



Study on genetic variability, heritability and genetic advance for agro-morphological traits of linseed (*Linum usitatissimum* L.)

Nimit Kumar*, Satish Paul and Ritika Singh Dhial

Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176062, India

*e-mail: nk.kakran@gmail.com

(Received: May 06, 2015; Revised received: October 25, 2015; Accepted: October 28, 2015)

Abstract: Twelve hybrids along with their seven parents were subjected to study the genetic variability indicated that genetic material in the present investigation possessed variability which provides sufficient basis for selection by breeder. High estimates of PCV and GCV were obtained for biological yield per plant and seed yield per plant indicated a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement. High heritability was observed for all the traits indicated that the characters under study are less influenced by environment in their expression. All the traits under study showed low genetic advance ranging from 1.68 to 2.05. High heritability coupled with high genetic advance as percentage of mean (GAM) were observed for straw yield per plant, seed yield per plant and 1000 seed weight, 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, F₁ generation, Genetic variability, Heritability, Genetic advance

Introduction

Linseed (*Linum usitatissimum* L.) belongs to the genus *Linum* is one of the oldest crop cultivated for its seeds and fibres. 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. The oil content of the seed generally varies from 33 to 45 per cent. About 20 per cent of the total linseed oil is used for edible and domestic purposes and 80 per cent 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 per hectare, where as in India its area is limited to 338 thousand hectares and production 147 thousand tons with the productivity of 434.91 kg per hectare, (Anonymous 2013). 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 resistance to biotic and abiotic stresses, etc.

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Genetic variability in a population is important for biodiversity because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction. The measurement of genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the breeding programme efficiently and effectively (Shah *et al.*, 2015). Heritability of any trait depends upon genetic properties of breeding material and environmental conditions in which experiments are carried out (Falconer and Mackay, 1996). 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. However, the variation patterns in these traits are considered to be the result of

both genetic and environmental attributes (Rohlf *et al.*, 1990). Genetic improvement of seed quality can make oilseed as a source for high quality edible oil for human consumption and high quality protein meal for feeding animals, nonedible industrial products, such as detergents, lubricants, cosmetics, hydraulic oils, biodiesel and bio energy (Ofori & Becker, 2008; Kimber & McGregor, 1995). The estimation of the value of heterosis and heterobeltiosis for understanding the genetic control of these parameters in different cross combinations under the prevailing conditions is very important. Success of any breeding program depends upon the presence of substantial amount of genetic variability and heritability (Sidra *et al.*, 2014; Laila *et al.*, 2014;) because the ultimate goal is to develop hybrid cultivars that can potentially use the total amount of heterosis available.

Therefore, the present study was conducted with the objective to determine the genetic variability of different genotypes and crosses of linseed based on their agro-morphological traits.

Materials and Methods

Genetic variability for various agro-morphological traits was studied in seven genotypes (T-397, Chambal, Kangra Local, HimAlsi-2, Nagarkot, HimAlsi-1 and EC-541194) and twelve crosses (T-397 x EC-541194, Chambal x EC-541194, Kangra Local x EC-541194, HimAlsi-2 x EC-541194, T-397 x Nagarkot, T-397 x HimAlsi-1, Chambal x Nagarkot, Chambal x HimAlsi-1, Kangra Local x Nagarkot, Kangra Local x HimAlsi-1, HimAlsi-2 x Nagarkot and HimAlsi-2 x HimAlsi-1) of Linseed during *rabi* 2013-14 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 three 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 was maintained by thinning. Normal cultural practices were carried out as recommended for linseed. Data were recorded on five randomly selected plants in each replication. For plant height data was recorded by measuring the distance from the soil to the tip of the plant, at a stage

when crop reached physiological maturity, Technical height recorded from the ground surface to the point from where the primary branches start at the stage of physiological maturity, Primary branches per plant is the numbers of branches emerging from the main stem were counted for each plant at maturity and then averaged, Secondary branches per plant was counted of branches arising from primary branches in selected plants of each genotype were recorded and mean value was obtained, Capsules per plant were counted total numbers of capsules in the plant and mean value was obtained, Biological yield was recorded by weighing five selected plant before threshing and then averaged Seeds per capsule were counted in ten randomly selected capsules and then averaged, Straw yield per plant was recorded by weighing five selected plant after threshing and then averaged, Seed yield per plant was recorded by weighing seed of five selected plant and averaged, Seed yield per plot was recorded on the plot basis, while 1000 seed per entry per replication were also weighed and Harvest index was calculated as:

