

Original Research Article

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Assessment of Stability Parameters in Linseed Genotypes

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ABSTRACT

An experiment was conducted in linseed during the rabi of 2022-23 with the aim was to assess the stability parameters of yield and related traits. It is important to screen and identify the stable and widely adoptable genotypes in respect to yield and yield contributing characters, which could perform uniformly under different environmental condition. Seven genotypes, along with three checks, were evaluated in three different environments with three replications each. Analysis of variance was performed for seven traits: days to 50% flowering, number of branches plant⁻¹, plant height, number of capsules plant⁻¹, root volume, seed yield plant⁻¹, and seed yield plot⁻¹. The results indicated significant differences for all traits in all six environments, suggesting randomness and diversity in agro-climatic conditions. Furthermore, significant mean squares due to environments were observed for all traits, reinforcing the distinctiveness of the selected environments. The interactions between genotypes and environments were found to be significant for all traits. Notably, genotype BAU 2021-06 secured the second position in seed yield and demonstrated stability in seed yield plant⁻¹, seed yield plot⁻¹, root volume, and the number of branches plant⁻¹. In contrast, genotype NL 371 claimed the first position in seed yield and exhibited stability in the number of branches plant⁻¹, number of capsules plant⁻¹, root volume, seed yield plant⁻¹, and seed yield plot⁻¹.

Keywords: Stable genotype, genotype x environment interaction, Linseed, Root volume, Root length

INTRODUCTION

Linseed (*Linum usitatissimum* L.) belongs to the genus *Linum* of the family Linaceae. The somatic chromosome number of the cultivated species is 2n=30. It is a multipurpose crop valued for its seed oil, fibre, probiotic and nutraceutical properties. It is a crop adapted to different environments and agroecologies. *Linum* is the largest.

genus of family Linaceae with about 200 species displaying great diversity in karyotype. Linnaeus in 1857 was the first to give a botanical name *Linum usitatissimum* L. to the cultivated species. *Linum usitatissimum* L. is the only species with non-dehiscent or semi-dehiscent capsules suitable for the modern cultivation of the family Linaceae [1]. The origin of the Indian type of linseed is traced to be in Ethiopia, though polyphyletic origin of the same is indicated. According to Vavilov, linseed was probably native to Southwest Asia consisting of India, Afghanistan, and Turkey. Among the oilseed crops grown during rabi, Linseed (*Linum usitatissimum* L.) is next important to rapeseed and mustard in the area as well as in production. Linseed is an annual, self-pollinating and non-edible oil crop. It occupies a greater importance among oil seeds owing to its various uses and qualities.

Around the globe this important crop occupies an area of 30.6 lakh ha yielding 31.56 lakh tones with an average productivity of 1031 kg hectare⁻¹ in the world.

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In our country, the crop occupies 1727 ha with a production of 990 tons culminating in low productivity of 574 kg ha⁻¹ in the committee of growing nations. (Annual Report, AICRP on Linseed 2021-2022). India contributes about 10.81 % and 5.3% to world area and production respectively. The total world production of linseed reached approximately 2.56 million tons in the year 2014. With Canada (34%), the Russian Federation (15%), China (13%). In India Madhya Pradesh, Karnataka, Chhattisgarh, Jharkhand, Bihar, Maharashtra, Odisha, Uttar Pradesh, West Bengal and Assam are major linseed-growing states. It is grown throughout the world including Canada, India, China, the United States, Ethiopia and all over Europe (FAOSTAT 2018). India is the second largest producer of linseed, next to Canada in the world.

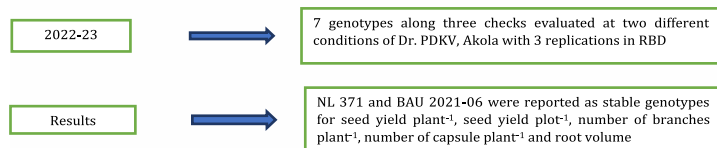
Flax is well known as linen flax or linseed around the World. It is grown in many countries for fibre as well as oilseeds. Linseed oil has been used as the basic component or additive of various paints and/or polymers industries [20]. Likewise, seeds of flax contain about 36-40% oleic acid (omega-6), linoleic and linolenic acids (omega-3) (unsaturated fatty acids), which are essential poly-unsaturated fatty acids for human beings and also for animals, because these acids cannot synthesize inside the body of both human and animals; thus it should include in human and animal diets [21].

