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Genetic variability for seed yield and its component traits in linseed (*Linum usitatissimum* L.)

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Abstract

To determine genetic variability of thirty linseed genotypes, an experiment was conducted using randomised block design under zero budget natural farming at CSKHPKV Palampur, Himachal Pradesh. Significant analysis of variance was found for yield and yield contributing traits. Primary branches per plant, secondary branches per plant, capsules per plant, biological yield per plant and seed yield per plant had higher PCV values whereas, traits secondary branches per plant and capsules per plant had high PCV and GCV values, indicating the possibility of genetic improvement through direct selection for these traits whereas, days to 50 per cent flowering, days to 75 per cent maturity, seeds per capsule, 1000 seed weight and oil content had low PCV. High heritability (>60%) was observed for oil content, days to 50 per cent flowering, days to 75 per cent maturity, secondary branches per plant, capsules per plant and 1000 seed weight. High heritability along with high genetic advance was observed for secondary branches per plant and capsules per plant indicating prevalence of additive gene action, which provides good scope for further improvement by selection.

Key words: Variability, heritability, genetic advance, linseed, PCV, GCV

Botanically referred to as *Linum usitatissimum* and commonly known as flax, linseed is an annual, self-pollinating crop, belonging to genus *Linum* in the family Linaceae (2n=2x=30). It is one of the important rabi oilseed crops of India. Both flax and linseed are specialized developments of a single species, which originates from the Mediterranean and Southwest Asian regions (Millam *et al.* 2005). Linseed has got great economic value for the commercial utility of its oil and fibre. Its oil is one of the richest sources of linolenic (omega-3) and linoleic (omega-6) polyunsaturated fatty acid (PUFA) which offer potential health benefits. Linseed contains 35 to 45 per cent oil with the α-linolenic acid (ALA) making up about 57 per cent of the total fatty acids. Omega-3 fatty acid lowers the level of triglycerides in the blood, thereby reducing heart diseases and also show promise in the battle against inflammatory diseases such as rheumatoid arthritis. It is also used in antibiotics and this has given linseed oil a new importance. Linseed oil is mostly used in paints and varnish industry (Biradar *et al.* 2016).

For the success of any plant breeding programme, understanding the genetic diversity inherent in a specific crop species for the attribute under development is vital. Crops become more susceptible to diseases and severe climate changes as genetic variability decreases. As a result, detailed knowledge on the kind and degree of genetic variability existing in linseed would aid in the selection of parents for developing superior varieties (Bayisa *et al.* 2020). Estimating direct selection factors such as coefficient of variation, heritability, and genetic advance can help a breeder come up with a good selection strategy for a greater yield. Heritability is a phenotypic variance metric that may be attributed to genetic factors and has predictive value in plant breeding. It tells us how well a given morphogenetic trait can be passed down over generations. The plant breeder's understanding of heritability influences the selection procedures he or she uses to determine which selection methods are most useful for improving the character, predicting gain from selection, and determining the relative importance of genetic effects (Bello *et al.* 2012). No variability analysis has been done for linseed genotypes under natural farming conditions. Therefore, the current study was designed to generate information on advanced linseed lines to assess the extent of genetic variability present in them under zero budget natural farming system (ZBNF).

Materials and Methods

Testing location and layout of experiment: The biological experimental materials comprised of 30 linseed genotypes including advanced breeding lines, elite varieties and exotic lines. They were evaluated for genetic variability under zero budget natural farming system at ZBNF farm of Department of Organic Agriculture and Natural Farming at Holta, CSKHPKV Palampur *rabi* 2019-20. The experiment was carried out in randomized block design with three replications with row to row and plant to plant spacing of 25cm × 5cm respectively with a 50 cm path gap between each replication. Recommended package of practices were followed to raise a good crop. The seeds were treated with *beejamrit* @10ml per kg of the seed before sowing which was prepared freshly at the Department of Organic Agriculture and Natural Farming CSKHPKV, Palampur. *Ghanjeevamrit* (microbial mix) was applied @ 250 kg/ha at the time of sowing and its liquid form *i.e. jeevamrit* (10%) was sprayed during the crop period with first spray at 21 days after sowing and the rest at an interval of 15 days till harvesting. The biometric observations were recorded using five randomly selected competitive plants of each genotype for traits *i.e.*, plant height, technical plant height, primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule, biological yield per plant, seed yield per plant, harvest index and 1000 seed weight.