Harvest index (%) = (Seed yield per plant / Aerial biomass per plant) x 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 and Chaudhary (1985):

$$\text{Genotypic variance (Vg)} = \frac{\text{Genotypes mean squares (GMS)} - \text{Error mean squares (EMS)}}{\text{No. of replicates (r)}}$$

$$\text{Environmental variance (Ve)} = \text{Error mean squares (EMS)}$$

Table-1: Analysis of variance for agro-morphological traits in linseed

Traits	Replication df = 2	Treatment df = 18	Error df = 36	CV (%)
Plant Height (cm)	4.99	329.63**	1.32	0.82
Technical Height (cm)	3.82	137.04**	1.32	1.67
Primary branches	1.14	21.74**	0.10	2.99
Secondary branches	0.84	13.71**	0.06	2.73
Capsules per plant	6.32	192.62**	1.30	1.05
Biological Yield per plant (g)	1.6	21.36**	0.09	3.01
Seeds per Capsule	1.32	1.65	0.08	3.61
Straw yield per plant (g)	0.34	4.66**	0.05	4.33
Seed yield per Plant (g)	0.26	3.93**	0.02	3.25
Seed yield per plot (g)	4.44	3368.96**	2.40	0.85
1000 Seed Weight (g)	0.76	7.07**	0.04	3.18
Harvest Index (%)	0.38	66.17**	1.63	3.46

* P<0.005 and ** P<0.001

Table-2: Genetic parameters of variability for different agro-morphological traits of linseed

Traits	Mean ± S.E.(m)	Range	PV	GV	PCV (%)	GCV (%)	h ² bs (%)	GA(%)	GAM
Plant Height (cm)	69.04 ± 0.33	44.79 - 79.75	110.09	109.77	15.20	15.17	99.71	2.05	2.97
Technical Height (cm)	34.02 ± 0.33	21.96 - 41.99	45.90	45.57	19.91	19.84	99.30	2.04	5.99
Primary branches	10.78 ± 0.19	6.60 - 16.29	7.32	7.21	25.09	24.91	98.58	2.02	18.70
Secondary branches	9.06 ± 0.14	5.77 - 13.31	4.61	4.55	23.70	23.54	98.67	2.02	22.28
Capsules per plant	52.52 ± 0.33	45.18 - 74.33	64.41	64.11	15.28	15.24	99.53	2.05	3.89
Biological Yield per plant (g)	10.31 ± 0.18	6.12 - 13.62	7.18	7.09	26.00	25.83	98.66	2.02	19.59
Seeds per Capsule	7.68 ± 0.16	5.87 - 8.90	0.60	0.52	10.08	9.41	87.17	1.68	21.82
Straw yield per plant (g)	5.19 ± 0.13	3.22 - 7.32	1.59	1.54	24.26	23.87	96.82	1.96	37.80
Seed yield per Plant (g)	3.80 ± 0.07	2.18 - 5.65	1.32	1.31	30.22	30.04	98.84	2.02	53.23
Seed yield per plot (g)	181.67 ± 0.89	116.33 - 218.67	1124.59	1122.19	18.46	18.44	99.79	2.05	1.13
1000 Seed Weight (g)	6.38 ± 0.12	3.49 - 8.13	2.38	2.34	24.18	23.97	98.27	2.01	31.44
Harvest Index (%)	36.91 ± 0.74	29.73 - 46.87	23.14	21.51	13.04	12.57	92.95	1.85	5.00

PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, h²bs Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as percent of mean

$$\text{Phenotypic variance (Vp)} = \text{Vg} + \text{Ve}$$

Heritability broad sense (H²) on plots mean basis was calculated as:

$$H^2 = \text{Vg} / \text{Vp}$$

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

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

Where: V_g = Genotypic variance; V_p = Phenotypic variance; GM = Grand mean of the trait; H² = Broad sense heritability for a trait.