Improvement in the genetic architecture of crops depends upon the nature and extent of genetic variability which is a prerequisite for selection. Genotype x Environment Interaction is a prevalent issue among farmers, breeders, geneticists, and production agronomists. Genotype x environment interaction is a major concern in plant breeding for two main reasons: first, it reduces progress from selection, and second, it makes cultivar recommendation difficult because it is statistically impossible

to interpret the main effects. The average response of varieties, thus depends largely upon the absence or presence of genotype x environment interaction, coupled with high yield indicating that the genotype is suitable for general adaptation in the range of environments considered. However, this ideal situation is rarely found because the phenotypic stability of a genotype is universally proportional to the mean yield. The varieties with high stability are generally low-yielders and vice versa. G x E interaction causes difficulty in demonstrating the significant superiority of any variety when varieties are compared over a series of environments. Hence, methods are in need to be investigated for reducing the G x genotype. On average interaction. One such method would be to select stable genotype that interact less with the environment in which they are grown. Hence, preliminary evaluation is to be done to identify the stable genotypes. However, selection for stability is not possible until a biometrical model with stable parameters is available to provide the criteria necessary to rank varieties for stability. Keeping the above points in consideration, the present investigation is to study genotype x environment interaction and stability parameters for yield and its related traits in linseed [6].

MATERIALS AND METHODS

The present research was conducted at Research farm of All India Co-ordinated Research Project on Linseed, College of Agriculture, Nagpur. The material for present study consisted of 7 genotypes (NL 367, NL 371, NL 407, NL 408, RL 18114, BAU 2021-06 and T 397) along with three checks (JLS 95, LSL 93 and PKV NL 260). Seven genotypes along with three checks were evaluated in randomized block design in 3 replications during the year 2022-23 with the net plot size was 18 m². The number of rows per plot was ten in rainfed and irrigated conditions with spacing between row to row 30 cm and plant to plant 5 cm. The data was reported on 7 seed yield and its contributing characters, viz days to 50% flowering, number of branches plant⁻¹, plant height (cm), number of capsule plant⁻¹, root volume (cm³), seed yield plant⁻¹ (g) and seed yield plot⁻¹ (kg/ha). The data for all the morphological characters was recorded on randomly selected 5 competitive plants in the middle 4 rows of each plot in all 3 replications except days to 50% flowering, where data was recorded on plot basis. The recommended package of practices for raising of linseed crop in Vidarbha region of Maharashtra was followed to raise a healthy crop. The recorded data after calculating mean were subjected to analysis of variance as per the method prescribed by [9]. Significant genotype-environment interactions were observed for all the characters under study, hence the data were further subjected for assessing the stability of different genotypes as per the procedure prescribed by Eberhart and Russel [2]. A genotype was considered to be a stable genotype having regression coefficient of unity (bi=1) and the deviation not significantly different from zero (S²di = 0).



RESULTS AND DISCUSSION

Analysis of Variance: A genotype can be taken as stable over environments if it gives a high mean yield, has unit regression and least deviation around the regression slope (Eberhart and Russell, 1966).

