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ESTIMATES OF VARIABILITY AND HERITABILITY IN LINSEED GERMPLASM

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ABSTRACT

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Keeping in view the lack of information on genetic variability in the Ethiopian linseed germplasm and need to study variability, heritability and genetic advance in this crop, the present investigation was undertaken on 81 geographically diverse Ethiopian accessions of linseed. These accessions were evaluated at the Agricultural Research Center, Sinana, and on farmers' field at Robe in the highlands of bale, Ethiopia during 2001-2002 cropping season. The accessions differed significantly for all the traits, under study at both locations. However, the genotypic differences were non-significant for number of primary branches, number of capsules per plant, number of seeds per capsules, seed yield per plant, biomass and percent oil content in the combined analysis over locations. Estimates of genotypic and phenotypic coefficients of variability at the two locations indicated significant variability for most of the traits under study. At Sinana, heritability estimates were high for most of the traits. Whereas moderate estimates of heritability were observed for plant height, percent oil content and biomass. At Robe, heritability estimates were high for seed yield per plant, days to flowering, number of secondary branches, seed yield per plot, harvest index, number of primary branches, number of capsules per plant, thousand seed weight, days to maturity, tillers per plants and number of seeds per capsule. These characters, therefore, may respond effectively to phenotypic selection.

Key words: *variability, heritability, linseed, genotypic and phenotypic variance, Ethiopian germplasm*

INTRODUCTION

Linseed, *Linum usitatissimum* L. (n=15), also called flax, is an important oilseed crop which belongs to the family linaceae having 14 genera and over 200 species. Linseed is the only widely grown and economically important species. It is believed that this crop species may have originated from *Linum angustifolium* Huds (n=15), native to the Mediterranean region. The genus Linum has both cultivated and wild species. The wild species have little economic value. Almost all the species are annual herbs and some are shrubs *Linum usitatissimum* L. is the only species with non-dehiscent or semi-dehiscent capsules suitable for modern cultivation of the family linaceae (Getinet and Nigussie, 1997). *Linum usitatissimum* L. is one of the oldest plant species cultivated for oil and fiber (Lay and Dybing, 1989). The crop is predominantly self pollinated, but out crossing (less than 2%) occasionally results from insect activity (Dillman 1928).

On the basis of growth habit, two types (long stemmed and short stemmed) are recognized. Long stem linseed produces a high quality fiber but the oil content of the seed is relatively low. On the other hand, short-stemmed linseed bears larger seeds of high oil content and has a branching tendency.

Selection is an integral part of a breeding program by which genotypes with high productivity in a given environment could be developed. However, selection for high yield is made difficult because of its complex nature. Yield per unit area is the end product of components of several characters, which are polygenic in inheritance and thus are highly influenced by environment. Therefore, only little progress could be made over a long span of time through direct selection for yield. Indirect selection through yield components has been proved more effective (Ford 1964).

Knowledge of the extent and pattern of variability, particularly of genetic variability present in a population of a given crop is essential for further improvement of the crop. Similarly, information on the extent and nature of interrelationship among characters help in formulating efficient scheme of multiple trait selection. Besides this, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization program. In Ethiopia, the information on these aspects in linseed is very scarce. Therefore, there is a need to generate information on phenotypic and genotypic variances as well as heritability and interrelationships of yield and yield related traits among linseed genotypes. Therefore, the present study was conducted to assess the nature and magnitude of variability, heritability and genetic advance in some Ethiopian linseed genotypes.

MATERIALS AND METHODS

Testing location and Season

The experiment was carried out at two locations. One of the experimental sites was at the research farm of Sinana Agricultural Research Center, Oromia Agriculture Research Institute, Sinana, and the other at a site in the farmer's field near Robe town, in the highlands of bale, Ethiopia. The experiment was conducted at each location on vertisol clay loam soil under rain fed conditions during the meher season (August-January) of 2001-2002 cropping season.

