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Estimation of genetic parameters in bold seeded linseed (*Linum usitatissimum* L.) genotypes

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Abstract

In linseed comparing bold seeded with medium and small-seeded, the advantage lies with better germination and seedling vigour giving robust plant growth which ultimately produces more branches and capsules and finally will produce more seed yield and seed oil yield respectively. Therefore, a field experiment was conducted at Research cum instructional farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during Rabi 2019-20 using randomized complete block design with three replications to evaluate forty-five genotypes (including checks) of bold seeded linseed for genetic variability and correlation analysis. Results revealed that analysis of variance for all traits had significant differences among the genotypes. High phenotypic coefficient of variation for the number of capsules/plant, number of secondary branches/plant, harvest index, and number of primary branches/plant whereas, high genotypic coefficient of variation for the number of capsules/plant and number of secondary branches/plant. High heritability coupled with high genetic advance for the number of primary branches/plant, number of secondary branches/plant, number of capsule/plant, and harvest index. The existence of variability among the breeding materials is highly essential for devising proper selection strategies and also useful in the selection of diverse parents for utilization in future hybridization programmes. Bold-seeded linseed genotypes were identified with good agro morphological characteristics.

Keywords: Bold seeded linseed, analysis of variance, genetic variability

Introduction

Linseed (*Linum usitatissimum* L.) is an annual self-pollinated crop originating either in the Middle East or the Indian regions (Vavilov, 1951)^[39]. The generic name *Linum* derives from the Celtic word, lin which means thread and the species name *usitatissimum* (the Latin word) means "very useful". *Linum usitatissimum*, the only cultivated species of the genus *Linum* of the family Linaceae is cultivated for oil from the beginning of agriculture eight thousand years ago and somewhat later for fiber (Zohary and Hopf, 1999)^[40].

Given the increasing demand for linseed because of several benefits for health, there is a steady need to increase the genetic potential for oilseed yield. As per the Food and Agriculture Organization statistical data (FAOSTAT, 2021)^[10], currently, the overall world production of linseed is around 3.34 million tonnes, with Canada (34%), Russia (15%), and China (13%) being the major producers. In the world, India is the 6th largest producer adding 13% and 5.5% to global linseed area and production respectively. In the world, India is the foremost growing country of linseed ranking 4th in area 19.65 mha and production of 12.96 mt followed by Russia, Kazakhstan, and Canada, with annual area whereas, in terms of productivity India (666.0 Kg/ha) far behind to Switzerland (2525 Kg/ha), Kyrgyzstan (2257.1 Kg/ha), Tunisia (2142.6 Kg/ha) and France (1909.1 Kg/ha) (FAOSTAT, 2021) ^[10]. In India, linseed is mostly occupied under rainfed (63%), utera (25%), and irrigated (17%) conditions, and in famished conditions in the major linseed-producing states of India are Madhya Pradesh, Chhattisgarh, Maharashtra, Jharkhand, Uttar Pradesh, and Odisha. Currently, linseed is grown in Chhattisgarh in 29900 ha with 1030 tonnes of production and average productivity of 344 Kg/ha (INDIASTAT, 2017). Production and area-wise, Chhattisgarh is one of the significant linseed-producing states of India. In Chhattisgarh, Durg, Rajnandgaon, Bilaspur, Raigarh, Raipur, Dhamtari, Sarguja, Raipur, and Kabirdham are the prime growing districts of linseed. In Chhattisgarh, linseed is grown as a rabi crop under rainfed (63%) and in utera (25%) under sub-marginal lands.

Fibre is widely used in linen for the textile industry, thread/rope and packaging materials; paper for cigarette, currency notes, and artwork (Mackiewicz-Talarczyk *et al.*, 2008) ^[20]. To use as a rope/thread, the strength, repeated flexibility, non-elasticity, and recyclable nature with a low density were quite desirable, and valuable in use. The oil extracted from the seeds has unique drying properties having utility in the production of varnish, inks, paints, and linoleum flooring (Newkirk, 2008; Czemplik *et al.*, 2011) ^[22, 8].

Linseed is rich in oil (fatty acids), dietary fiber, and protein. An examination of brown seeded linseed reported 41% fat, 20% protein, 28% total dietary fiber, 7.7% moisture, and 3.4% ash, which is the mineral-rich residue left after the burning of samples. The oil content of seeds differs significantly from 33-45% (Gill, 1987)^[13].

The medicinal value of linseed is also very rich. Most often, it is used in conditions such as high cholesterol and laxative. It has a beneficial effect on platelets, which induce coagulation of the blood vessel. It is considered beneficial for the treatment of cancer too. In painkillers, linseed is very common to use.