There are many stability parameters, but Eberhart and Russell's [2] model's parameter S²di was found to be very important for assessing the stability of genotype. Since the variance of S²di is a function of a number of environments numerous environments along with minimum replications per environment are necessary to calculate reliable estimates of S²di. In the present study, for each environment, analysis of variance for seed yield and its contributing characters was computed individually along pooled over the years and conditions. Analysis of variance showed the significant differences among genotypes for all the characters under study in each of the 6 environments. Pooled analysis of variance for 6 environments was also estimated to verify the presence of G x E interactions is presented in Table 1. Analysis of variance for genotype x environment interactions suggested that all the genotypes exhibited highly significant genetic variability for all the characters viz. days to 50% flowering, number of branches plant⁻¹, plant height (cm), number of capsule plant⁻¹, root volume, seed yield plant⁻¹ (g) and seed yield plot⁻¹ (kg/ha). Significant mean squares due to environments for seed yield and its contributing characters indicated that selected environments were random and having different agro-climatic conditions. Significant interaction of genotypes with the environment + (G x E) were observed for seed yield and its contributing traits, hence genotypes performed differently for all the characters under study at different conditions (Table 2). The mean sum squares due to environment (linear) were found significant for all thirteen characters. Therefore, it is concluded that the environments were random and different variation could have arisen due to the linear response of regression. The significance of linear component of variance due to environment has also been reported by [8], [13], [11] and [3]. The mean squares due G x E (linear) were significant for five characters viz. number of capsule plant⁻¹, root volume, relative water content, seed yield plant⁻¹ and seed yield plot⁻¹ revealing that behaviour of the genotypes could be predicted over the environment more precisely. However, the magnitude of the linear component i.e., environment (linear) and genotype x environment (linear) was many times higher than the non-linear component (pooled deviation) for all the thirteen characters revealing that the prediction of stability could be reliable though it may get affected to some extent. In accordance to this result [19] and [5] also reported significant and non-significant pooled deviation for various characters. The deviation of each genotype from its regression when tested by an appropriate 'F' test was found to be significant and non-significant for some genotypes and for some characters.

Stability Parameter

The genotypes having regression coefficient value of unity (bi=1), non-significant deviations from linear regression deviation (S²di =0) along with higher mean values were considered to be stable for the traits and showed adaptability to variety of environmental conditions was used as criteria for selection of stable genotype in the present study. Similarly, genotypes having regression coefficient near to unity, higher mean value along with non-significant deviations from linear regression were considered suitable and approachable for favourable environmental conditions. While, the genotypes along with higher mean, regression coefficient less than one or negative and non-significant deviations from linear regression were classified as responsive and fit for poor environmental conditions.

According to these criteria, genotypes under study were grouped into different classes which fit for varied environmental condition. None of the genotypes having lower mean than population mean, regression coefficient value of unity ($b_i=1$) and non-significant deviations from linear regression deviation ($S^2d_i=0$) for days to 50% flowering, while among the checks, only LSL 93 (C) had lower mean (51.67 days) than population mean (60.56 days) and non-significant deviation from regression ($S^2d_i=0$) along with regression coefficient less than unity. Hence, check LSL 93 found to be fit for favourable environment. In accordance to these result, [12] also identified stable genotypes for days to 50% flowering in mustard and [13] identified stable genotype in linseed. None of the genotypes possessed regression coefficient of less than one (unity) or negative and non-significant deviations from linear regression for plant height. Therefore, no genotypes were considered stable for this trait. For a number of branches plant⁻¹ five genotypes NL 371 (5.67), BAU 2021-06 (5.83), T 397 (6.13), JLS 95 (C) (7.91) and LSL 93 (C) (5.43) showed higher mean than the population mean (5.33). Among these five genotypes, non-significant deviation from regression along with regression coefficient about unity observed in three genotypes viz., NL 371 (5.67), BAU 2021-06 (5.83), T 397 (6.13), JLS 95 (C) (7.91). Thus, these genotypes exhibited their fitness for average environment. Similar findings were also reported by [13], [8] and [7] identified stable genotypes for number of branches plant⁻¹ in linseed. For the trait, number of capsule plant⁻¹, JLS 95 (65.02) and NL 371 (72.32) exhibited non-significant regression co-efficient but closer to unity and non-significant S^2d_i hence these genotypes were identified as stable genotype. [13], [3] and [11] also earlier reported stable genotypes for number of capsules plant⁻¹ in linseed. Mean number of root volume produced by plants ranged from 3.33 (PKV NL-260 (C)) to 7.12 (NL-371) with a population mean of 5.22 is shown in table. The genotypes BAU-2021-06 (5.46), NL-408 (5.75), JLS-95 (C) (5.77), NL-407 (6.12) and NL-371 (7.12) exhibited higher mean value than population mean. Out of these five genotypes NL-408, JLS-95 (C), NL-407, NL-371 had significant S^2d_i with non significant b_i and closer to unity but BAU-2021-06 had non-significant b_i with non significant S^2d_i and closer to unity. Hence these genotypes were identified as stable.