Statistical Analysis: The data obtained were subjected to analysis as per Panse and Sukhatme (1984) and were analysed using using statistical software package OPSTAT available online (Sheoran *et al.* 1998). The genetic parameters phenotypic, genotypic and environmental coefficients of variation were analyzed as suggested by Burton and De Vane (1953) and Johnson *et al.* (1955) along with heritability (h^2_{bs}) which was calculated as a ratio of genotypic variance to the sum of genotypic and environmental variance. The expected genetic advance for various traits was calculated as per Burton and De Vane (1953) and Johnson *et al.* (1955).

Results and Discussion

Analysis of Variance: ANOVA is a collection of statistical models used to analyze the differences between group means and their associated procedures (such as variation among and between groups), developed by R.A. Fisher. The seed yield is a highly variable, complex quantitative trait (influenced by environment) and is a cumulative effect of its component. The analysis of variance is a way to partition the variation into different components such as replications, treatments/ genotypes and error.

Table 1. The list of thirty linseed genotypes under investigation

S. No.	Genotypes	Parentage	S.No.	Genotypes	Parentage
1	KL-236	Jeevan ×Janki	16	Him Alsi-1	K2 × TLP-1
2	KL-241	Giza-7 ×KLS-1	17	Janki	Palampur
3	KL-244	(RLC 29 × Jeevan) × RLC-29	18	Surbhi	LC-216 × LC-185
4	KL-257	LC-2323 × KLS-1	19	Canada	Exotic collection
5	KL-263	KL-223 × KL-224	20	Binwa	Flak-1 × SPS 47/7-10-3
6	KL-269	EC-21741 × LC-216	21	Giza-7	Exotic collection
7	KL-278	Giza-5 × Aayogi	22	Giza-8	Exotic collection
8	KL-279	Mariena × Giza-5	23	Belinka	-
9	KL-280	Giza-7 × Belinka	24	Nagarkot	New River × LC – 216
10	KL-284	Rjeena × Him Alsi-2	25	Himani	DPL-20 × KLS-1
11	KL-285	Binwa × Him Alsi-2	26	Jeewan	Sumit × LC-216
12	K-1 Raja	CSIRO, Canberra, Australia	27	Baner	EC-21741 × LC-214
13	JRF-4	CRIJAF, Barrackpore	28	Bhagsu	RL-50-3 × Surbhi
14	Him Alsi-1	K2 × TLP-1	29	Himalini	K2 × Kangra Local
15	Him Alsi-2	EC-21741 × LC-216	30	Nagarkot	New River × LC – 216

Analysis of variance for various yield and yield attributing traits in linseed have been given in Table 2. The analysis revealed that the mean sum of square due to genotypes was significant for all the traits studied. This indicates that the genotypes selected for the experiment were quite variable and considerable amount of variability existed among them. Hence, it provides ample scope for selection of different quantitative and qualitative characters for yield improvement in linseed. These results were in accordance with Bibi *et al*. (2013), Kumar and Paul (2016), Patial *et al*. (2018), Banjare *et al*. (2019), Dabalo *et al*. (2020), Paul *et al*. (2020), Terfa *et al*. (2020) and Thakur *et al*. (2020).

