



# ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR SEED YIELD AND IT'S ATTRIBUTES IN LINSEED (*LINUM USITATISSIMUM* L.)

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## Abstract

Seventeen linseed (*Linum usitatissimum* L.) genotypes were evaluated during *rabi* 2014-15, at the Experimental Farm of the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India, to examine the nature and magnitude of variability, heritability and genetic advance. The analysis of variance revealed that highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study and indicating the scope for selection of suitable initial breeding material for crop improvement. High estimates of PCV and GCV were obtained for seed yield per plant and harvest index indicated a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement. High estimates of PCV and GCV were obtained for seed yield per plant and harvest index indicating, great amount of variability in these characters and selection for improvement of such characters will be rewarding. Heritability and genetic advance are important selection parameters and selection success is a reflectance of selection response. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. High heritability coupled with high genetic advance as percentage of mean (GAM) were observed for seed yield per plant, biological yield per plant and harvest index, indicating predominance of additive gene action for these characters. Hence, simple selection based on phenotypic performance of these characters would be more effective.

**Key words :** Linseed, genetic variability, heritability, genetic advance.

## Introduction

Linseed (*Linum usitatissimum* L. : n = 15) commonly known as Alsi, belongs to the genus *Linum* of the family Linaceae having 14 genera. Out of these only *Linum usitatissimum* is the only cultivated species of genus *Linum*. All other species in this genus are wild and are less important economically. India is considered as centre of origin of linseed, from where it spreaded to other parts of the world including Ethiopia (Wakjira *et al.*, 2004). Two morphologically distinct cultivated species of linseed are recognised, namely Flax and Linseed. The flax types are commercially grown for the extraction of fibres, whereas the linseed is meant for the extraction of oil from seeds. The oil content of the seed generally varies from 33 to 45 per cent, which is predominantly useful as drying oil in manufacturing of paints and varnishes, manufacturing of linoleum, printer's ink, soap, patent leather, oilcloth etc. Use of linseed as antibiotic

(Anonymous, 1968) has given a new dimension as an antibiotic "Lentive" found in the linseed can cure diseases of human being as well as of animals. Recently, linseed has gained a new interest in the emerging market of functional food due to its high fatty acids content, alpha linolenic acid (ALA), an essential Omega-3 fatty acid and lignin oligomers which constitute about 57% of total fatty acids in linseed. Linseed oil is used for a variety of industrial purposes and the oil free meal is fed to livestock. Across the world, it covers 2270.35 thousand hectare area with production of 2238.94 thousand tons having productivity of 986.16 kg per hectare, whereas in India, it covers 338 thousand hectares area and a production of 147 thousand tons with the productivity of 434.91 kg per hectare (Anonymous, 2013). The average productivity is very low as compared to other countries, hence, there is an urgent need to increase the productivity by breaking the present yield barrier and developing high yielding varieties. Success of any breeding program depends upon the presence of substantial amount of genetic variability

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and heritability (Sidra *et al.*, 2014 and Laila *et al.*, 2014) because the ultimate goal is to develop hybrid cultivars that can potentially use the total amount of heterosis available. Development of high yielding varieties requires the knowledge of existing genetic variability. The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype for further breeding programme. A character which has higher range of genetic variability, high heritability and high genetic advance would be an effective tool to improve economic yield (Aytaç and Kinaci, 2009). Morphological traits have been used to assess the genetic variation and relationships among populations of different oilseed species, for example, Linseed, Brassica and Soybean (Iqbal *et al.*, 2008; Rabbani *et al.*, 1998 & 1999; Kop *et al.*, 2003) etc. Assessment of variability for yield and its component characters becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. It helps in determining the influence of environment on the expression of the genotypic and reliability of characters. With the above background information the present investigation was undertaken to study the genetic parameters among the seventeen linseed genotypes.

### Materials and Methods

Genetic variability for various traits was studied in seventeen genotypes (table 1) of Linseed during *rabi* 2014-15 at Experimental Farm of the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India (32°8' N, 76°3' E) represents humid sub-temperate climate zone with annual rainfall of 2500mm and acidic soil with pH of 5.0 to 5.6. The experiment was conducted using randomized complete block design with two replications. Each replication consisted of three rows of each genotype. Row to row distance was 30 cm with row length of 3 meter and plant to plant distance was 10 cm maintained by thinning. The crop was raised following the standard package of practices.