Eighty-one geographically diverse populations of linseed collected from different part of the country were used for this study (Table 1). In this investigation, 9 x 9 simple lattice design with two replications was used. Each experimental plot consisted of two 4m long rows with inter-row spacing of 20-cm. Seeding rate was applied at the rate of 25g kg/ha whereas fertilizers were applied at the rate of 23/23 kg/ha N/P_2O_5. Weeds were controlled by hand weeding once or as per need.

Data were recorded on both plant and plot basis. The following data was taken on plant basis, i.e. data was collected from five plants which were tagged just before heading and all data to be collected on plant basis were recorded on these five plants. Then the collected plant based data was expressed as average of five plants in each experimental plot. The parameters taken at plant basis are plant height (cm), number of primary branches, number of secondary branches, number of capsules per plant, number of seeds per capsule, seed yield (g/plant), and number of tillers. Where as days to flower, days to maturity, biological yield (g/plot), harvest index (%), thousand seed weight (g), seed yield (g/plot), and percent oil content (%) was taken on plot basis.

Estimation of genetic parameters

Assessing the genetic variability among 81 linseed genotypes for the characters under study and to work out the environmental effects on various characters under study, the following parameters were estimated:

Environmental variance (σ^2 e) = Error mean square

Phenotypic variance (σ^2 p) = σ^2 g + σ^2 e for individual location

$$\sigma^2 p = \sigma^2 g + \frac{\sigma^2{}_{gl}}{l} + \frac{\sigma^2{}_{e}}{rl}$$ for across locations

Genotypic variance $\left(\delta^2{}_g\right) = \frac{\left(MS_g - MS_e\right)}{r}$ for individual location, where MS_g is mean square for the genotypes and MS_e is mean square for error

$$\sigma^2{}_g = \left(\frac{M_g - M_{gl}}{rl}\right)$$ for across location

$$\sigma^2{}_{gl} = \frac{\left(M_{g_l} - M_e\right)}{r}$$ for G X E

Phenotypic Coefficient of Variation (PCV) = $\dfrac{\left(\sqrt{\sigma^2 p}\right) \text{X } 100}{\overline{\text{X}}}$

Genotypic Coefficient of Variation (GCV) = $\dfrac{\left(\sqrt{\sigma^2 g}\right) \text{X } 100}{\overline{\text{X}}}$

Heritability (h^2)

Heritability in broad sense for all character was estimated by the formula suggested by Allard (1960) as given

$(h^2) = \left[\dfrac{\sigma^2 g}{\sigma^2 p}\right]$ X 100

Where $\sigma^2{}_g$ = Genetic variance

$\sigma^2{}_p$ = Phenotypic variance

Expected Genetic Advance (GA)

Expected genetic advance was estimated using the formula of Johnson *et al.* (1955). Predicted effects from selecting the superior 5% of the germplasm accessions were calculated from the formula:

GA $= k\,\delta_p h^2$

Where, σ_p = the phenotypic standard deviation of the character,

h^2 = heritability estimate and

k = the standardized selection differential at 5% selection intensity (2.063)

To determine the extent of predicted genetic advance of different characters under selection, genetic advance as percent of mean was computed as devised by Johanson *et al*. (1955).

$$GAM = \frac{GA}{\overline{X}} X100$$

Where, GAM= genetic advance as percent of mean
GA = Genetic advance
$\overline{X}$ = grand mean for the character

RESULTS AND DISCUSSION

The results pertaining to variability studies, divergence among the 81 accessions and associations among yield, yield related traits and percent oil content in linseed are presented here. The important implications of these observations in breeding linseed for high grain yield and oil content are discussed as follows:

Studies on Variability

The estimates of range, mean, genotypic, phenotypic and environmental variances, heritability in broad sense, genetic advance and genetic advance expressed as a percentage of means for all the characters are presented in Table 2, Table 3 and Table 4 for Sinana, Robe and combined analysis across locations, respectively.