PCV and GCV

Table 3 shows the phenotypic coefficient of

Table 2. Analysis of variance for different quantitative characters in linseed

Sr. No.	Traits	Mean sum of squares		
		Replications d.f.=2	Genotypes d.f.=29	Error d.f.=58
1	Days to 50 % flowering	22.71	26.18**	8.65
2	Days to 75% maturity	6.01	67.60**	11.85
3	Plant height (cm)	25.04	104.99**	25.36
4	Technical plant height (cm)	61.28	30.61**	13.04
5	Primary branches	0.04	3.12**	0.59
6	Secondary branches	0.04	14.58**	2.03
7	Capsules per plant	37.76	101.73**	9.34
8	Seeds per capsule	0.24	0.19**	0.15
9	Biological yield/plant(g)	2.26	1.30**	0.58
10	Seed yield/plant(g)	0.11	0.22**	0.13
11	Harvest index (%)	22.90	42.84**	17.97
12	1000 seed weight (g)	0.13	0.62**	0.08
13	Oil content (%)	0.003	6.86**	0.001

Table 3. Estimation of genetic parameters for thirteen quantitative traits in linseed genotypes

Sr. No.	Traits	Mean ± S.E. (m)	Range	PCV (%)	GCV (%)	Heritability (%)(h^2_{bs})	Genetic Advance	Genetic Advance as per cent of mean
1	Days to 50 % flowering	135.51 ±0.94	128.00 -140.67	2.39	2.06	74.72	4.98	3.68
2	Days to 75% maturity	172.68 ±1.98	162.00 -180.00	3.19	2.49	61.06	6.93	4.02
3	Plant height (cm)	53.05±2.90	39.92 -71.09	13.58	9.71	51.15	7.59	14.31
4	Technical plant height (cm)	34.95±2.08	25.32 -51.42	15.44	11.47	55.23	6.14	17.56
5	No. of primary branches	5.97±0.44	3.87 -8.09	20.05	15.38	58.84	1.45	24.31
6	No. of secondary branches	9.77±0.82	6.93 -17.40	25.51	20.92	67.29	3.45	35.35
7	Capsules/plant	26.64±1.76	16.40 -39.33	23.78	20.83	76.74	10.01	37.59
8	Seeds/capsule	8.24±0.22	7.67 - 8.73	4.94	1.36	7.61	0.06	0.77
9	Biological yield/plant(g)	4.07±0.44	2.71-5.24	22.29	12.02	29.04	0.54	13.34
10	Seed yield/plant (g)	1.30±0.20	0.75-1.91	30.62	13.39	19.13	0.15	12.06
11	Harvest index (%)	31.94±1.55	22.28-38.90	19.70	3.98	4.09	0.53	1.66
12	1000 seed weight (g)	7.64±0.16	6.75-8.40	6.65	5.55	69.83	0.73	9.56
13.	Oil content (%)	40.77±0.15	38.04-43.98	3.71	3.71	99.98	3.11	7.64

PCV=Phenotypic co-efficient of variability, GCV= Genotypic co-efficient of variability variation (PCV), genotypic coefficient of variation (GCV), heritability in the broad sense (h^2_{bs}), and predicted genetic advance expressed as a percentage of mean for thirteen morphological traits. PCV values were high for the parameters seed yield per plant (30.62%), secondary branches per plant (25.51%), capsules per plant (23.78%), biological yield per plant (22.29%), primary branches per plant (20.05%). Whereas, days to 50 per cent flowering (2.39%), days to 75 per cent maturity (3.19%), oil content (3.71%), seeds per capsule (4.94%) and 1000 seed weight (6.65%) had the lowest PCV. However, traits plant height, technical plant height and harvest index showed moderate PCV values. These findings were supported by Akbar *et al*. (2003), Khan *et al*. (2007), Kumar *et al*. (2012) and Manggoel *et al.* (2012) and Kumar *et al.* (2019).

Secondary branches per plant (20.92%) and capsules per plant (20.83%) had the highest GCV also observed by Tadesse *et al.* (2010), while days to 50 per cent flowering (2.06%), days to 75 percent maturity (2.49%), plant height (9.71%), seeds per capsule (1.36%), harvest index (3.98%), 1000 seed weight (5.55%) and oil content (3.71%) had the lowest GCV in line with the findings of Terfa and Gurmu (2020). Moderate GCV was observed for traits technical plant height, primary branches per plant, biological yield per plant and seed yield per plant. These findings were in line with those of Kumar *et al.* (2015) who also reported moderate GCV for biological yield per plant in similar studies in linseed.