Generally, in linseed comparing bold-seeded with medium and small-seeded, the advantage lies with better germination and seedling vigor giving robust plant growth which ultimately produces more branches and capsules and finally will produce more seed yield and seed oil yield respectively. The present investigation focused on this hypothesis that in linseed the bold seeded ness alone has never been exploited for yield improvement of crop and its oil yield potential. Hence, for the present investigation the different sources for variability of bold seed character in germplasm. Segregating material and varieties have been collected and studied for various genetic parameters *viz;* PCV, GCV, heritability, and genetic advance, *etc.* for bold seededness with other yield attributes in the development of bold seeded varieties.

Material and Methods

Experimental area and materials

The experimental materials consist of forty-five lines of boldseeded linseed genotypes including check variety taken from linseed germplasm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur Chhattisgarh, India. The genotype was obtained by selection of seed from linseed germplasm in rabi 2019-20. The selection was made according to linseed 1000-seed weight (more than 6.5 grams). During rabi 2019-20, the experiment was in a randomized complete block design (RCBD) with 3 replication. The forty-five lines were sown including check variety (RLC-92 and R-552) on 7th December 2019 in three rows of 2.5m length with a spacing of 30 cm between rows and 6 cm between plants the recommended packages of practices were followed for raising a healthy crop and all necessary plant protection measures were taken to control the pest and diseases.

Trait measured

In this study, observations on seed yield and its components along with morphological traits based on linseed descriptor, Kanpur (2010) ^[5]. "National guidelines for the conduct of tests for Distinctness, Uniformity and Stability in linseed, India" published as per Catalogue on linseed germplasm, Project Coordinating Unit (Linseed), Kanpur, (2010) ^[5] have to record.

Following traits were evaluated plant height (cm), days to 50 percent flowering, number of capsules per plant, days to maturity, number of primary branches/plant, number of secondary branches/plant, the total number of branches/plant, 1000 seed weight (g), oil content (%), harvest index (%), seed yield/ plant (g). Climatic variations were monitored using a meteorological station set up close to the experimental area.

Genetic-statistical analysis

All the statistical analysis has to be done with the aid of windostat version 9.2 from indostat service, Hyderabad." The data were processed with the aid of different standard statistical procedures as mentioned below.

Analysis of Variance was carried out as per the method suggested by Panse and Sukhatme (1985).

Whereas,

 $\begin{array}{l} Y_{ij} = Yield \ of \ j^{th} \ genotype \ in \ i^{ts} \ replication. \ \mu = General \ mean \\ g_i = Effect \ of \ i^{th} \ genotype \ r_j = Effect \ if \ j^{th} \ replication \ e_{ij} = Error \\ component \end{array}$

Assessment of variability parameters

All the observed traits were analyzed for each of the test genotypes taken under study and were evaluated with the help of various variability parameters as mentioned below:

$$X = \frac{\Sigma X i}{n}$$

Where, X = Mean, $\Sigma X_i = Sum \text{ of all observations}$, N = Total number of all observations

$$SD = \sqrt{\frac{\Sigma d2}{N}}$$

Where, SD= Standard deviation N= Total number of observations

$$CV(\%) = \frac{SD}{X} \times 100$$

Where, SD =Standard deviation X = Mean

Heritability in terms of broad sense (bs) was evaluated by using the formula given by Allard (1960) $^{[1]}$. It is expressed as%.

Heritability
$$(h_{bs}^2) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

 $\sigma^2 g$ = genotypic variances, $\sigma^2 p$ = phenotypic variances. Genetic advance (GA) = $h^2_{(bs)} \times K \times \sigma_p$

Where,

 $h^{2}_{(bs)}$ = Heritability in terms of broad sense

 σ_p = Phenotypic standard deviation of the original population K = Selection intensity at 5% = 2.06 suggested by "Allard (1960) [1]."

Genetic advance as a percentage of $\overline{\mathbf{x}} = \frac{GA}{\overline{\mathbf{x}}} \times 100$

Whereas, GA = Genetic advance \bar{x} = Population mean

The genotypic coefficient of variation and phenotypic coefficient of variation was computed as per Burton (1952), heritability (broad sense), and genetic advance as a percent of the mean as per Allard (1960) ^[1]. The genotypic and phenotypic coefficient of correlation was calculated using the method given by Johnson *et al.* (1955) ^[15].

Result and Discussion

Genetic variability

Analysis of variance for all characters indicated that the mean sum of squares due to genotypes was highly significant for all the characters indicating the presence of a sufficient amount of variability in all genotypes (Table 1).

