	0.0661	0.3032*	-0.3144**	-0.0111	0.2132
	G			0.4769**	0.0748	0.4021**	-0.4482**	-0.0067	0.2164
PB	P				0.6481**	0.3554 **	0.0638	0.2873*	0.4839**
	G				0.7686**	0.4521 **	0.0449	0.3426**	0.5664**
SB	P					0.3829**	0.3625**	0.2591*	0.6873**
	G					0.4631**	0.3804**	0.2495*	0.6994**
CPP	P						0.0249	-0.0508	0.2165
	G						0.0572	-0.1064	0.0679
SPC	P							0.0906	0.0553
	G							0.0511	0.0422
SW	P								0.0608
	G								0.0189

*Significant at 5% level; **Significant at 1% level

DTF-Days to 50% flowering; DTM-Days to 75% maturity; PH-Plant height; PB-Primary branches per plant ; SB-Secondary branches per plant; CPP-Capsules per plant; SPC-Seeds per capsule; SW-1000 Seed weight; SY-Seed yield per plant

Path Coefficient Analysis

Correlation coefficient measures the mutual association between two variables but does not permit the cause and effect relationship of traits contributing directly or indirectly towards economic yield. Whereas, the path coefficient analysis specifies the causes and measures their relative importance (Shivanna *et al.*, 2007). The economic characters like seed yield is dependent on several component characters which are mutually related. Slight changes in any one component will ultimately disturb the complex. Hence character hence to be analysed for its action namely direct effect of component character on seed yield and the indirect effect through other component characters on seed yield. Therefore, correlations were partitioned into direct and indirect effects (Table 5). Such an analysis helps the breeders to identify the characters that could be used as selection criteria in linseed breeding programmes. The direct and indirect effects of genotypic path coefficients were mostly higher in magnitude than the corresponding phenotypic path coefficients. Similar finding with respect to path coefficients have been reported (Gauraha and Rao, 2011; Reddy *et al.,* 2013). Secondary branches per plant had higher and positive direct effect on seed yield per plant. This traits also had significant positive correlation with seed yield per plant indicating that selection for secondary branches per plant would indirectly select for higher seed yield. On partitioning the components for correlation of seed yield per plant with characters showing positive correlation, direct effects were found to be low indicating that while selecting these characters seed yield per plant cannot be improved through these characters. Their indirect effects through secondary branches per plant were high, therefore primary branches per plant contributed indirectly through secondary branches per plant. Path coefficient analysis revealed the importance of secondary branches per plant as major yield contributing component in linseed.

Principal Component Analysis of Seed Yield and other Traits

The principal component analysis (PCA) was performed for traits (Table 6 and Fig. 2.) which revealed five most informative principal components with eigenvalues 2.796, 1.868, 1.326, 1.144 and 0.614 respectively, which together accounted 86.089% of the total variance (Fig. 1), for all the characters. Thus, according to principal component 1, characters such as primary branches per plant, secondary branches per plant and seed yield per plant had relatively higher contributions to the total morphological variability, a truth which proved by other statistical approaches similar to path coefficients analysis which discussed at earlier parts of this paper. The first two principal components biplot including loadings of the various characters along with the genotypes spread over is given in Fig. 2. This Figure indicates that the

Table 5. Estimates of direct and indirect phenotypic (P) and genotypic (G) effects of different traits on seed yield in linseed