Genetic Advance

The degree of gain achieved in a character under a certain selection pressure is referred to as genetic advance. With respect to the genetic advance expressed as percentage of mean, the value ranged from 0.77 per cent (seeds per capsule) to 37.59 per cent (capsules per plant). High genetic advance was shown by traits primary branches per plant (24.31%), secondary branches per plant (35.35%) and capsules per plant (37.59%). Plant height (14.31%), technical plant height (17.56%), biological yield per plant (13.34%) and seed yield per plant (12.06%) showed moderate genetic advance as percentage of mean, whereas low estimates for genetic advance were reported for days to 50 per cent flowering (3.68%), days to 75 per cent maturity (4.02%), seeds per capsule (0.77%), harvest index (1.66%), 1000 seed weight (9.56%) similar to the findings of Dhirhi and Mehta (2019) and oil content (7.64%). Low genetic advance for 1000 seed weight and oil content was also observed by Ahmad *et al.* (2014) and Thakur *et al*. (2020).

Heritability

Heritability is the percentage of phenotypic variance that is attributed to genetic variance. In the present study heritability in broad sense ranged from 4.09 per cent (harvest index) to 99.98 per cent (oil content) (Table 3). High heritability was observed for traits oil content (99.98%), capsules per plant (76.74%), days to 50 per cent flowering (74.72%), 1000 seed weight (69.83%), secondary branches per plant (67.29%), days to 75 per cent maturity (61.06%). High heritability for days to 75 per cent maturity was also observed by Ahmad *et al*. (2014) and Paul *et al* (2020). Moderate estimates of heritability were observed for plant height (51.15%), technical plant height (55.23%) and primary branches per plant (58.84%). The heritability estimates for the remaining characters were low (below 10%). It meant that environmental factors played a larger role in phenotypic variability in these traits. The results were supported by Tadesse *et al.* (2010) and Mirza *et al.* (2011), Tyagi *et al.* (2014), Singh *et al.* (2015) and Bhushan *et al.* (2019).

High genetic advance coupled with high heritability estimates offers the most suitable condition for selection as heritability estimates in the broad sense are reliable if accompanied by a high genetic advancement. Traits secondary branches per plant and capsules per plant showed high heritability coupled with high genetic advance implying that these traits are heritable and can be enhanced through selection. Whereas, for seed yield per plant low heritability was observed with moderate genetic advance. Low heritability with low genetic advance was observed for harvest index and seeds per capsule which indicated that low heritability was a result of some variances constituting the environment variance and therefore, selection would be ineffective for these traits which was in agreement with Kanwar *et al.* (2014), Kumar *et al.* (2019). However, most of the traits showed high heritability with low genetic advance *i.e.,* days to 50 per cent flowering, days to 75 per cent maturity, 1000 seed weight and oil content which was in accordance to the findings of Bibi *et al.* (2013) and Thakur *et al.* (2020). This revealed that selection would be inefficient because the environment had a stronger influence on these characters.

Conclusion

The current study's findings on variability, heritability and genetic advance revealed potential for improving linseed yield through selection, using parameters such as the genetic coefficient of variation, heritability, and GA. For all of the traits studied, the analysis of variance revealed very significant differences across the tested genotypes, showing that there is variability among the tested genotypes for these characters. High PCV and GCV estimations imply that there is enough variation among genotypes to allow for effectiveness of selection and crop improvement. From the present study it could be concluded that for secondary branches per plant and capsules per plant strong heritability combined with high genetic advance demonstrated additive gene effects in inheritance. These parameters are critical when developing an efficient linseed breeding programme, because when there is enough genetic variation, breeders can take advantage of additive gene effects, transgressive segregation, and heterosis to improve yield. Whereas, traits harvest index and seeds per capsule were observed as characters irresponsive to selection due to low heritability and low genetic advance. For seed yield moderate genetic advance was observed along with low heritability which indicated the presence of environmental effects on the expression of the trait. Hence, direct selection for improvement of the trait would not be possible.

Conflict of interest: There is no conflict of interest among the authors.

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