In accordance to these results, [22] and [5] also identified stable genotypes for root volume in mustard. The mean value for seed yield plant⁻¹ ranged from 9.00 g (NL 407) to 14.95 g (BAU 2021-06) respectively with an average of 11.32 g shown in table 3. The genotypes NL 367(11.55 g), NL 371 (11.95 g), NL 408 (11.47 g) and BAU 2021-06 (14.95 g) exhibited high seed yield plant⁻¹ over population mean. Out of these genotypes, NL 371, NL 367 and BAU 2021-06 exhibited high mean value, non-significant ' b_i ' but closer to unity and significant S^2d_i for seed yield plant⁻¹ and hence these genotypes can be considered as stable. [14], [23], [8] and [10] identified stable genotype for seed yield plant⁻¹ in linseed. The mean value for seed yield plot⁻¹ ranged from 500.2 kg/ha (NL-407) to 830.5 kg/ha (BAU-2021-06) respectively with an average of 631.2 kg/ha is shown in table 7m. The genotypes NL-367 (641.5 kg/ha), NL-371 (663.6 kg/ha), NL-408 (637.4 kg/ha) and BAU-2021-06 (830.5 kg/ha) exhibited high seed yield plot⁻¹ over population mean. Out of these genotypes, NL-367, NL-371 and BAU-2021-06 exhibited high mean value, non-significant ' b_i ' but closer to unity and significant S^2d_i for seed yield plot⁻¹ and hence these genotypes can be considered as stable. [14] and [23] identified a stable genotype for seed yield plot⁻¹ in linseed.

From overall study of stability parameters (Table 3) concluded that not a single genotype was ideally stable for all the five characters under investigation. The stability parameters for seed yield plant⁻¹ exhibited that three genotypes viz., NL 367, BAU-2021-06 and NL-371 were stable over the different locations over years. These genotypes showed higher mean seed yield plant⁻¹, non-significant deviation from regression and regression coefficient not deviating from one. The genotype NL 371 was found ideally stable for number of capsule plant⁻¹, for number of branches plant⁻¹, root volume, seed yield plant⁻¹ and seed yield plot⁻¹ and it was the second ranking in terms of seed yield while the genotype for BAU 2021-06 was found stable for number of capsule plant⁻¹, root volume, seed yield plant⁻¹ and seed yield plot⁻¹. Similarly, BAU 2021-06 and NL 371 genotypes were observed to be stable for seed yield plant⁻¹ and seed yield plot⁻¹. Therefore, the genotype BAU 2021-06 and NL 371 may be identified as the stable genotype with high seed yield per plant and stability for other desirable characters over two agronomic situations *i.e* rainfed and irrigated conditions.

Table 1: Pooled Analysis of variance over one years for seven yield contributing characters in linseed

Sources of variation	d.f.	Mean sum of squares						
		Days to 50% flowering	Plant height (cm)	No. of branches plant ⁻¹	No. of capsule plant ⁻¹	Root volume (cm) ³	Seed yield plant ⁻¹	Seed yield plot ⁻¹
Environments	5	129.00**	108.99**	4.41**	528.07**	23.54**	106.92**	323298.01**
Genotypes	9	144.84**	609.98**	8.39**	234.53**	6.87**	14.17	42622.93
Genotype x Environments	45	10.76**	17.74	1.35**	200.76**	2.23**	23.72**	72423.88**
Pooled Error	108	3.06	12.50	0.33	38.20	0.37	0.84	2345.32

Note: **Significant at 1% and *Significant at 5%

Table 2: Analysis of variance (mean sum of squares) for genotype x environment interactions

Sources of variation	d.f.	Mean sum of squares						
		Days to 50% flowering	Plant height (cm)	No. of branches plant ⁻¹	No. of capsule plant ⁻¹	Root volume (cm) ³	Seed yield plant ⁻¹	Seed yield plot ⁻¹
Genotypes	9	144.84**	609.98**	8.39**	234.53**	6.87**	14.17	42622.93
Environments	5	129.00**	108.99**	4.41**	528.07**	23.54**	106.92**	323298.01**
Genotype x Environments	45	10.76**	17.74	1.35**	200.76**	2.23**	23.72**	72423.88**
Environment + (G x E)	50	22.584**	26.862*	1.654	233.491*	4.364**	32.041*	97511.291*
Env (Linear)	1	645.01**	544.95**	22.03**	2640.37**	117.69**	534.58**	1616490.057**
Genotype x Environments (Lin)	9	15.10	25.49	1.10	398.14**	3.68*	43.08*	134706.93*
Pooled Deviation	40	8.70**	14.22	1.27**	136.27**	1.69**	16.99*	51167.80**
Pooled Error	108	3.06	12.50	0.33	38.20	0.37	0.84	2345.32