		DTF	DTM	PH	PB	SB	CPP	SPC	SW	Correlation with SYP
DTF	P	-0.0321	-0.0638	0.0060	0.0004	-0.1331	-0.0363	0.0068	-0.0011	-0.2532*
	G	0.4448	-0.0018	-0.0039	-0.0899	-0.3240	-0.3664	0.0095	-0.0060	-0.3377**
DTM	P	-0.0079	-0.2586	0.0703	0.0017	0.0712	-0.0137	0.0275	-0.0191	-0.1287
	G	0.1438	-0.0054	0.2473	-0.2954	0.2964	-0.4531	0.0702	-0.0978	-0.0939
PH	P	-0.0009	-0.0841	0.2160	0.0029	0.0550	-0.0407	0.0641	0.0009	0.2132
	G	-0.0027	-0.0021	0.6295	-0.3572	0.1465	-0.3757	0.1762	0.0020	0.2164
PB	P	-0.0015	-0.0573	0.0804	0.0078	0.5392	-0.0477	-0.0130	-0.0240	0.4839**
	G	0.0534	-0.0021	0.3002	-0.7491	1.001	-0.4223	-0.0176	-0.1012	0.5664**
SB	P	0.0051	-0.0221	0.0143	0.0050	0.8319	-0.0514	-0.0739	-0.0216	0.6873**
	G	-0.0736	-0.0008	0.0471	-0.5757	1.000	-0.4326	-0.1496	-0.0737	0.6994**
CPP	P	-0.0087	-0.0265	0.0655	0.0028	0.3185	-0.1343	-0.0051	0.0042	0.2165
	G	0.1745	-0.0026	0.2531	-0.3386	0.9068	-0.9342	-0.0225	0.0314	0.0679
SPC	P	0.0011	0.0348	-0.0679	0.0005	0.3016	-0.0034	-0.2039	-0.0076	0.0553
	G	-0.0107	0.0010	-0.2821	-0.0336	0.7450	-0.0534	-0.3932	-0.0151	0.0422
SW	P	-0.0004	-0.0591	-0.0024	0.0022	0.2156	0.0068	-0.0185	-0.0834	0.0608
	G	0.0090	-0.0018	-0.0042	-0.2566	0.4886	0.0994	-0.0201	-0.2954	0.0189

*Significant at 5% level; **Significant at 1% level

DTF-Days to 50% flowering; DTM-Days to 75% maturity; PH-Plant height; PB-Primary branches per plant ; SB-Secondary branches per plant; CPP-Capsules per plant; SPC-Seeds per capsule; SW-1000 Seed weight; SY-Seed yield per plant

Table 6. Eigenvectors and eigenvalues of 5 principal components for nine characters of 35 linseed genotypes

	DTF	DTM	PH	PB	SB	CPP	SPC	SW	SYP	Eigen value	Proportion	Cumulative %
PC1	0.003	0.215	0.280	0.528	0.516	0.348	0.074	0.197	0.406	2.796	31.065	31.065
PC2	0.448	0.476	0.383	0.039	-0.291	0.253	-0.390	0.006	-0.350	1.868	20.759	51.824
PC3	0.450	0.186	-0.456	0.012	0.117	0.103	0.561	0.345	-0.311	1.326	14.735	66.559
PC4	-0.287	0.285	0.020	0.074	-0.060	-0.525	-0.201	0.713	-0.042	1.144	12.707	79.267
PC5	0.552	-0.498	-0.251	0.162	-0.024	-0.065	-0.468	0.246	0.273	0.614	6.822	86.089

DTF-Days to 50% flowering; DTM-Days to 75% maturity; PH-Plant height; PB-Primary branches per plant ; SB-Secondary branches per plant; CPP-Capsules per plant; SPC-Seeds per capsule; SW-1000 Seed weight; SY-Seed yield per plant