Results and Discussion

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus, the primary objective of germplasm conservation is to collect and preserve the genetic variability in indigenous collection of crop species to make it available to present and future generations. The analysis of variance (Table-1) 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. 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 2 Mean values and range showed great variation for all the traits indicating sufficient variability in material.

Estimates of genotypic variance (GV) and phenotypic variance (PV) of different traits are given in table-2. The results indicated that phenotypic variances (PV) are slightly higher than the genotypic variances (GV). This means that the traits under study were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. The results are in accordance with the findings of Dayal *et al.* (1975) and Kumar *et al.* (2012). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. The traits which expressed difference between genotypic and phenotypic variance as compare to the other have maximum influence of environment on seed yield and harvest index. All the genetic variations are heritable and can be exploited in any breeding programme as reported by Akbar *et al.* (2003).

The PCV values were slightly higher than the respective GCV for all the characters denoting little influence of environmental factors on their expression. The difference between values of PCV and GCV

were less for all traits in present investigation. It means that these traits were less influenced by environment and hence, they could be improved by following different phenotypic selections like directional, disruptive and stabilized selections. The highest PCV and GCV values were found particularly for seed yield per plant due to very high variability available in this traits (Table 2). Higher estimates of PCV and GCV (>25%) are obtained for biological yield per plant and seed yield per plant. Whereas, higher PCV and moderate GCV was recorded for primary branches. Moderate PCV and GCV (15 – 25%) values for plant height, technical height, secondary branches, capsules per plant, straw yield per plant, seed yield per plot and 1000 seed weight the presence of moderate genetic variability for these characters respectively in Linseed. Low PCV and GCV (<15) for seeds per capsule and harvest index indicating less variability existed in these characters. This moderate to low variability indicates the need for improvement of base population through intercrossing in F_2 generation followed by recurrent selection to increase the gene flow and to fix favourable alleles.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. Therefore, high heritability helps in effective selection for a particular character. 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 87.17 to 99.71 percent for seeds per capsules and plant height respectively. 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 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. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.*, 1955). Present study revealed that all the traits under study showed low genetic advance (<15) ranging from 1.68 to 2.05. 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. 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 straw yield per plant, seed yield per plant and 1000 seed weight, indicating predominance of additive gene action for these characters. Simple selection based on phenotypic performance of these characters would be more effective. High heritability and moderate GAM (15-30) as per cent of mean values were observed for the characters, primary branches, secondary branches, biological yield per plant and seeds per capsule. This indicates the influence of non-additive gene action and considerable influence of environment in the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis. Other characters showed high heritability along with low GAM (<15) indicated the presence of non-additive gene action. Hence selection could be postponed for these characters or these characters could be

improved by intermating of superior genotypes of segregation population from recombination breeding.

Present investigation signified that seed yield per plant expressed high GCV and PCV, high heritability coupled with high genetic advance as per cent of mean which indicated the presence of sufficient variability a pre requisite for any successful breeding programme. Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes especially in case of Linseed.

Acknowledgements

The authors gratefully acknowledges the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishwavidyalaya, Palampur, India for providing the research facilities for this research.