Note: **Significant at 1% level and *Significant at 5% level

Table 3: Estimates of stability parameters

Sr.No.	Genotypes	Days to 50% Flowering			Plant Height (cm)			No. of Branches Plant ⁻¹		
		Mean	Bi	S ² di	Mean	Bi	S ² di	Mean	Bi	S ² di
1	NL 367	58.22	1.20	24.16**	48.40	0.49	-4.50	4.43	0.83	1.04*
2	NL 371	58.33	0.59	-1.01	67.89	1.23	3.28	5.67	0.99	0.56
3	NL 407	62.72	2.06	17.13**	51.84	1.30	13.24	4.90	0.72	-0.23
4	NL 408	60.39	0.94	8.06*	59.69	1.91	4.84	4.02	1.44	1.10*
5	RL 18114	58.50	0.57	-1.54	51.09	0.58	0.84	5.07	1.47	0.29
6	BAU 2021-06	65.00	0.38	-0.05	61.31	1.47	-2.05	5.83	1.04	-0.04
7	T 397	64.33	0.99	0.20	43.75	0.40	0.51	6.13	2.35	0.43
8	JLS 95 (Check)	69.17	1.33	4.54	42.52	2.07	11.88	7.91	0.04	4.42**
9	LSL 93 (Check)	51.67	1.19	-2.41	33.43	0.14*	-7.25	5.43	1.19	1.01*
10	PKV NL 260 (Check)	57.28	0.73	1.46	48.32	0.41	5.36	3.87	-0.08	0.58
Population mean		60.56			50.82			5.33		

Note: **Significant at 1% level and *Significant at 5% level

Sr. No.	Genotypes	No. of Capsule plant ⁻¹			Root Volume (cm ³)			Seed yield plant ⁻¹			Seed yield plot ⁻¹		
		Mean	Bi	S ² di	Mean	Bi	S ² di	Mean	Bi	S ² di	Mean	Bi	S ² di
1	NL 367	56.36	0.73	-2.35	4.57	0.36	0.74*	11.55	0.55	14.18**	641.5	0.56	43852.0**
2	NL 371	72.32	1.14	-1.13	7.12	1.27	3.26**	11.95	0.88	14.16**	663.6	0.89	44038.8**
3	NL 407	72.06	0.14	105.11*	6.12	0.96	0.97*	9.00	0.72	6.82**	500.2	0.75	20112.3**
4	NL 408	68.70	3.65*	124.74*	5.75	2.03	5.32**	11.47	2.97*	20.89**	637.4	2.99*	65351.6**
5	RL 18114	62.40	0.37	-12.63	5.15	1.05	-0.13	11.22	0.72	11.77**	623.3	0.72	36976.7**
6	BAU 2021-06	61.70	0.98	44.03	5.46	0.91	-0.22	14.95	1.32	19.92**	830.5	1.32	62792.1**
7	T 397	61.50	2.51*	18.99	4.77	1.18	0.19	11.15	1.91	12.96**	619.6	1.96	35790.8**
8	JLS 95 (Check)	65.02	0.80	329.69**	5.77	1.47	1.45**	10.50	0.97	28.98**	608.1	0.86	81019.6**
9	LSL 93 (Check)	58.80	0.27	383.72**	4.19	0.74	1.46**	10.08	0.08	13.23**	559.8	0.09	41001.6**
10	PKV NL 260 (Check)	54.00	0.58*	6.44	3.33	0.04*	-0.13	11.31	-0.11	18.58**	628.5	-0.15	57247.2**
Population Mean		63.29			5.22			11.32			631.2		

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CONFLICT OF INTEREST

We hereby certify that there is no conflict of interest in submission of the research article.

AUTHOUR'S CONTRIBUTION

Achal B. Jagzape: Data analysis, writing and conducted the study

Beena M. Nair: Desinging and proof reading

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