Observations were recorded on five randomly

selected plants per entry and per replication for plant height, technical height, primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule, biological yield per plant, straw yield per plant, fibre yield per plant, 1000-seed weight, seed yield per plant, whereas days to 50 per cent flowering and days to 75 per cent maturity were recorded on plot basis and and harvest index was calculated as per the formula given below:

$$\text{Harvest index (\%)} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

### Statistical analysis

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

### Genetic variability

Genotypic and phenotypic variances, genotypic (GCV), phenotypic coefficients of variance (PCV) and heritability (broad sense) were computed according to Burton & Devane (1953), Johnson *et al.* (1955) and Singh & Chaudhary (1985).

$$\text{Genetic variance (\%)} = \frac{\text{Genotypes mean squares (GMS)} - \text{Error mean square (EMS)}}{\text{No. of replications (r)}}$$

Environmental variance ( $V_e$ ) = Error mean squares (EMS).

$$\text{Phenotypic variance (} V_p \text{)} = V_g + V_e$$

Heritability broad sense ( $h^2$  bs) on plots mean basis was calculated as:

$$\frac{V_g}{V_p}$$

$$\text{Genotypic coefficient of variation} = \sqrt{V_g/GM} \times 100.$$

$$\text{Phenotypic coefficient of variation} = \sqrt{V_p/GM} \times 100.$$

Where,

$V_g$  = Genotypic variance.

$V_p$  = Phenotypic variance.

GM = Grand mean of the trait.

$h^2$  bs = Broad sense heritability for a trait.

$$\text{Genetic advance (GA)} = K \sigma_p h^2$$

Where,

K = 2.06 (selection differential at 5% selection intensity)

$\sigma_p$  = phenotypic standard deviation

$h^2$  = heritability (broad sense)

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

## Results and Discussion

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant.

The analysis of variance (table 2) revealed significant differences among the genotypes for all the traits studied indicating wide range of genetic variability and scope for selection of these traits, as earlier reported by Khorgade and Pillai (1994) for capsules per plant.

However, the absolute variability in different characters does not permit identification of the characters showing the highest degree of variability. Mean performance and range of genotypes studied are given in table 3. Mean values and range expressed great variation for all the traits indicating presence of variability in material. Estimation of genetic parameters are presented in table 3. The results indicated that phenotypic variances (PV) are greater than the genotypic variances (GV). This means that the traits under study were influenced by the environment, as earlier reported by Khan *et al.* (2007) and Manggoel *et al.* (2012). All the genetic variations are heritable and can be exploited in any breeding programme. Similar findings were also reported by Akbar *et al.* (2003).

The PCV values were greater than the GCV values for all the traits studied indicating that the apparent variation is not only due to genotypes but, also due to the influence of environment. 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. These investigations were supported by the previous workers (Akbar *et al.*, 2003; Khan *et al.*, 2007; Kumar *et al.*, 2012; Manggoel *et al.*, 2012). The highest PCV (36.37) and GCV (32.90) values were found particularly for seed yield per plant due to very high variability available in this traits. Higher estimates of PCV and GCV (>25%) are obtained for seed yield per plant and harvest index. Moderate PCV and GCV (15–25%) values for biological yield per plant, straw yield per plant and fibre yield per plant indicated the presence of moderate genetic variability for these characters in linseed. Whereas, moderate PCV and low GCV was recorded for 1000 seed weight. Low PCV and GCV (<15) for days to 50% flowering, days to 75% maturity, plant height, technical height, primary branches per plant, secondary branches per plant, capsules per plant and seeds per capsule suggesting less variability

**Table 1 :** List of linseed accessions/lines and their parentage/ source used in the study.

S. no.	Genotype	Source/Pedigree
1.	Himani	DPL-20 × KLS-1
2.	Araine	Exotic collection
3.	Belinka	Exotic flax material
4.	Belinka-60	LC-216 × LC-185
5.	Chambal	Local × RR 45
6.	KL-213	Aoyogi × JRF-2
7.	KL-216	Polf-16 × Surbhi
8.	KL-217	Flak-1 × Janaki
9.	KL-218	RL-50-3 × RL-33-4
10.	KL-219	L-1321 × Flak-1
11.	KL-220	89D-2B/4
12.	Giza-5	Exotic flax material
13.	Giza-6	Exotic flax material
14.	Giza-7	Exotic flax material
15.	Giza-8	Exotic flax material
16.	Flak-1	Exotic flax material
17.	Jeevan	Summit × LC-216

**Table 2 :** Analysis of variance for various traits in linseed.

	Traits	Replication (df= 1)	Genotypes (df= 16)	Error (df= 16)
1	Days to 50% flowering	10.63	8.08**	.80
2	Days to 75% maturity	47.06	10.00**	1.43
3	Plant height	127.77	54.87**	1.08
4	Technical height	77.73	48.76**	2.40
5	Primary branches per plant	.92	.25**	.04
6	Secondary branches per plant	.57	.24**	.03
7	Capsules per plant	27.54	19.08**	.85
8	Seeds per capsule	.57	.24**	.02
9	Biological yield per plant	1.18	.78**	.06
10	Straw yield per plant	.86	.15**	.02
11	Fibre yield per plant	.05	.01**	.01
12	1000 seed weight	15.09	1.77**	.15
13	Harvest index	192.58	81.66**	14.57
14	Seed yield per plant	.57	.14**	.01