At Sinana, the range for seed yield per plot varied from 115.8g to 382.0g (Table 2). PGRC/E 10048 gave the highest seed yield per plot (382.0g). Out of the top twenty high yielding germplasm accessions, 45% were early maturing (125-137 days) and 10% were late maturing (146-166 days). The range for days to flowering was from 51.5 days to 103.0 days. When germplasm accessions were grouped based on number of days for flowering, 12.35% were early (51-70 days), 32.09% were medium (71-78 days) and 55.56% were late flowering (79-103 days). The variation for the germplasm accessions with respect to maturity was very wide and the maximum days needed to reach physiological maturity was 166 days and the minimum days needed was 121 days. The range for number of capsules per plant was 28.5-113.0. This range was very wide which indicated that the germplasm showed high variability for this trait. The range for seed yield per plant was 0.49g to 2.35g. PGRC/E 10104 gave the maximum seed yield per plant followed by PGRC/E 10120. The lowest seed yield per plant was for accession PGRC/E 10240 (0.49g). Thousand seed weight ranged from 2.65g to 5.70g. For harvest index the range was from 14.0 to 29.5%. The range for percent oil content in seed was from 29.6-34.9%. In general, the percent oil content at Sinana was lower than that of Robe.

Similarly, at Robe (Table 3) the range for seed yield per plot was very wide and it ranged from 85.65g to 588.58g. PGRC/E 10039 gave the maximum seed yield (588.58g) followed by PGRC/E 10051 (286.20g). At this location, when germplasm lines were grouped on the basis of days for flowering, 23.6% of the germplasm lines were considered as early (61-70 days), 38.2% were medium (71-78 days) and 32.8% were late flowering (79-89 days). The maximum days needed to reach physiological maturity was 162 days whereas it was 126 days for the earliest accession.

Estimates of Phenotypic and Genotypic Variation

As it is indicated in Table 2 for Sinana, the range of variation for different characters observed by the germplasm accessions was very wide. High genotypic coefficient of variation (GCV) was observed for number of secondary branches, seed yield per plant and number of primary branches. However, GCV was moderate for tillers per plant, number of capsules per plant, number of seeds per capsule and seed yield per plot. It was low for days to maturity, plant height and percent oil content.

Singh (1984) reported high genetic coefficient of variation for capsules per plant followed by tillers per plant, branches per plant, thousand seeds weight, plant height and days to flowers. While Mirza *et al.* (1996) reported high estimates of GCV and PCV for seed yield per plant, harvest index, capsules per plant and plant height. Similarly, Mishra and Yadva (1999), Chandrashekhar *et al.* (1998) and Mahto and Mahto (1998) reported high estimates of GCV for yield per plant, capsules per plant and branches per plant. This was partial in agreement with the present finding.

High phenotypic coefficient of variation (PCV) was observed for number of secondary branches, seed yield per plant, number of primary branches and number of capsules per plant. The estimated PCV was low for days to maturity, plant height and percentage of oil content which was supported by Satapathi *et al.* (1987).

At Robe (Table 3), the highest GCV was observed for seed yield per plant followed by number of primary branches, number of secondary branches, number of primary branches and number of capsules per plant. Considerable genetic variability in these traits offers good opportunity for improvement through selection. This was in agreement with the finding of Satapathi *et al*. (1987) who had reported high estimates of PCV than GCV for most of the characters.

For across locations (Table 4), highest genotypic coefficient of variation was observed for number of secondary branches (17.8%) followed by seed weight (14.1%). High genotypic and phenotypic variance estimates for the characters indicated that the germplasm accessions under investigation possess very high potential difference and this might be due to their genetic origin and differential adaptability.

Estimates of Heritability in Broad sense

Estimates of heritability for Sinana, Robe and across location are summarized in Table 2, Table 3 and Table 4 respectively. These values are helpful in predicting the expected progress to be achieved through the process of selection (Wright 1921)**.** Genetic coefficient of variation along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Burton *et al.* 1953).

At Sinana, heritability estimates were high for seed yield per plant (87.0%), followed by number of secondary branches (86.7%), seed yield per plot (78.3%), number of primary branches (75.6%), days to flowering (74.0%), number of capsules per plant (61.1%), number of seeds per capsules (60.6%), tillers per plants (60.6%), days to maturity (53.3%) and harvest index (52.4%). Whereas moderate estimates of heritability were observed for plant height (30.0%), percent oil content (31.3%) and biomass (32.9%).