References

- Akbar, M., Mahmood, T., Anwar, M., Ali, M., Shafiq, M. and Salim, J.: Linseed improvement through genetic variability, correlation and path coefficient analysis. *Inter. J. Agri. Biol.*, **5**: 303-305 (2003).
- Anonymous.: Annual report linseed. AICRP (All India Coordinated Research Project) on linseed. Kanpur, India. (2013).
- Aytac, Z. and Kinaci, G.: Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). *Afr. J. Biotech.*, **8**: 3547-3554 (2009).
- Burton, G.W. and Devane, E.H.: Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, **45**: 478-481 (1953).
- Dayal, B., Tikka, S.B.S., Jaimini, S.N. and Goyal, S.N.: Heritability estimates in linseed (*Linum usitatissimum* L.). *Oilseeds. J.*, **5**: 3-4 (1975).
- Falconer, D.S. and Mackay, T.F.C.: Introduction to quantitative genetics, 4th edition, Longman, Essex, UK. (1996).
- Iqbal, Z., Arshad, M., Ashraf, M., Mahmood, T. and Waheed, A.: Evaluation of soybean (*Glycine max* L.) germplasm for some important morphological traits using multivariate analysis. *Pak. J. Bot.*, **40**: 2323-2328 (2008).
- Johnson, H.W., Robinson, H.F. and Comstock, R.E.: Estimation of genetic and environmental variability in soybeans. *Agron. J.*, **47**: 314-318 (1955).
- Kimber, D.S. and McGregor, D.I.: The species and their origin, cultivation and world production. In: Brassica Oilseed; Production and Utilization. D. S. Kimber and D. I. McGregor (Eds.) Centre for Agriculture and Biosciences International. University Press, Cambridge, pp. 1-7 (1995).
- Kop, E.P., Teakle, G.R., McClenaghan, E.R., Lynn, J.R. and King, G.J.: Genetic analysis of the bracting trait in cauliflower and broccoli. *Plant Sci.*, **164**: 803-808 (2003).
- Kumar, S., Kerkhi, S.A., Gangwar, L.K., Chand, P. and Kumar, M.: Improvement in the genetic architecture through study of Variability, heritability and genetic advance in Linseed Crop (*Linum usitatissimum* L.). *IJREISS.*, **2**: 58-65 (2012).
- Laila, F., Farhatullah, Shah, S., Iqbal, S., Kanwal, M. and Ali, S.: Genetic variability studies in brassica F2 populations developed through inter and intra-specific hybridization. *Pak. J. Bot.*, **46**: 265-269 (2014).
- Ofori, A. and Becker, H. C.: Breeding of *Brassica rapa* for biogas production: heterosis and combining ability of biomass yield. *Bioenergy Res.*, **1**: 98-104 (2008).
- Panse V. G. and Sukhatme P. V.: Statistical Methods for Agricultural Workers. ICAR Publication, New Delhi, India. (1985)
- Rabbani, M.A., Iwabuchi, A., Murakami, Y., Suzuki, T. and Takayanagi, K.: Phenotypic variation and the relationships among mustard (*Brassica juncea* L.) germplasm from Pakistan. *Euphytica*, **101**: 357-366 (1998).
- Rabbani, M.A., Iwabuchi, A., Murakami, Y., Suzuki, T. and Takayanagi, K.: Collection, evaluation and utilization of oilseed mustard (*Brassica juncea* L.) *Pak. J. Biol. Sci.*, **2**: 88-94 (1999).
- RamaKant, Singh, P., Tiwari, S. K. and Sharma, R. M.: Study of heritability and genetic advance for yield components and oil content in diallel cross of linseed (*Linum usitatissimum* L.). *Agricult. Sci. Digest.*, **25**: 290-292 (2005).
- Rohlf, F., Chang, W., Sokal, R. and Kim, J.: Accuracy of estimated phylogenies: Effects of tree topology and evolutionary model. *Evolution*, **44**: 1671-1684 (1990).
- Shah, K. A., Farhatullah, Shah, L., Ali, A., Ahmad, Q. and Zhou, L.: Genetic variability and heritability studies for leaf and quality characters in flue cured virginia tobacco. *Acad. J. Agric. Res.*, **3**: 044-048 (2015).
- Sidra, I., Farhatullah, Nasim, A., Kanwal, M. and Fayyaz, L. Heritability studies for seed quality traits in introgressed segregating populations of brassica. *Pak. J. Bot.*, **46**: 239-243 (2014).
- Singh, R. K. and Chaudhary, B. D.: Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, Ludhiana, India. (1985).