\*P = 0.005 and \*\*P = 0.001

**Table 3 :** Genetic parameters of variability for different traits of linseed.

S. no.	Traits	Mean±S.E.(m)	Range	PV	GV	PCV (%)	GCV (%)	h <sup>2</sup> bs (%)	GA	GAM
1.	Days to 50% flowering	124.09±0.63	121.00-128.50	4.44	3.64	1.70	1.54	81.89	3.56	2.87
2.	Days to 75% maturity	176.00±.085	172.00-180.50	5.72	4.28	1.36	1.18	74.92	3.69	2.10
3.	Plant height	73.76±0.73	63.75-84.80	27.97	26.89	7.17	7.03	96.15	10.48	14.20
4.	Technical height	43.10±1.10	33.30-49.60	25.58	23.18	11.73	11.17	90.63	9.44	21.91
5.	Primary branches per plant	5.46±0.14	4.95-6.05	0.14	0.11	6.95	5.94	73.16	.57	10.47
6.	Secondary branches per plant	4.35±0.12	3.95-5.05	0.13	0.10	8.38	7.37	77.41	.58	13.36
7.	Capsules per plant	35.19±0.65	30.00-39.30	9.97	9.11	8.97	8.58	91.45	5.95	16.90
8.	Seeds per capsule	6.24±0.10	5.45-6.95	0.13	0.11	5.83	5.28	82.03	.61	9.85
9.	Biological yield per plant	3.30±0.17	2.05-4.44	0.42	0.36	19.62	18.23	86.36	1.15	34.90
10.	Straw yield per plant	1.60±0.10	1.22-2.20	0.08	0.07	18.12	16.04	78.34	.47	29.24
11.	Fibre yield per plant	0.32±0.07	0.23-0.46	0.00	0.00	18.40	15.01	66.51	.08	25.21
12.	1000-seed weight	6.39±0.27	5.31-8.92	0.96	0.81	15.31	14.10	84.78	1.71	26.74
13.	Harvest index	23.07±2.70	11.89-37.21	48.11	33.54	30.07	25.11	69.71	9.96	43.19
14.	Seed yield per plant	0.77±0.07	0.25-1.21	0.08	0.06	36.37	32.90	81.84	.47	61.32

**PV:** Phenotypic variance, **GV:** Genotypic variance, **PCV:** Phenotypic coefficient of variation, **GCV:** Genotypic coefficient of variation, **h<sup>2</sup>bs:** Broad sense heritability, **GA:** Genetic advance, **GAM:** Genetic advance as percent of mean.

existed in these characters. This moderate to low variability indicates the need for improvement of base population through intercrossing in F<sub>2</sub> generation followed by recurrent selection to increase the gene flow and to fix favourable alleles. Heritability is the only genetic parameter to predict direct and correlated response (Dudley and Moll, 1969). Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). All the characters studied in the present investigation expressed high heritability estimates ranging from 66.51 to 96.15 per cent. Heritability estimates were found maximum (96.15) for plant height among all other characters, which means that 96.15% of genetic portion may be heritable from parents to offspring. High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these characters in the individual plant by adopting simple selection methods. 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) and RamaKant *et al.* (2005).

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Present study revealed that all the characters under study showed low genetic advance (<15) ranging from 0.08 to 10.48. High heritability coupled with high genetic advance as percentage of mean (GAM) were more useful than heritability alone in predicting the resultant effect during selection of best individual genotype (Johnson *et al.*, 1955). Genetic advance is the measure of genetic gain under selection and expression in percentage of mean. In the present experiment, high heritability and GAM (>30) was recorded for seed yield per plant, biological yield per plant and harvest index. High heritability and moderate GAM (15-30) as per cent of mean values were observed for the characters, technical height, capsules per plant, 1000 seed weight, fibre yield per plant and straw yield per plant. Other characters showed high heritability along with low GAM (<15) indicated the presence of non-additive gene action. Selection for the characters having high heritability coupled with high GAM is likely to accumulate more additive genes leading to further improvement of their performance. In the present investigation, high heritability along with high GAM was

noticed for three characters (seed yield per plant, biological yield per plant and harvest index). Other characters indicated high heritability along with moderate or low GAM, which can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadia, 2005).

### Conclusion

Important economic traits *viz.*, seed yield per plant, biological yield per plant and harvest index were controlled by additive gene action and can be improved through simple selection methods. The traits showing high heritability with low genetic advance indicated 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 segregation population from recombination breeding.

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