Similarly, at Robe (Table 3) heritability estimates were high for seed yield per plant (90.9%), days to flowering (83.2%), number of secondary branches (79.8%), seed yield per plot (74.8%), harvest index (70.7%), number of primary branches (70.2%), number of capsules per plant (64.8%), thousand seed weight (64.3%), days to maturity (62.3%), tillers per plants (62.3%) and number of seeds per capsule (59.5%). In the present study low estimate of heritability was observed for biomass thereby indicating limited possibility of the improvement of this character through selection.

The heritability estimates for across locations as it is indicated in Table 4, were high for days to flowering (90.8%), days to maturity (85.2%), thousand seed weight (83.1%) and plant height (65.3%). Meanwhile, moderate estimates of heritability were observed for number of secondary branches (33.6%), seed yield per plot (34.2%), harvest index (40.4%) and tillers per plant (45.2%).

Estimates of Expected Genetic Advance

As indicated in Table 2 for Sinana, the genetic advance expressed as percentage of mean was highest for number of secondary branches (80.1%) followed by seed yield per plant (68.4%) and number of primary branches (56.5%). These traits had high GCV and PCV as well as high heritability. Low estimates were observed for days to maturity (7.1%), plant height (5.0%) and percent oil content (2.9%). The low expected genetic advance for days to maturity was observed due to low variability in this trait indicated by low GCV and PCV.

Similarly, at Robe (Table 3), genetic advance as percentage of mean was highest for seed yield per plant followed by number of secondary branches, number of primary branches and number of capsules per plant. In this case also the low expected genetic advance for characters like days to maturity and plant height, inspite of their more than 50% heritability, is due to low variability for these traits indicated by respective low GCV's and PCV's.

For across locations, the estimate of genetic advance expressed as percentage of mean was highest for thousand seed weight (26.5%) followed by number of secondary branches (21.3%). As observed for individual locations, the low expected genetic advance for days to maturity and plant height was due to low variability for these traits. Therefore, even if heritability estimates provide basis for selection on the phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously, as high heritability is not always associated with high genetic advance (Johnson *et al*. 1955). In the present study, the number of secondary branches had higher heritability and lower estimate of genetic advance as compared to the other yield contributing traits. This suggests that it may serve as an important trait in indirect selection for high seed yield.