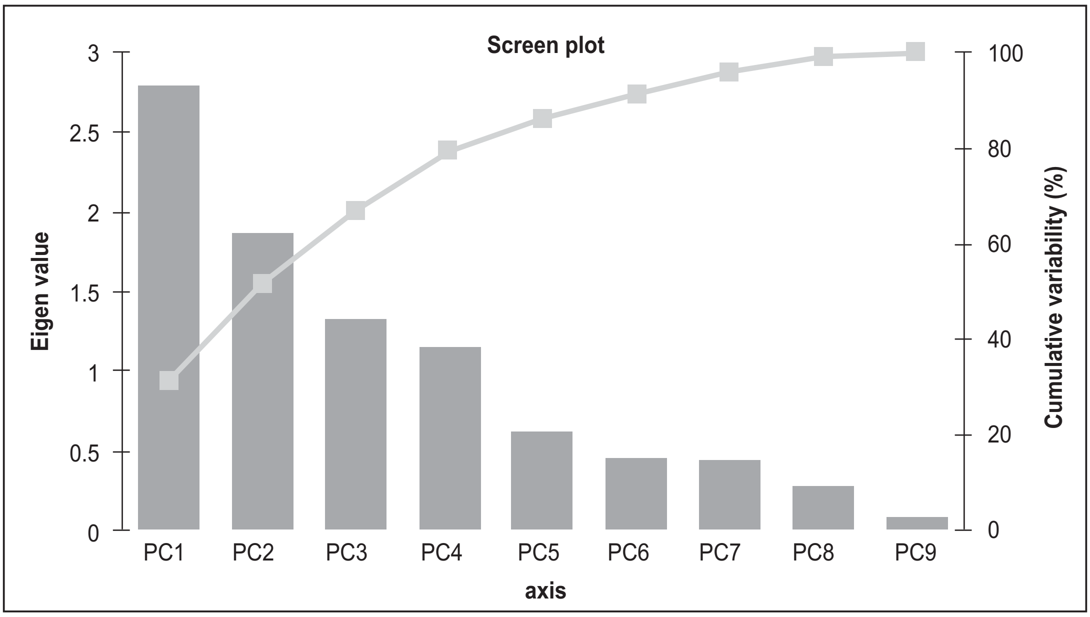

Fig. 1. Eigenvalues of principal components

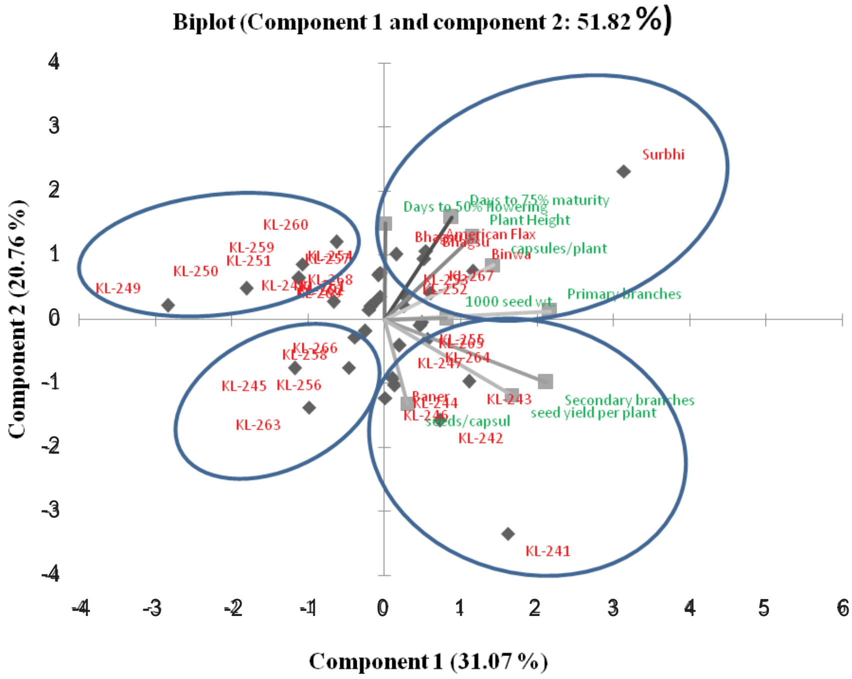

Fig. 2. Biplot of principal component

35 genotypes could be categorized at four groups. The group comprising of Surbhi, Nagarkot, Bhagsu, Binwa, American Flax, KL-252, KL-253 and KL-267 had higher days to 50% flowering, days to 75% maturity, plant height, primary branches per plant, capsules per plant and 1000 seed weight; the second group including varieties Baner, KL-241, KL-242, KL-243, KL-244, KL-241, KL-246, KL-247, KL-255, KL-264 and KL-265 contained more secondary branches per plant, seeds/capsules and seed yield per plant and rest of the genotypes were found in third and fourth group. PCA showed a clear differentiation between flax cultivars from each other. The variation (31.065%) is explained by first principal component and in total this biplot explained 51.82% of the variation. Thus, this biplot can interpret the near-real differentiation of the linseed cultivars and morphological characters studied in this experiment. Vromans (2006) also reported that the biplot can be used as a vital instrument to categorize, differentiate and address the genetic entities in breeding decisions.

From the present investigation it is observed that analysis of variance showed significant differences between genotypes for all the characters, indicating the scope for selection from diverse genotypes for various important traits. There were positive significant correlation between seed yield per plant with primary branches per plant and secondary branches per plant. The PCA showed that the first two components explained 51.82 percent of the existing variation in genotypes as depicted by biplot. The present studies and its results can play an important role in effective selection and breeding strategies for linseed improvement in future endeavours.

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