Genotypic and phenotypic coefficient of variation

The estimates of genetic parameters (Table 2 and Fig. 1) revealed that there were close correspondences between GCV and PCV for all the characters. Thus, the results indicated that most of the characters were largely under genetic control. The highest magnitude of genotypic coefficient of variation was noticed for the number of capsules per plant (26.6%) which is followed by the number of secondary branches per plant (20.4%). The moderate magnitude for the number of primary branches per plant (19.3%) is followed by the harvest index (18.9%), total number of branches per plant (14.4%), and seed yield per plant (10.7%). The low magnitude of genotypic coefficient of variation was noticed in plant height (8.9%) followed by 1000 seed weight (6.6%), oil content (6.4%), days to 50% flowering (4.7%), and days to maturity (3.8%). The highest magnitude of the phenotypic coefficient of variation was noticed for the number of capsules per plant (28.1%) followed by the number of secondary branches per plant (21.4%), harvest index (21.1%), and number of primary branches per plant (20.1%). The moderate magnitude of the phenotypic coefficient of variation for the total number of branches per plant (18.8%) and seed yield per plant (14.1%). The low magnitude of the phenotypic coefficient of variation was found in plant height (9.0%) followed by oil content (7.6%), 1000 seed weight (6.6%), days to 50% flowering (5.2%), and days to maturity (4.7%). These findings were by the report of Belete and Yohannes (2013) ^[2], Bibi et al., (2013)^[4], Reddy et al., (2013)^[30], Pali and Mehta (2014)^[23],

Kanwar *et al.* (2014) ^[17], Patel *et al.* (2015) ^[25], Chandrawati *et al.* (2016) ^[6], Paul and Kumari (2018) ^[26], Singh *et al.* (2019) ^[34], Tewari and Singh (2018) ^[36] and Upadhyay *et al.* (2019 a) ^[37] and Upadhyay *et al.* (2019 b) ^[38].

Heritability and Genetic Advance

Heritability in a broad sense was recorded for each of the yield-contributing traits under study (Table 2 and Fig. 2). The highest heritability was recorded for 1000 seed weight (98.7%), plant height (94.9%), number of primary branches per plant (92.0%) and number of secondary branches per plant (90.7%), days to 50% flowering (82.3%), harvest index (80.8%) and oil content (71.4%). Moderate heritability was noticed for days to maturity (64.8%), total number of branches per plant (58.7%), and seed yield per plant (57.1%). These results fall in line with those of Pali and Mehta (2014) ^[23], Chandarwati et al. (2016), Singh et al. (2019) ^[34] and Upadhyay et al. (2019) [37, 38] reported high heritability for 1000 seed weight, plant height, number of primary branches per plant and number of secondary branches per plant. The high amount of genetic advance as a mean percent was observed for the number of capsules per plant (52.1%) followed by the number of secondary branches per plant (39.9%), number of primary branches per plant (38.2%), harvest index (35.0%) and total number of branches per plant (22.7%). A moderate amount of genetic advance was recorded for plant height (17.6%) followed by 1000 seed weight (13.5%), seed yield per plant (16.7%), and oil content (11.1%). The low genetic advance was recorded for the trait days to 50% flowering (8.8%) followed by days to maturity (6.3%). Kumar et al. (2012), Kasana et al. (2016), Siddiqui et al. (2016) ^[33], Kumar et al. (2017) ^[19], Singh et al. (2019) ^[34] and Upadhyay et al. (2019) [37, 38] reported "high genetic advance for the number of capsules per plant, number of secondary branches per plant, number of primary branches per plant and harvest index". High heritability coupled with genetic advance as a percent of mean has been noticed for the number of primary branches/plant, number of secondary branches/plant, number of capsule/plant, and harvest index indicating lesser influence of environment and prevalence of additive gene action in their expression. Thus selection for improvement of those characters would be more effective. Kanwar et al. (2014) ^[17], Pali and Mehta (2014) ^[23], Rajanna et al. (2014)^[28], Kumar et al. (2015)^[18], Kasana et al. (2016), Tewari and Singh (2018) [36] and Singh et al. (2019) [34] reported high heritability and high genetic advance for number of capsules per plant, number of primary branches per plant, number of secondary branches per plant and seed yield per plant.