Table 1. The List of linseed accessions and their origin used in the study

No.	Accession No.	Collection place/area	No.	Accession No.	Collection place/area
1.	PGRC/E 10002	Shewa/J.meacha	42.	PGRC/E 13736	Wello/Ambasel
2.	PGRC/E 10005	Sidamo	43.	PGRC/E 10155	Gonder
3.	PGRC/E 10007	Kefa/Jima	44.	PGRC/E 10013	Harerge
4.	PGRC/E 10008	Gonder/D.tabor	45.	PGRC/E 10015	Illubabor
5.	PGRC/E 10010	Kefa	46.	PGRC/E 10012	Gojjam
6.	PGRC/E 10022	Wollo	47.	PGRC/E 13673	Gojjam/Mota
7.	PGRC/E 10026	Gojjam/ Koladamot	48.	PGRC/E 13658	Bako
8.	PGRC/E 10037	Sidamo/Jemjem	49.	PGRC/E 10014	Shewa
9.	PGRC/E 10039	Eritria/Seraye	50.	PGRC/E 10082	Harerge/Alemaya
10.	PGRC/E 10041	Bale/Ginner	51.	PGRC/E 10173	Gojjam/Bichena
11.	PGRC/E 10046	Wellega/Nekamt	52.	PGRC/E 10122	Sidamo/Arero
12.	PGRC/E 10061	Gamogofa	53.	PGRC/E 10092	Shewa/Yefitana timug
13	PGRC/E 10068	Gojjam/ Bahrdar	54.	PGRC/E 10044	Tigray/Shire
14.	PGRC/E 10080	Harar	55.	PGRC/E 10158	Sidamo/awassa
15.	PGRC/E 10085	Harar	56.	PGRC/E 10047	Illubabor/Bunobedelle
16.	PGRC/E 10104	Shewa/J.M	57.	PGRC/E 10133	Tigray/Agame
17.	PGRC/E 10109	Shewa/J.Meacha	58.	PGRC/E 10048	Tigray/Shire
18.	PGRC/E 10111	Shewa/ Merabete	59.	PGRC/E 10081	Harerge/Habro
19.	PGRC/E 10118	Shewa/J.Mmeacha	60.	PGRC/E 10172	Gamugofa/Garadula
20.	PGRC/E 10120	Sidamo	61.	PGRC/E 10139	Welega/Horegudru
21.	PGRC/E 10125	Tigray/Inderta	62.	PGRC/E 10132	Tigray/Agame
22.	PGRC/E 10138	Wellega/Horogudru	63.	PGRC/E 13673	Gojjam/Mota
23.	PGRC/E 10144	Wellega	64.	PGRC/E 10073	Gojjam/Debremarkos
24.	PGRC/E 10159	Gonder/Wegera	65.	PGRC/E 10161	Gonder/Denbi
25.	PGRC/E 10162	Gonder	66.	PGRC/E 10180	Shewa/Menagesha
26.	PGRC/E 10169	Gonder	67.	PGRC/E 10182	Shewa
27.	PGRC/E 10176	Gojjam/Metekel	68.	PGRC/E 10178	Shewa/K.Hadiya
28.	PGRC/E 10179	Shewa	69.	PGRC/E 10043	Gojjam/Koladdamot
29.	PGRC/E 10204	Wollo/Awsa	70.	PGRC/E 10191	Shewa/Jibatenameach
30.	PGRC/E 10006	Illubabor	71.	PGRC/E 10171	Gamugofa/Gamu
31.	PGRC/E 10042	Tigray/Axum	72.	PGRC/E 10088	Shewa/Teguletnabulga
32.	PGRC/E 10047	Illubabor/Buno	73.	PGRC/E 10051	Bale/Genale
33.	PGRC/E 10062	Bale/Meliyu	74.	PGRC/E 10177	Gojam/Debremarkos
34.	PGRC/E 10235	Gonder	75.	PGRC/E 10071	Gojam/Dejen
35.	PGRC/E 10064	Gamogofa/Hamrbako	76.	PGRC/E 10174	Gojam/Koladegadamo
36.	PGRC/E 10072	Gojam/Debremarkos	77.	PGRC/E 10164	Gonder/Wegera
37.	PGRC/E 10073	Gojam/Debremarkos	78.	PGRC/E 10121	Sidamo/Jemjem
38.	PGRC/E 10060	Gonder	79.	PGRC/E 10147	Wello/Yeju
39.	PGRC/E 13737	Wello/Ambasel	80.	PGRC/E 10207	Wello/Kallu
40.	PGRC/E 13731	Wello/Ambasel	81.	PGRC/E 10200	Wello/Kalu
41.	PGRC/E 13738	Wello/Ambasel			

Table 2. Estimates of range, mean, genotypic and phenotypic coefficients of variability, heritability and genetic advance in 14characters of linseed at Sinana

Variables	Range	Mean ± SE.	δ^2g	δ^2e	δ^2p	GCV %	PCV %	h^2	GA	GA %
DF	51.5-103.0	79.11 ± 2.93	49.97	17.3	67.2	8.9	10.6	74.4	12.6	15.9
DM	120.5-166.0	141.45 ± 4.39	44.1	38.6	82.7	4.7	6.4	53.3	9.9	7.1
PH(cm)	58.5-92.0	73.24 ± 3.90	13.1	30.5	43.6	4.9	9.01	30.0	4.1	5.6
TPP	2.5-7.0	3.61 ± _0.39	0.49	0.3	0.8	19.4	24.9	60.6	1.1	31.2
NPB	11.5-65.5	20.48 ± 2.59	41.42	13.44	55.2	31.5	36.2	75.6	11.6	56.5
NSB	1.0-4.0	1.52 ± 0.18	0.4	0.06	0.47	41.8	44.9	86.7	1.2	80.1
NCPP	28.5-113.0	50.32 ± 6.78	144.8	92.1	236.8	23.9	30.8	61.1	19.4	38.5
NSPC	3.0-9.5	5.27 ± 0.59	1.1	0.7	1.8	19.9	25.5	60.6	1.7	31.9
TSW (g)	2.65-5.7.0	3.97 ± 0.42	0.24	0.4	0.6	12.4	19.5	40.3	0.6	16.2
SY/pl(g)	0.49-2.35	1.31 ± 0.11	0.16	0.02	0.2	35.6	38.1	87.1	0.8	68.4
HI (%)	14.0-29.5	19.9 ± 1.7	6.8	6.2	13.0	13.1	18.1	52.4	3.9	19.6
SY/plot(g)	115.8-382.3	238.4 ± 17.8	2300.9	636.0	2936.9	20.1	22.7	78.3	87.6	36.7
BM g/plot(g)	725-1825	1228.5 ± 134.9	17842.9	36448.5	54291.4	10.9	18.9	32.9	157.8	12.8
POC (%)	29.6-34.9	32.12 ± 0.57	0.65	1.42	2.07	2.50	4.50	31.30	0.90	2.90

Where: δ^2g , δ^2e and δ^2p genotypic, environmental and phenotypic variance, respectively; GCV= Genotypic coefficient of variability, PCV= Phenotypic coefficient of variability; GA= Genetic advance; GA%= Genetic advance expressed as percentage of mean; DF= Days to flowering; DM= Days to maturing; PH= Plant height (cm); TPP= Tillers per plant; NPB= No. of primary branches; NSB= No. of secondary branches; NCPP= No. of capsules per plant; NSPC= No. of seeds per capsule; TSW= Thousand seed weight (g); SY/pl= Seed yield per plant; HI = Harvest index per plot (%); SY/plot= Seed yield per plot (g/plot); BM = Biomass per plot; POC= Percent oil content.

Table 3. Estimates of range, mean, genotypic and phenotypic coefficients of variability, heritability and genetic advance in 14 characters of linseed at Robe

Variables	Range	Mean ± SE.	δ^2g	δ^2e	δ^2p	GCV %	PCV %	h^2 %	GA	GA %
DF	61-89	75.64 ± 1.987	38.99	7.90	46.89	8.25	9.05	83.15	11.73	15.5
DM	126.5-162	137.87 ± 3.66	44.28	26.82	71.10	4.83	6.12	62.27	10.82	7.9
TPP	2-6	3.93 ± 0.44	0.64	0.39	1.03	20.37	25.82	62.25	1.30	33.1
PH(cm)	48-77	63.85 ± 2.71	18.40	14.69	33.09	6.72	9.01	55.61	6.59	10.3
NPB	8.0-33	14.99 ± 2.04	19.59	8.31	27.90	29.53	35.24	70.22	7.64	50.9
NSB	1-3	1.93 ± 0.23	0.42	0.11	0.53	33.56	37.56	79.87	1.19	61.8
NCPP	22.5-84.5	42.53 ± 5.96	130.96	71.03	201.99	26.91	33.42	64.83	18.98	44.6
NSPC	3.5-10	7.136 ± 0.72	1.54	1.05	2.59	17.38	22.54	59.48	1.97	27.6
TSW(g)	2.8-5.9	4.13 ± 0.34	0.41	0.23	0.63	15.45	19.27	64.30	1.05	25.5
SY/pl(g)	0.35-4.34	1.28 ± 0.126	0.33	0.03	0.36	44.77	46.96	90.92	1.13	87.9
HI (%)	9.5-47.5	21.96 ± 1.96	18.59	7.72	26.31	19.63	23.35	70.65	7.47	33.9
SY/plot(g)	85.65-588.58	217.51 ± 21.75	2804.97	946.25	3751.23	24.35	28.16	74.77	94.34	43.4
BM(g)	673.6-1651.5	1001.84 ± 119.65	7625.69	28633.44	36259.13	8.72	19.01	21.03	82.50	8.2
POC (%)	31.6-40	33.96 ± 0.54	0.59	2.02	2.61	2.27	4.76	22.68	0.75	2.2