Table 1: Analysis of variance for seed yield and it's contributing traits in bold-seeded linseed

S. N	Source of variance	DF	PH	DTF	DM	PB	SB	ТВ	С	SW	OC	SY	HI
1.	Replication	2	1.5	5.2	9.4	0.1	3.0	4.2	79.6	0.07	5.4	0.01	1.7
2.	Genotype	44	92.6**	25.1**	74.7**	1.2**	32.0**	62.0**	743.6**	0.7**	17.3**	0.1**	62.9**
3.	Error	88	1.6	1.7	11.4	0.03	1.05	11.8	26.1	0.003	2.0	0.03	4.6

*Significant at 5% level, **Significant at 1% level

PH- Plant height (cm)C- NDTF- Days to 50% floweringSW-DM- Days to maturityOC-PB- Primary branches per plantSY-SB- Secondary branches per plantHI- HTB- Total branches per plantDF-

C- Number of capsules per plant SW- 1000 Seed weight (g) OC- Oil content (%) SY- Seed yield per plant (g) HI- Harvest index (%) DF- Degree of freedom

S.N.	Characters	Moon	Range		Critical Differences (5%)	Coefficient of Variation (%)PCV (%)GCV (%)		$h^{2}(h_{s})^{0/2}$	GA	GA% mean
9.14.	Characters	wream	Max. Min.		Critical Differences (578)	PCV (%) GCV (%)		II (DS) 70		
1	Plant height (cm)	62.7	70.7	48.5	2.1	9.0	8.8	94.9	11.0	17.6
2	Days to 50% flowering	59.0	69.0	55.3	2.1	5.2	4.7	82.3	5.2	8.8
3	Days to maturity	119.9	133.3	111.3	5.5	4.7	3.8	64.8	7.6	6.3
4	No. of primary branches/plant	3.2	4.8	1.4	0.3	20.2	19.3	92.0	1.2	38.2
5	No. of secondary branches/plant	15.8	27.3	11.0	1.7	21.4	20.4	90.7	6.3	39.9
6	Total no. of branches/plant	28.4	40.6	18.2	5.6	18.8	14.4	58.7	6.5	22.7
7	No. of capsule/plant	58.0	87.5	36.3	8.3	28.1	26.6	90.1	30.2	52.1
8	1000-Seed weight (g)	7.3	8.7	6.7	0.1	6.6	6.5	98.7	0.1	13.5
9	Oil content (%)	35.2	42.7	30.3	2.3	7.6	6.4	71.4	3.9	11.2
10	Seed yield (g)	1.8	2.3	1.4	0.3	14.2	10.7	57.1	0.3	16.7
11	Harvest Index (%)	23.3	35.0	17.1	3.5	21.1	18.9	80.8	8.2	35.1

Table 2: Genetic Parameter of variation for seed yield and its contributing traits in bold-seeded linseed

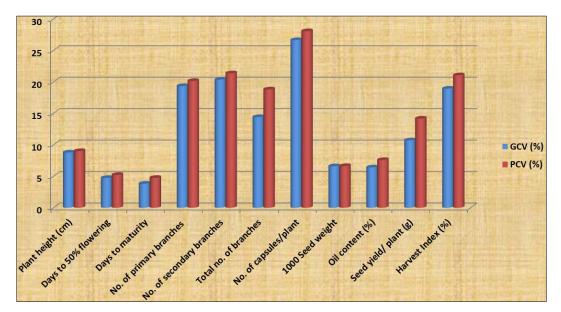


Fig 1: Graphical representation of a comparison of PCV (Phenotypic coefficient of variation) and GCV (Genotypic coefficient of variation) of seed yield and it's contributing trait in bold seeded linseed during 2019-20 at Raipur (C.G.)

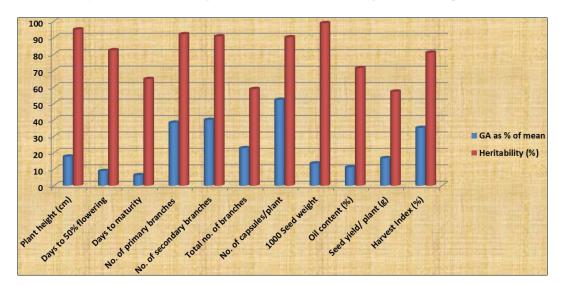


Fig 2: Heritability and genetic advance as a mean percent for seed yield and its contributing characters in bold seeded linseed

Conclusions

Bold-seeded linseed genotypes may be used as a parent in breeding programmes. The existence of variability among the breeding materials is highly essential for devising proper selection strategies and also useful in the selection of diverse parents for utilization in future hybridization programmes. Bold-seeded linseed genotypes were identified with good agro morphological characteristics. This will help to initiate the research work with bold-seeded linseed genotypes in our state. Chhattisgarh state has a huge amount of linseed germplasms containing diverse alleles of important genes which could be utilized soon for improving the nutritional status of the crop.

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