Where: δ^2g, δ^2e and δ^2p genotypic, environmental and phenotypic variance, respectively; GCV= Genotypic coefficient of variability, PCV= Phenotypic coefficient of variability; GA= Genetic advance; GA%= Genetic advance expressed as percentage of mean; DF= Days to flowering; DM= Days to maturity; PH= Plant height (cm); TPP= Tillers per plant; NPB= No. of primary branches; NSB= No. of secondary branches; NCPP= No. of capsules per plant; NSPC= No. of seeds per capsule; TSW= Thousand seed weight (g); SY/pl= Seed yield per plant; HI = Harvest index per plot (%); SY/plot= Seed yield per plot (g/plot); BM = Biomass per plot; POC= Percent oil content.

Table 4. Estimates of range, mean, genotypic and phenotypic coefficients of variability, heritability and genetic advance in 14 characters of linseed at across locations

Variables	Range	Mean ± SE.	δ^2g	δ^2e	δ^2p	GCV %	PCV %	h^2 %	GA	GA %
DF	58-96	77.4 ± 1.77	42.21	12.57	46.49	8.39	8.81	90.81	12.75	16.48
DM	124-164	139.6 ± 2.85	44.88	32.71	52.70	4.80	5.20	85.16	12.74	9.12
PH (cm)	61.3-83.5	68.5 ± 2.38	13.08	22.57	20.05	5.28	6.54	65.25	6.02	8.79
TPP	3-6	3.8 ± 0.29	0.22	0.35	0.48	12.24	18.22	45.17	0.64	16.95
NSB	1-3	1.7 ± 0.14	0.09	0.08	0.27	17.82	30.72	33.64	0.36	21.29
TSW(g)	3.2-5.8	3.2 ± 5.8	0.33	0.29	0.40	14.10	15.47	83.10	1.09	26.48
HI (%)	12-36	20.9 ± 1.31	4.09	6.95	10.13	9.68	15.23	40.36	2.65	12.66
SY/plot(g)	111-430	227.9 ± 14.06	607.46	791.14	1777.99	10.81	18.50	34.17	29.68	13.02

Where: δ^2g , δ^2e and δ^2p genotypic, environmental and phenotypic variance respectively; GCV= Genotypic coefficient of variability, PCV= Phenotypic coefficient of variability; GA= Genetic advance; GA%= Genetic advance expressed as percentage of mean; DF= Days to flowering; DM= Days to maturity; PH= Plant height (cm); TPP= Tillers per plant; NSB= No. of secondary branches; TSW= Thousand seed weight (g); HI = Harvest index (%); SY/plot= Seed yield per plot (g/plot).

CONCLUSION

The accessions differed significantly for all the traits at both locations. However, in the combined analysis of variance over locations the genotypes differed significantly for eight out of 14 traits only. The differences among accessions were non significant for number of primary branches, number of capsules per plant, number of seeds per capsules, seed yield per plant, biomass and percent oil content. At Sinana, maximum variability was observed for number of secondary branches which had highest genotypic coefficient of variability (GCV) as well as phenotypic coefficient of variability (PCV). Both GCV and PCV were higher than 20% for number of primary branches, number of capsules per plant, seed yield per plant and seed yield per plot. At Robe, GCV and PCV were highest for seed yield per plant followed by number of secondary branches. The expected genetic advance was high for seed yield per plant and number of secondary branches at both locations. However, in combined analysis seed weight had highest estimate for expected genetic advance followed by number of secondary branches. In general, maximum genetic advance through selection was expected for number of secondary branches.

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